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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:20:27 ; Search time 23.6667 Seconds  
(without alignments)  
28.022 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 110780

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/prodata/1/aaa/5A-COMB.pep.\*  
2: /cgn2\_6/prodata/1/aaa/5B-COMB.pep.\*  
3: /cgn2\_6/prodata/1/aaa/6A-COMB.pep.\*  
4: /cgn2\_6/prodata/1/aaa/6B-COMB.pep.\*  
5: /cgn2\_6/prodata/1/aaa/PTUS-COMB.pep.\*  
6: /cgn2\_6/prodata/1/aaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	57.7	10	4 US-09-535-852-1357	Sequence 1357, Ap
2	15	57.7	10	4 US-09-535-852-1366	Sequence 1366, Ap
3	15	57.7	10	4 US-09-535-852-1375	Sequence 1375, Ap
4	15	57.7	10	4 US-09-535-852-1385	Sequence 1385, Ap
5	15	57.7	10	4 US-09-535-852-1395	Sequence 1395, Ap
6	15	57.7	10	4 US-09-535-852-1825	Sequence 1825, Ap
7	15	57.7	10	4 US-09-535-852-1829	Sequence 1829, Ap
8	15	57.7	10	4 US-09-535-852-1833	Sequence 1833, Ap
9	14	53.8	10	2 US-08-764-640-77	Sequence 77, Appl
10	14	53.8	10	3 US-08-973-225-77	Sequence 77, Appl
11	14	53.8	10	3 US-09-244-298A-77	Sequence 77, Appl
12	14	53.8	10	3 US-09-516-704-77	Sequence 77, Appl
13	14	53.8	10	3 US-09-187-859-3644	Sequence 3644, Ap
14	14	53.8	10	3 US-09-187-859-3646	Sequence 3646, Ap
15	14	53.8	10	4 US-09-549-090-77	Sequence 77, Appl
16	14	53.8	10	4 US-09-832-230A-77	Sequence 77, Appl
17	14	53.8	10	4 US-09-839-542B-3644	Sequence 3644, Ap
18	14	53.8	10	4 US-09-839-542B-3646	Sequence 3646, Ap
19	14	53.8	10	4 US-09-535-852-1352	Sequence 1352, Ap
20	14	53.8	10	4 US-09-535-852-1361	Sequence 1361, Ap
21	14	53.8	10	4 US-09-535-852-1370	Sequence 1370, Ap
22	14	53.8	10	4 US-09-535-852-1380	Sequence 1380, Ap
23	14	53.8	10	4 US-09-535-852-1390	Sequence 1390, Ap
24	14	53.8	10	4 US-09-620-091-49	Sequence 49, Appl
25	13	50.0	10	2 US-08-764-640-102	Sequence 102, Appl
26	13	50.0	10	2 US-08-764-640-120	Sequence 120, Appl
27	13	50.0	10	2 US-08-764-640-121	Sequence 121, Appl

28	13	50.0	10	3 US-08-925-002-67	Sequence 67, Appl
29	13	50.0	10	3 US-08-973-225-102	Sequence 102, App
30	13	50.0	10	3 US-08-973-225-120	Sequence 120, App
31	13	50.0	10	3 US-08-973-225-121	Sequence 121, App
32	13	50.0	10	3 US-08-973-225-207	Sequence 207, App
33	13	50.0	10	3 US-08-973-225-208	Sequence 208, App
34	13	50.0	10	3 US-08-377-781A-17	Sequence 17, Appl
35	13	50.0	10	3 US-08-377-781A-18	Sequence 18, Appl
36	13	50.0	10	3 US-09-244-298A-102	Sequence 102, App
37	13	50.0	10	3 US-09-244-298A-120	Sequence 120, App
38	13	50.0	10	3 US-09-244-298A-121	Sequence 121, App
39	13	50.0	10	3 US-09-516-704-102	Sequence 102, App
40	13	50.0	10	3 US-09-516-704-120	Sequence 120, App
41	13	50.0	10	3 US-09-516-704-121	Sequence 121, App
42	13	50.0	10	3 US-09-187-859-834	Sequence 834, App
43	13	50.0	10	3 US-09-187-859-836	Sequence 836, App
44	13	50.0	10	3 US-09-187-859-1075	Sequence 1075, Ap
45	13	50.0	10	3 US-09-187-859-1077	Sequence 1077, Ap

ALIGNMENTS

RESULT 1  
US-09-535-852-1357  
; Sequence 1357, Application US/09535852  
; Patent No. 6638911  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James M.  
; TITLE OF INVENTION: COMPOUNDS AND ETHODS FOR MODULATING  
; FILE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C6  
; CURRENT APPLICATION NUMBER: US/09/535,852  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1357  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclized modulating agent comprising  
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence  
US-09-535-852-1357

Query Match 57.7%; Score 15; DB 4; Length 10;  
Best Local Similarity 20.0%; Pred. No. 15;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
Db 1 CAYATDGC 10

RESULT 2  
US-09-535-852-1366  
; Sequence 1366, Application US/09535852  
; Patent No. 6638911  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James M.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND ETHODS FOR MODULATING  
; FILE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C6  
; CURRENT APPLICATION NUMBER: US/09/535,852  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1366  
; LENGTH: 10

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1366

Query Match          57.7%; Score 15; DB 4; Length 10;
Best Local Similarity 20.0%; Pred. No. 15;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
   |             |
Db 1 CYAYATTAC 10

RESULT 3
US-09-535-852-1375
; Sequence 1375, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1375
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1375

Query Match          57.7%; Score 15; DB 4; Length 10;
Best Local Similarity 20.0%; Pred. No. 15;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
   |             |
Db 1 CLYAYATTAC 10

RESULT 4
US-09-535-852-1385
; Sequence 1385, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1385
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1385
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Query Match          57.7%; Score 15; DB 4; Length 10;
Best Local Similarity 20.0%; Pred. No. 15;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
   |             |
Db 1 CVYAYATTAC 10

RESULT 5
US-09-535-852-1395
; Sequence 1395, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1395
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1395

Query Match          57.7%; Score 15; DB 4; Length 10;
Best Local Similarity 20.0%; Pred. No. 15;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
   |             |
Db 1 CIYAYATTAC 10

RESULT 6
US-09-535-852-1825
; Sequence 1825, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James M.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND EMTHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C6
; CURRENT APPLICATION NUMBER: US/09/535,852
; CURRENT FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1825
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-535-852-1825

Query Match          57.7%; Score 15; DB 4; Length 10;
Best Local Similarity 20.0%; Pred. No. 15;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
   |             |
Db 1 CXXXXXXXC 10
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Db 1 CAYASTADGC 10

## RESULT 7

US-09-535-852-1829  
; Sequence 1829, Application US/09535852  
; Patent No. 6638911  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James M.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND ETHODS FOR MODULATING  
; FILE REFERENCE: 100086.407C6  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1829  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion  
; OTHER INFORMATION: recognition sequence  
US-09-535-852-1829

Query Match 57.7%; Score 15; DB 4; Length 10;  
Best Local Similarity 20.0%; Pred. No. 15;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10

Db 1 CIAYASTADC 10

## RESULT 8

US-09-535-852-1833  
; Sequence 1833, Application US/09535852  
; Patent No. 6638911  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James M.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND ETHODS FOR MODULATING  
; FILE REFERENCE: 100086.407C6  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1833  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion  
; OTHER INFORMATION: recognition sequence  
US-09-535-852-1833

Query Match 57.7%; Score 15; DB 4; Length 10;  
Best Local Similarity 20.0%; Pred. No. 15;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10

Db 1 CLIAVASTAC 10

## RESULT 9

US-08-764-640-77

; Sequence 77, Application US/08764640  
; Patent No. 5869451  
; Patent No. 5869451 5837683  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Gates, Christian  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Balasubramanian, Palaniappan  
; APPLICANT: Wagstrom, Christopher R.  
; APPLICANT: Hendren, Richard W.  
; APPLICANT: Deprince, Randolph B.  
; APPLICANT: Poddaturi, Surekha  
; APPLICANT: Yin, Qun  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; NUMBER OF SEQUENCES: 244  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/764,640  
; FILING DATE: 11-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3281  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-764-640-77

Query Match 53.8%; Score 14; DB 2; Length 10;  
Best Local Similarity 20.0%; Pred. No. 69;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10

Db 1 CSRADFLAAC 10

## RESULT 10

US-08-973-225-77  
; Sequence 77, Application US/08973225A  
; Patent No. 6083913  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwiria, Steven E.  
; APPLICANT: Duffin, David J.  
; APPLICANT: Gates, Christian  
; APPLICANT: Haselden, Sherril S.  
; APPLICANT: Mattheakis, Larry C.  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Wagstrom, Christopher R.  
; APPLICANT: Wrighton, Nicholas C.

; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; THROMBOPOIETIN RECEPTOR  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/973,225A  
; FILING DATE: 04-Dec-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3065USW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:  
US-08-973-225-77  
  
Query Match 53.8%; Score 14; DB 3; Length 10;  
Best Local Similarity 20.0%; Pred. No. 69;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 CXXXXXXXC 10  
Db 1 CSRADFLAAC 10  
  
RESULT 11  
US-09-244-298A-77  
; Sequence 77, Application US/09244298A  
; Patent No. 6121238  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Gates, Christian  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Balasubramanian, Palaniappan  
; APPLICANT: Wagstrom, Christopher R.  
; APPLICANT: Hendren, Richard W.  
; APPLICANT: Deprince, Randolph B.  
; APPLICANT: Podduturi, Surekha  
; APPLICANT: Yin, Qun  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; NUMBER OF SEQUENCES: 244  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/244,298A  
; FILING DATE: 11-DEC-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3281  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-244-298A-77  
  
Query Match 53.8%; Score 14; DB 3; Length 10;  
Best Local Similarity 20.0%; Pred. No. 69;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 CXXXXXXXC 10  
Db 1 CSRADFLAAC 10  
  
RESULT 12  
US-09-516-704-77  
; Sequence 77, Application US/09516704  
; Patent No. 6251664  
; GENERAL INFORMATION:  
; APPLICANT: Dower, William J.  
; APPLICANT: Barrett, Ronald W.  
; APPLICANT: Cwirla, Steven E.  
; APPLICANT: Gates, Christian  
; APPLICANT: Schatz, Peter J.  
; APPLICANT: Balasubramanian, Palaniappan  
; APPLICANT: Wagstrom, Christopher R.  
; APPLICANT: Hendren, Richard W.  
; APPLICANT: Deprince, Randolph B.  
; APPLICANT: Podduturi, Surekha  
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A  
; NUMBER OF SEQUENCES: 244  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Glaxo Wellcome  
; STREET: Five Moore Drive, P.O. Box 13398  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/516,704  
; FILING DATE: 01-Mar-2000  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hrubiec, Robert T.  
; REGISTRATION NUMBER: 36,392  
; REFERENCE/DOCKET NUMBER: PK3281  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-248-1000  
; INFORMATION FOR SEQ ID NO: 77:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid

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; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-516-704-77
Query Match 53.8%; Score 14; DB 3; Length 10;
Best Local Similarity 20.0%; Pred. No. 69;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 1 CSRADFLAAC 10

RESULT 13
US-09-187-859-3644
; Sequence 3644, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3644
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-187-859-3644
Query Match 53.8%; Score 14; DB 3; Length 10;
Best Local Similarity 20.0%; Pred. No. 69;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 1 CFTIDSSGC 10

RESULT 14
US-09-187-859-3646
; Sequence 3646, Application US/09187859A
; Patent No. 6358920
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C1
; CURRENT APPLICATION NUMBER: US/09/187,859A
; CURRENT FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 4052
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3646
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Representative cyclic modulating agent based on
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion
; OTHER INFORMATION: recognition sequence
US-09-187-859-3646
Query Match 53.8%; Score 14; DB 3; Length 10;
Best Local Similarity 20.0%; Pred. No. 69;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 1 CKFTIDSSSC 10

RESULT 15
US-09-549-090-77
; Sequence 77, Application US/09549090
; Patent No. 6465430
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; Barrett, Ronald W.
; Cwiria, Steven E.
; Duffin, David J.
; Gates, Christian
; Haselden, Sherril S.
; Matheakis, Larry C.
; Schatz, Peter J.
; Wagstrom, Christopher R.
; Wighton, Nicholas C.
; TITLE OF INVENTION: PEPTIDES AND COMPOUNDS THAT BIND TO A
; TITLE OF INVENTION: THROMBOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Glaxo Wellcome
; STREET: Five Moore Drive, P.O. Box 13398
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/549,090
; FILING DATE: 13-Apr-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/973,225
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Hrubiec, Robert T.
; REGISTRATION NUMBER: 36,392
; REFERENCE/DOCKET NUMBER: PK3065USW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-248-1000
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-09-549-090-77
Query Match 53.8%; Score 14; DB 4; Length 10;
Best Local Similarity 20.0%; Pred. No. 69;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10
DB 1 CSRADFLAAC 10

Search completed: December 29, 2004, 21:36:43
Job time : 23.6667 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 21:36:53 ; Search time 82 Seconds  
(without alignments)  
43.869 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 182644

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
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20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	15	57.7	10	17	US-10-654-578-1357
3	15	57.7	10	17	US-10-654-578-1366
4	15	57.7	10	17	US-10-654-578-1375
5	15	57.7	10	17	US-10-654-578-1385
6	15	57.7	10	17	US-10-654-578-1395
7	15	57.7	10	17	US-10-654-578-1825
8	15	57.7	10	17	US-10-654-578-1829
9	14	53.8	10	17	US-10-654-578-1833
10	14	53.8	10	10	US-09-572-404B-2111
11	14	53.8	10	13	US-10-046-922-2169
12	14	53.8	10	14	US-10-006-869-58
13	14	53.8	10	14	US-10-006-869-3646

14	14	53.8	10	14	US-10-083-768-77	Sequence 77, Appl
15	14	53.8	10	14	US-10-395-032-3644	Sequence 3644, Ap
16	14	53.8	10	14	US-10-395-032-3646	Sequence 3646, Ap
17	14	53.8	10	17	US-10-654-578-1352	Sequence 1352, Ap
18	14	53.8	10	17	US-10-654-578-1361	Sequence 1361, Ap
19	14	53.8	10	17	US-10-654-578-1370	Sequence 1370, Ap
20	14	53.8	10	17	US-10-654-578-1380	Sequence 1380, Ap
21	14	53.8	10	17	US-10-654-578-1390	Sequence 1390, Ap
22	13	50.0	10	9	US-09-234-395-220	Sequence 220, App
23	13	50.0	10	9	US-09-234-395-222	Sequence 222, App
24	13	50.0	10	9	US-09-305-928-220	Sequence 220, App
25	13	50.0	10	9	US-09-305-928-222	Sequence 222, App
26	13	50.0	10	9	US-09-264-516A-244	Sequence 244, App
27	13	50.0	10	9	US-09-264-516A-246	Sequence 246, App
28	13	50.0	10	9	US-09-910-552-67	Sequence 67, Appl
29	13	50.0	10	10	US-09-572-404B-1223	Sequence 1223, Ap
30	13	50.0	10	10	US-09-572-404B-1225	Sequence 1225, Ap
31	13	50.0	10	10	US-09-572-404B-1231	Sequence 1231, Ap
32	13	50.0	10	10	US-09-572-404B-1235	Sequence 1235, Ap
33	13	50.0	10	10	US-09-572-404B-1239	Sequence 1239, Ap
34	13	50.0	10	10	US-09-572-404B-1291	Sequence 1291, Ap
35	13	50.0	10	10	US-09-572-404B-1293	Sequence 1293, Ap
36	13	50.0	10	10	US-09-572-404B-1295	Sequence 1295, Ap
37	13	50.0	10	10	US-09-572-404B-1309	Sequence 1309, Ap
38	13	50.0	10	10	US-09-572-404B-1335	Sequence 1335, Ap
39	13	50.0	10	10	US-09-572-404B-1337	Sequence 1337, Ap
40	13	50.0	10	10	US-09-572-404B-1417	Sequence 1417, Ap
41	13	50.0	10	10	US-09-572-404B-1427	Sequence 1427, Ap
42	13	50.0	10	10	US-09-572-404B-1451	Sequence 1451, Ap
43	13	50.0	10	10	US-09-572-404B-1489	Sequence 1489, Ap
44	13	50.0	10	10	US-09-572-404B-1505	Sequence 1505, Ap
45	13	50.0	10	10	US-09-572-404B-1521	Sequence 1521, Ap

#### ALIGNMENTS

RESULT 1  
US-10-654-578-1357  
; Sequence 1357, Application US/10654578  
; Publication No. US20040229811A1  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C10  
; CURRENT APPLICATION NUMBER: US/10/654,578  
; CURRENT FILING DATE: 2003-09-03  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1357  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence  
US-10-654-578-1357

Query Match 57.7%; Score 15; DB 17; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
Db 1 CAYATTADGC 10

RESULT 2  
US-10-654-578-1366  
; Sequence 1366, Application US/10654578

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; Publication No. US20040229811A1
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C10
; CURRENT APPLICATION NUMBER: US/10/654,578
; CURRENT FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1366
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-10-654-578-1366

Query Match          57.7%; Score 15; DB 17; Length 10;
Best Local Similarity 20.0%; Pred. No. 1.2e+02;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 1 CYAYATTAC 10

RESULT 3
US-10-654-578-1375
; Sequence 1375, Application US/10654578
; Publication No. US20040229811A1
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C10
; CURRENT APPLICATION NUMBER: US/10/654,578
; CURRENT FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1375
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-10-654-578-1375

Query Match          57.7%; Score 15; DB 17; Length 10;
Best Local Similarity 20.0%; Pred. No. 1.2e+02;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 1 CLYAYATTAC 10

RESULT 4
US-10-654-578-1385
; Sequence 1385, Application US/10654578
; Publication No. US20040229811A1
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
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; FILE REFERENCE: 100086.407C10
; CURRENT APPLICATION NUMBER: US/10/654,578
; CURRENT FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1385
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-10-654-578-1385

Query Match          57.7%; Score 15; DB 17; Length 10;
Best Local Similarity 20.0%; Pred. No. 1.2e+02;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 1 CVYAYATTAC 10

RESULT 5
US-10-654-578-1395
; Sequence 1395, Application US/10654578
; Publication No. US20040229811A1
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C10
; CURRENT APPLICATION NUMBER: US/10/654,578
; CURRENT FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1395
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-10-654-578-1395

Query Match          57.7%; Score 15; DB 17; Length 10;
Best Local Similarity 20.0%; Pred. No. 1.2e+02;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 1 CIYAYATTAC 10

RESULT 6
US-10-654-578-1825
; Sequence 1825, Application US/10654578
; Publication No. US20040229811A1
; GENERAL INFORMATION:
; APPLICANT: Blachuk, Orest W.
; APPLICANT: Symonds, James Matthew
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
; FILE REFERENCE: 100086.407C10
; CURRENT APPLICATION NUMBER: US/10/654,578
; CURRENT FILING DATE: 2003-09-03
; NUMBER OF SEQ ID NOS: 2009
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1825
; LENGTH: 10
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; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion  
; OTHER INFORMATION: recognition sequence  
US-10-654-578-1825

Query Match 57.7%; Score 15; DB 17; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
DB 1 CAYASTADGC 10

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US-10-654-578-1829  
; Sequence 1829, Application US/10654578  
; Publication No. US20040229811A1  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C10  
; CURRENT APPLICATION NUMBER: US/10/654,578  
; CURRENT FILING DATE: 2003-09-03  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1829  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion  
; OTHER INFORMATION: recognition sequence  
US-10-654-578-1829

Query Match 57.7%; Score 15; DB 17; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
DB 1 CIAYASTADC 10

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US-10-654-578-1833  
; Sequence 1833, Application US/10654578  
; Publication No. US20040229811A1  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; FILE REFERENCE: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C10  
; CURRENT APPLICATION NUMBER: US/10/654,578  
; CURRENT FILING DATE: 2003-09-03  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1833  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmocollin-3 or desmocollin-4 cell adhesion

; OTHER INFORMATION: recognition sequence  
US-10-654-578-1833

Query Match 57.7%; Score 15; DB 17; Length 10;  
Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
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DB 1 CLIAVASTAC 10

## RESULT 9

US-09-572-404B-2111  
; Sequence 2111, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 2111  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in C6 at 873-882 and may interact with Sequence ;  
; OTHER INFORMATION: this patent.  
US-09-572-404B-2111

Query Match 53.8%; Score 14; DB 10; Length 10;  
Best Local Similarity 20.0%; Pred. No. 4.9e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
DB 1 CSASTSKCVC 10

## RESULT 10

US-09-572-404B-2169  
; Sequence 2169, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProtPatent version 1.0  
; SEQ ID NO 2169  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in C6 at 873-882 and may interact with Sequence ;  
; OTHER INFORMATION: this patent.  
US-09-572-404B-2169

Query Match 53.8%; Score 14; DB 10; Length 10;  
Best Local Similarity 20.0%; Pred. No. 4.9e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
DB 1 CSASTSKCVC 10

## RESULT 11



Best Local Similarity 20.0%; Pred. No. 4.9e+02; Mismatches 8; Indels 0; Gaps 0;  
Matches 2; Conservative 0;

QY 1 CXXXXXXXC 10  
|  
Db 1 CSRADFLAAC 10

## RESULT 15

US-10-395-032-3644  
; Sequence 3644, Application US/10395032  
; Publication No. US20030229199A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 10086.407C9  
; CURRENT APPLICATION NUMBER: US/10/395,032  
; CURRENT FILING DATE: 2003-03-21  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3644  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-related neuronal receptor cell adhesion  
; OTHER INFORMATION: recognition sequence  
US-10-395-032-3644

Query Match 53.8%; Score 14; DB 14; Length 10;  
Best Local Similarity 20.0%; Pred. No. 4.9e+02; Mismatches 8; Indels 0; Gaps 0;  
Matches 2; Conservative 0;

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Db 1 CFTDSSGC 10

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Job time : 83 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 21:30:17 ; Search time 19 Seconds  
(without alignments)  
50.640 Million cell updates/sec

Title: US-10-046-922-33

Perfect score: 26

Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62

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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	9	34.6	4	I51049	metallothionein-A
3	9	34.6	4	S43959	Ig mu chain V regi
4	9	34.6	4	S52338	pallidipin - assas
5	9	34.6	5	B22565	R-phycoerythrin al
6	9	34.6	5	R22565	R-phycoerythrin ga
7	9	34.6	5	A33882	cadmium-binding pe
8	9	34.6	5	B45525	actin I - malaria
9	9	34.6	5	S63726	hemoglobin, extrac
10	9	34.6	6	JU0355	lipopeptide WS1279
11	9	34.6	6	C22565	R-phycoerythrin be
12	9	34.6	6	I37027	protamine p1 - gor
13	9	34.6	6	I37263	Y protein - human
14	9	34.6	6	H48394	glycoprotein compo
15	9	34.6	6	I67345	MHC H2-K-k cell su
16	9	34.6	6	I65546	MHC H2-L antigen -
17	9	34.6	6	FT0652	T-cell receptor be
18	9	34.6	6	F41946	T-cell receptor ga
19	9	34.6	6	I49421	laminin B1 - weste
20	9	34.6	6	S29881	Na+/K+-exchanging
21	9	34.6	6	I79564	hypothetical TGL3
22	9	34.6	7	PH1408	Ig heavy chain V r
23	9	34.6	7	S38516	mabinlin II chain
24	9	34.6	7	B34818	vicilin 57K chain
25	9	34.6	7	B33882	cadmium-binding he
26	9	34.6	7	A34026	acetylcholinestera
27	9	34.6	7	A12016	formylglycinamide
28	9	34.6	7	PH1602	Ig H chain V-D-J r
29	9	34.6	7	PH0932	T-cell receptor be

30	9	34.6	7	2	A58512	venom heptapeptide
31	9	34.6	7	2	S08606	hypothetical prote
32	9	34.6	7	4	I56695	hypothetical I2 pr
33	9	34.6	8	2	PH1407	Ig heavy chain V r
34	9	34.6	8	2	S59622	metallothionein is
35	9	34.6	8	2	PH1618	Ig H chain V-D-J r
36	9	34.6	8	2	PH0803	T-cell receptor al
37	9	34.6	8	2	PH0934	T-cell receptor be
38	9	34.6	8	2	PC1002	leucine-trNA ligas
39	9	34.6	8	2	S19288	acylase - Kluvyvera
40	9	34.6	8	2	A37521	R-phycoerythrin ga
41	9	34.6	8	2	C61512	variant surface gl
42	9	34.6	8	2	D61512	variant surface gl
43	9	34.6	8	2	I57018	gene Cfr protein
44	9	34.6	8	2	A25836	L-serine ammonia-1
45	9	34.6	8	2	XGHUEU	urine glycopeptide

ALIGNMENTS

RESULT 1

A22565  
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)  
C:Species: Gastroclonium coulteri  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: A22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; MUID:85182601; PMID:3886644  
A:Accession: A22565  
A:Molecule type: protein  
A:Residues: 1-3 <KLO>

Query Match 34.6%; Score 9; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 1 C 1

RESULT 2

I51049  
metallothionein-A - rainbow trout (fragment)  
C:Species: Oncorhynchus mykiss (rainbow trout)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jul-2000  
C:Accession: I51049  
R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.  
Eur. J. Biochem. 230, 344-349, 1995  
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) met  
A:Reference number: I51049; MUID:95324545; PMID:7601121  
A:Accession: I51049  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-4 <OLS>  
A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 34.6%; Score 9; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 4 C 4

RESULT 3

S43959  
Ig mu chain V region (clone 13) - human (fragment)  
C:Species: Homo sapiens (man)

C;Date: 20-Oct-1994 #sequence\_revision 26-Jul-1996 #text\_change 17-Mar-1999  
C;Accession: S43959  
R;Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.;  
Nucleic Acids Res. 22, 1389-1393, 1994  
A;Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.  
A;Reference number: S43956; MUID:94248036; PMID:8190629  
A;Accession: S43959  
A;Molecule type: DNA  
A;Residues: 1-4 <WAG>  
C;Keywords: Immunoglobulin

Query Match 34.6%; Score 9; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 2 C 2

RESULT 4  
S55238  
pallidipin - assassin bug (fragment)  
C;Species: Triatoma pallidipennis (assassin bug)  
C;Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 19-May-2000  
C;Accession: S55238  
R;Haendler, B.; Becker, A.; Noeske-Jungblut, C.; Kraetzschmar, J.; Donner, P.; Schleunin  
Biochem. J. 307, 465-470, 1995  
A;Title: Expression of active recombinant pallidipin, a novel platelet aggregation inhib  
A;Reference number: S55238; MUID:95251610; PMID:7733884  
A;Accession: S55238  
A;Molecule type: protein  
A;Residues: 1-4 <HAE>

Query Match 34.6%; Score 9; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 3 C 3

RESULT 5  
B22565  
R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)  
C;Species: Gastroclonium coulteri  
C;Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C;Accession: B22565  
R;Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A;Reference number: A22565; MUID:85182601; PMID:3886644  
A;Accession: B22565  
A;Molecule type: protein  
A;Residues: 1-5 <KLO>

Query Match 34.6%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 2 C 2

RESULT 6  
F22565  
R-phycoerythrin gamma-A chain - red alga (Gastroclonium coulteri) (fragment)  
C;Species: Gastroclonium coulteri  
C;Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C;Accession: F22565  
R;Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985  
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A;Reference number: A22565; MUID:85182601; PMID:3886644  
A;Accession: F22565  
A;Molecule type: protein  
A;Residues: 1-5 <KLO>

Query Match 34.6%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 3 C 3

RESULT 7  
A33882  
cadmium-binding pentapeptide - downy thornapple  
C;Species: Datura innoxia (downy thornapple)  
C;Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 18-Jun-1993  
C;Accession: A33882  
R;Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.  
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987  
A;Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant ce  
A;Reference number: A94182; MUID:88016144; PMID:3477793  
A;Accession: A33882  
A;Molecule type: protein  
A;Residues: 1-5 <JAC>

Query Match 34.6%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 2 C 2

RESULT 8  
B45525  
actin I - malaria parasite (Plasmodium falciparum) (fragments)  
C;Species: Plasmodium falciparum  
C;Date: 03-Jun-1993 #sequence\_revision 28-Oct-1994 #text\_change 09-Jun-2000  
C;Accession: B45525  
R;Kesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoenmake  
Mol. Biochem. Parasitol. 35, 167-176, 1989  
A;Title: Stage-specific expression and genomic organization of the actin genes of the ma  
A;Reference number: A45525; MUID:89364996; PMID:2671721  
A;Accession: B45525  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-5 <WES>  
A;Cross-references: GB:J03988  
A;Note: the authors translated the codon GAA for residue 3 as Gly  
C;Comment: The actin I gene contains no introns.

Query Match 34.6%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 4 C 4

RESULT 9  
S65726  
hemoglobin, extracellular, chain b - earthworm (Lumbricus terrestris) (fragment)  
C;Species: Lumbricus terrestris (common earthworm)  
C;Date: 06-Dec-1996 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C;Accession: S65726  
R;Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.

Biochim. Biophys. Acta 1292, 273-280, 1996  
A>Title: Characterization of the constituent polypeptides of the extracellular hemoglobin  
A:Reference number: S65721; MUID:96176855; PMID:8597573  
A:Accession: S65726  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <PUS>

Query Match 34.6%; Score 9; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 4 C 4

RESULT 10  
JU0355  
lipopeptide WS1279 [validated] - Streptomyces willmorei  
C:Species: Streptomyces willmorei  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: JU0355  
C:Reference number: JU0355; MUID:91300586; PMID:2070441  
A>Title: Structure and synthesis of an immunoreactive lipopeptide, WS1279, of microbial origin  
A:Reference number: JU0355; MUID:91300586; PMID:2070441  
A:Accession: JU0355  
A:Molecule type: protein  
A:Residues: 1-6 <TSU>  
A>Note: the structure was confirmed by synthesis  
C:Keywords: blocked amino end; lipoprotein  
F:1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental  
F:1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 34.6%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 1 C 1

RESULT 11  
C22565  
R-phycoerythrin beta-1 chain - red alga (Gastroclonium coulteri) (fragment)  
C:Species: Gastroclonium coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: C22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A>Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; MUID:85182601; PMID:3886644  
A:Accession: C22565  
A:Molecule type: protein  
A:Residues: 1-6 <KLO>

Query Match 34.6%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 4 C 4

RESULT 12  
I37027  
protamine P1 - gorilla (fragment)  
C:Species: Gorilla gorilla (gorilla)  
C:Date: 04-Oct-1996 #sequence\_revision 04-Oct-1996 #text\_change 21-Jul-2000  
C:Accession: I37027

R:Queralt, R.; Oliva, R.  
Gene 133, 197-204, 1993  
A>Title: Identification of conserved potential regulatory sequences of the protamine-encephalin gene  
A:Reference number: I37013; MUID:94040810; PMID:8224908  
A:Accession: I37027  
A>Status: preliminary; translated from GB/EMBL/DBBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-references: EMBL:Z12145; NID:G22910; PIDN:CAA78129.1; PID:G579612

Query Match 34.6%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 6 C 6

RESULT 13  
I37263  
Y protein - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 12-Aug-1996 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I37263  
R:Waeber, G.; Habener, J.F.  
Endocrinology 131, 2010-2015, 1992  
A>Title: Novel testis germ cell-specific transcript of the CREB gene contains an alternative exon  
A:Reference number: I37263; MUID:93010691; PMID:1396344  
A:Accession: I37263  
A>Status: preliminary; translated from GB/EMBL/DBBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-references: EMBL:X68994; NID:G396171; PIDN:CAA48780.1; PID:G579816  
C:Genetics:  
A:Gene: CREB

Query Match 34.6%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 4 C 4

RESULT 14  
H48394  
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fra  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Feb-1997  
C:Accession: H48394  
R:Mather, I.H.; Banghart, L.R.; Lane, W.S.  
Biochem. Mol. Biol. Int. 29, 545-554, 1993  
A>Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig  
II-like sequences.  
A:Reference number: A48394; MUID:93250576; PMID:8485470  
A:Accession: H48394  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-6 <MAT>  
A:Experimental source: milk  
A>Note: sequence extracted from NCBI backbone (NCBIP:131518)  
C:Keywords: glycoprotein

Query Match 34.6%; Score 9; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
DB 6 C 6

```

RESULT 15
I67345
MHC H2-K-k cell surface glycoprotein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I67345
R;Archibald, A.L.; Thompson, N.A.; Kvist, S.
EMBO J. 5, 957-965, 1986
A;Title: A single nucleotide difference at the 3' end of an intron causes differential
A;Reference number: I53243; MUID:86247587; PMID:3013627
A;Accession: I67345
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: GB:M26859; NID:g199439; PIDN:AAA39612.1; PID:g387458
C;Genetics:
A;Introns: 6/1
C;Keywords: glycoprotein

Query Match      34.6%  Score 9; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 C 1
Db      4 C 4

Search completed: December 29, 2004, 21:42:53
Job time : 20 secs

```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:27:57 ; Search time 100 Seconds  
(without alignments)  
57.537 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 2971

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	34.6	7	1 ASCL ALLAS	P84071 allium asca
2	9	34.6	7	1 BRHP CONIM	P58803 conus imper
3	9	34.6	7	2 Q9C5B3	Q9C5B3 arabidopsis
4	9	34.6	7	2 P70804	P70804 azotobacter
5	9	34.6	7	2 Q8G112	Q8G112 borrelia bu
6	9	34.6	7	2 Q55184	Q55184 rattus norv
7	9	34.6	7	2 Q66113	Q66113 cherry leaf
8	9	34.6	7	2 Q67113	Q67113 influenza a
9	9	34.6	7	2 Q9YIQ9	Q9YIQ9 human adeno
10	9	34.6	7	2 Q9YIR0	Q9YIR0 human adeno
11	9	34.6	7	2 Q9YVE3	Q9YVE3 human adeno
12	9	34.6	7	2 Q42564	Q42564 fugu rubrip
13	9	34.6	7	2 Q8JU20	Q8JU20 gallus gall
14	9	34.6	8	1 ACT CARMA	P80709 carcinus ma
15	9	34.6	8	1 COW2 CONPU	P58785 conus purpu
16	9	34.6	8	1 GLUR_HUMAN	P02729 homo sapien
17	9	34.6	8	2 Q6EGT1	Q6EGT1 stemphylium
18	9	34.6	8	2 Q6EGV0	Q6EGV0 stemphylium
19	9	34.6	8	2 Q6EGV2	Q6EGV2 stemphylium
20	9	34.6	8	2 Q6EGV3	Q6EGV3 stemphylium
21	9	34.6	8	2 Q6EGW2	Q6EGW2 stemphylium
22	9	34.6	8	2 Q15888	Q15888 homo sapien
23	9	34.6	8	2 Q15890	Q15890 homo sapien
24	9	34.6	8	2 Q15900	Q15900 homo sapien
25	9	34.6	8	2 Q71LUR9	Q71LUR9 homo sapien
26	9	34.6	8	2 Q81V87	Q81V87 homo sapien
27	9	34.6	8	2 Q9Y4X6	Q9Y4X6 homo sapien
28	9	34.6	8	2 Q9BYV5	Q9BYV5 homo sapien
29	9	34.6	8	2 Q7M3S2	Q7M3S2 trypanosoma
30	9	34.6	8	2 Q7M3S3	Q7M3S3 trypanosoma
31	9	34.6	8	2 Q7RBP6	Q7RBP6 plasmodium

32	9	34.6	8	2 Q7RC74	Q7RC74 plasmodium
33	9	34.6	8	2 O02831	O02831 oryctolagus
34	9	34.6	8	2 Q9TRY3	Q9TRY3 sus sp. ins
35	9	34.6	8	2 Q9BF82	Q9BF82 ursus arcto
36	9	34.6	8	2 Q9BF83	Q9BF83 canis famil
37	9	34.6	8	2 Q9BF84	Q9BF84 panthera on
38	9	34.6	8	2 Q9BF85	Q9BF85 leopardus p
39	9	34.6	8	2 Q9BF86	Q9BF86 felis silve
40	9	34.6	8	2 Q9BF87	Q9BF87 tapirus ind
41	9	34.6	8	2 Q9BF88	Q9BF88 equus cabal
42	9	34.6	8	2 Q9BF89	Q9BF89 okapia john
43	9	34.6	8	2 Q9BF90	Q9BF90 tragelaphus
44	9	34.6	8	2 Q9BF91	Q9BF91 hippopotamu
45	9	34.6	8	2 Q9BF92	Q9BF92 tursiops tr

ALIGNMENTS

RESULT 1  
ASCL ALLAS STANDARD; PRT; 7 AA.  
AC P84071;  
DT 01-OCT-2004 (Rel. 45, Created)  
DT 01-OCT-2004 (Rel. 45, Last sequence update)  
DE Ascalin (Fragment).  
OS Allium ascalonicum (Shallot) (Allium cepa var. aggregatum).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;  
OC Allium.  
OX NCBI\_TaxID=28911;  
RN [1]  
RP SEQUENCE, AND FUNCTION.  
RC TISSUE=Bulb;  
RX PubMed=12126728;  
RA Wang H.X., Ng T.B.;  
RT "Ascalin, a new anti-fungal peptide with human immunodeficiency virus  
type 1 reverse transcriptase-inhibiting activity from shallot bulbs.";  
RL Peptides 23:1025-1029(2002).  
CC -!- FUNCTION: Has antifungal activity against B.cinerea. Inhibits HIV-  
1 reverse transcriptase.  
CC -!- MISCELLANEOUS: Inhibits HIV-1 reverse transcriptase with an IC(50)  
of 10 uM.  
CC Direct protein sequencing; Fungicide.  
KW NON TER 7  
SQ SEQUENCE 7 AA; 712 MW; 687866D87EA6CB30 CRC64;  
Query Match 34.6%; Score 9; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 C 1  
Db 3 C 3  
RESULT 2  
BRHP CONIM STANDARD; PRT; 7 AA.  
AC P58803;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE Broncheptapeptide Im.  
OS Conus imperialis (Imperial cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=35631;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;

```

RX MEDLINE=97184108; PubMed=9030520;
RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,
RA Abogadie P.C., Porter J., Rivier J.E., Cruz L.J., Oliveira B.M.,
RA McIntosh J.M.;
RT "A novel post-translational modification involving bromination of
RT tryptophan. Identification of the residue, L-6-bromotryptophan, in
RT peptides from Conus imperialis and Conus radiatus venom.";
RL J. Biol. Chem. 272:4689-4698(1997).
CC -1- FUNCTION: Does not elicit gross behavioral symptoms when injected
CC centrally or peripherally in mice.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=853.19; METHOD=LSI; RANGE=1-7; NOTE=Ref.1.
DR PIR: A58512; A58512.
KW Amidation; Bromination; Direct protein sequencing;
KW Pyrrolidone carboxylic acid.
FT DISULFID 2 7
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 6 6 6'-bromotryptophan.
FT MOD_RES 7 7 Cysteine amide.
FT MOD_RES 7 7
SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;

Query Match 34.6%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 2 C 2

RESULT 3
Q9C5B3 PRELIMINARY; PRT; 7 AA.
AC Q9C5B3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein bDd1 10A-2b (Fragment).
GN Name=bDd1 10A-2b;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Roots;
RX MEDLINE=21171025; PubMed=11277426;
RA Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;
RT "Arabidopsis thaliana genes expressed in the early compatible
RT interaction with root-knot nematodes.";
RL Mol. Plant Microbe Interact. 14:288-299(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Roots;
RX MEDLINE=21171025; PubMed=11277426;
RA Vercauteren I.J.R.;
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286350; CAB71014.2; -.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 719 MW; 6732C7287EB325D0 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 3 C 3

```

```

RESULT 4
P70804 PRELIMINARY; PRT; 7 AA.
AC P70804;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Algt protein (Fragment).
GN Name=algt;
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E;
RX MEDLINE=96427318; PubMed=8830682;
RA Rehm B.H.A., Estesvag H., Valla S.;
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is
RT part of an alg gene cluster physically organized in a manner similar
RT to that in Pseudomonas aeruginosa.";
RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87973; CAA61230.1; -.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 1 C 1

RESULT 5
Q8GL12 PRELIMINARY; PRT; 7 AA.
AC Q8GL12;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PF-50 protein (Fragment).
GN Name=PF-50;
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Spirochaetia; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N40;
RX MEDLINE=22990544; PubMed=14629041;
RA Stevenson B., Miller J.C.;
RT "Intra- and interbacterial genetic exchange of Lyme disease spirochete
RT exp genes generates sequence identity amidst diversity.";
RL J. Mol. Evol. 57:309-324(2003).
DR EMBL; AY142100; AA017911.1; -.
KW Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 7 AA; 849 MW; 6337244330569ED0 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1
Db 1 C 1

RESULT 6
O55184 PRELIMINARY; PRT; 7 AA.
ID O55184

```

O55184;  
01-JUN-1998 (TrEMBLrel. 06, Created)  
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
Orphan receptor TR4-NS (Fragment).  
Name=TR4;  
Rattus norvegicus (Rat).  
Eukaryota; Metazoa; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
NCBI\_TaxID=10116;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=96198747; PubMed=8612486;  
RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,  
Detera-Wadleigh S.D.;  
RT "Splice variants of rat TR4 orphan receptor: differential expression  
of novel sequences in the 5'-untranslated region and C-terminal  
domain.";  
RL Endocrinology 137:1562-1571 (1996).  
RN [2]  
SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley;  
RX MEDLINE=96299786; PubMed=86611150;  
RA Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.;  
RT "New variants of the human and rat nuclear hormone receptor, TR4:  
expression and chromosomal localization of the human gene.";  
RL Genomics 35:361-366 (1996).  
DR EMBL; U59454; AAB91433.1; -;  
DR GO; GO:0004872; Fireceptor activity; IEA.  
KW Receptor.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 3 C 3

## RESULT 7

ID Q66113 PRELIMINARY; PRT; 7 AA.  
AC Q66113;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE C-terminus of the viral replicase (Fragment).  
OS Cherry leaf roll virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;  
OC Nepovirus; Subgroup C.  
OX NCBI\_TaxID=12615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Walnut;  
RX MEDLINE=96124520; PubMed=8560786;  
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;  
RT "Long, nearly identical untranslated sequences at the 3' terminal  
regions of the genomic RNAs of cherry leafroll virus (walnut  
strain).";  
RL Virus Genes 10:245-252 (1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Walnut;  
RA Borja M.;  
RL Thesis (1992); Biologia Molecular y Virologia Vegetal, CIT-INIA.  
DR EMBL; Z34265; CAA84019.1; -;  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 C 1  
|  
Db 4 C 4  
RESULT 8  
ID Q67113 PRELIMINARY; PRT; 7 AA.  
AC Q67113;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Influenza virus type A (Udorn/72) hemagglutinin (seg 4) cDNA, 3' end.  
DE (Fragment).  
OS Influenza A virus.  
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
OC Influenzavirus A.  
OX NCBI\_TaxID=11320;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81001892; PubMed=7407922;  
RA Dhar R., Chanock R.M., Lai C.-J.;  
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza  
viral mRNA deduced from cloned complete genomic sequences.";  
RL Cell 21:495-500 (1980).  
DR EMBL; M25045; AAA43202.1; -;  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1  
|  
Db 3 C 3

## RESULT 9

ID Q9YIQ9 PRELIMINARY; PRT; 7 AA.  
AC Q9YIQ9;  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
DE PVI core protein (Fragment).  
GN Name=pVI;  
OS Human adenovirus type 4.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=28280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Z-G T95-873;  
RX MEDLINE=99175282; PubMed=10074533;  
RA Crawford-Miksza L.K., Nang R.N., Schnurr D.P.;  
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute  
respiratory disease.";  
RL J. Clin. Microbiol. 37:1107-1112 (1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Z-G T95-873;  
RA Crawford-Miksza L.K.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF065064; AAD03659.1; -;  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1

Db 6 C 6

#### RESULT 10

Q9YI90 PRELIMINARY; PRT; 7 AA.  
AC Q9YI90  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)  
DE PVI core protein (Fragment).  
GN Name=pvi;  
OS Human adenovirus type 7a.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus;  
OC Human adenovirus type 7.  
OX NCBI\_TaxID=85755;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Kn T96-0620;  
RX MEDLINE=99175282; PubMed=10074533;  
RA Crawford-Mikaza L.K., Nang R.N., Schnurr D.P.;  
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute respiratory disease.";  
RL J. Clin. Microbiol. 37:1107-1112(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Kn T96-0620;  
RA Crawford-Mikaza L.K.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF065068; AAD03668.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.5e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1

Db 6 C 6

#### RESULT 11

Q9YVE3 PRELIMINARY; PRT; 7 AA.  
AC Q9YVE3  
DT 01-MAY-1999 (TrEMBLrel. 10, Created)  
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE PVI core protein (Fragment).  
GN Name=pvi;  
OS Human adenovirus type 7.  
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.  
OX NCBI\_TaxID=10519;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gomen;  
RX MEDLINE=99175282; PubMed=10074533;  
RA Crawford-Mikaza L.K., Nang R.N., Schnurr D.P.;  
RT "Strain variation in adenovirus serotypes 4 and 7a causing acute respiratory disease.";  
RL J. Clin. Microbiol. 37:1107-1112(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Gomen;  
RA Crawford-Mikaza L.K.;  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF065065; AAD03662.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.5e+06;

SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.5e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1

Db 6 C 6

#### RESULT 12

O42564 PRELIMINARY; PRT; 7 AA.  
AC O42564  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).  
GN Name=Scn8a;  
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraodontidae; Tetraodontidae; Takifugu.  
OX NCBI\_TaxID=31033;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97442476; PubMed=9295353;  
RA Plummer N.W., McBurney M.W., Meisler M.H.;  
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";  
RL J. Biol. Chem. 272:24008-24015(1997).  
DR EMBL; U97673; AAB0916.1; -.  
DR GO; GO:0005216; F:ion channel activity; IEA.  
KW Ionic channel.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.5e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 C 1

Db 5 C 5

#### RESULT 13

Q8JU20 PRELIMINARY; PRT; 7 AA.  
AC Q8JU20  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Extracellular fatty acid binding protein (Fragment).  
GN Name=EXFABP;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RA Wang Q., Li N., Li H.;  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF487519; AAL96665.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 780 MW; 72CB1AB2D5BEBB70 CRC64;

Query Match 34.6%; Score 9; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.5e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1

Db 2 C 2

## RESULT 14

ACT CARMA  
ID ACT CARMA STANDARD; PRT; 8 AA.  
AC P80709;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Actin (Fragment).  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.  
OX NCBI\_TaxID=6759;  
RN [1]  
RP SEQUENCE.  
RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,  
RA Baghdasarian D.;  
RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";  
RL Endocrine 5:23-32(1996).  
CC -!- FUNCTION: Actins are highly conserved proteins that are involved  
CC in various types of cell motility and are ubiquitously expressed  
CC in all eukaryotic cells.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein is:  
CC 6.8, its MW is: 46 kDa.  
CC -!- SIMILARITY: Belongs to the actin family.  
DR InterPro: IPR004001; Actin.  
DR InterPro: IPR004000; Actin\_like.  
DR PROSITE: PS00406; ACTINS\_1; PARTIAL.  
DR PROSITE: PS00432; ACTINS\_2; PARTIAL.  
DR PROSITE: PS01132; ACTINS\_ACT LIKE; PARTIAL.  
KW Direct protein sequencing; Structural protein.  
FT NON\_TER 1  
FT NON\_TER 8  
SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAB3 CRC64;

Query Match 34.6%; Score 9; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.5e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1

Db 2 C 2

## RESULT 15

COM2\_CONPU  
ID COM2\_CONPU STANDARD; PRT; 8 AA.  
AC P58785;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Leu-contryphan-P.  
OS Conus purpurascens (Purple cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=41690;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC STRAIN=Clipperton Island; TISSUE=Venom;  
RX MEDLINE=9938839; PubMed=10461743;  
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,  
RA Olivera B.M.;  
RT "A novel D-leucine-containing Conus peptide: diverse conformational  
RT dynamics in the contryphan family.";

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:55:07 ; Search time 69.6226 Seconds  
(without alignments)  
51.525 Million cell updates/sec

Title: US-10-046-922-33

Perfect score: 26

Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	69.2	89	8 ADP30533	Adp30533 Human sec
2	18	69.2	89	8 ADP30531	Adp30531 Human sec
3	18	69.2	109	4 AAM93527	Aam93527 Human pol
4	18	69.2	109	8 ADL31230	Adl31230 Human pro
5	18	69.2	109	8 ADP30690	Adp30690 Human sec
6	18	69.2	144	8 ADP31474	Adp31474 Human sec
7	18	69.2	167	7 ABO69151	Abo69151 Pseudomon
8	18	69.2	171	8 ADP30794	Adp30794 Human sec
9	18	69.2	171	8 ADP30793	Adp30793 Human sec
10	18	69.2	183	8 ADP30806	Adp30806 Human sec
11	18	69.2	191	7 ABO76619	Abo76619 Pseudomon
12	18	69.2	228	8 ADP30921	Adp30921 Human sec
13	18	69.2	252	8 ADP31485	Adp31485 Human sec
14	18	69.2	258	8 ADP30479	Adp30479 Human sec
15	18	69.2	264	8 ADP31412	Adp31412 Human sec
16	18	69.2	270	8 ADP30500	Adp30500 Human sec
17	18	69.2	270	8 ADP31321	Adp31321 Human sec
18	18	69.2	294	8 ADP31473	Adp31473 Human sec
19	18	69.2	327	8 ADP31192	Adp31192 Human sec
20	18	69.2	328	4 AAM25285	Aam25285 Human pro
21	18	69.2	339	8 ADP30702	Adp30702 Human sec
22	18	69.2	348	8 ADP31441	Adp31441 Human sec
23	18	69.2	356	4 ABG21039	Abg21039 Novel hum
24	18	69.2	357	8 ADP31267	Adp31267 Human sec
25	18	69.2	357	8 ADP30505	Adp30505 Human sec

#### ALIGNMENTS

##### RESULT 1

ADP30533

ID ADP30533 standard; protein; 89 AA.

XX AC ADP30533;

XX DT 12-AUG-2004 (first entry)

XX DE Human secreted protein SEQ ID #1300.

XX KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;

XX KW cancer; inflammatory; immune; human secreted protein.

XX OS Homo sapiens.

XX PN WO2004035732-A2.

XX PD 29-APR-2004.

XX PF 28-AUG-2003; 2003WO-US026780.

XX PR 29-AUG-2002; 2002US-0406576P.

XX PR 29-AUG-2002; 2002US-0406579P.

XX PR 29-AUG-2002; 2002US-0406585P.

XX PR 29-AUG-2002; 2002US-0406588P.

XX PR 29-AUG-2002; 2002US-0406608P.

XX PR 29-AUG-2002; 2002US-0406611P.

XX PR 29-AUG-2002; 2002US-0406612P.

XX PR 29-AUG-2002; 2002US-0406618P.

XX PR 29-AUG-2002; 2002US-0406640P.

XX PR 29-AUG-2002; 2002US-0406642P.

XX PR 29-AUG-2002; 2002US-0406646P.

XX PR 29-AUG-2002; 2002US-0406653P.

XX PR 29-AUG-2002; 2002US-0406655P.

XX PR 29-AUG-2002; 2002US-0406668P.

XX PR 17-SEP-2002; 2002US-0410946P.

XX PR 17-SEP-2002; 2002US-0410947P.

XX PR 17-SEP-2002; 2002US-0410948P.

XX PR 17-SEP-2002; 2002US-0410949P.

XX PR 17-SEP-2002; 2002US-0410953P.

XX PR 17-SEP-2002; 2002US-0410957P.

XX PR 17-SEP-2002; 2002US-0410958P.

XX PR 17-SEP-2002; 2002US-0410959P.

XX PR 17-SEP-2002; 2002US-0410960P.

XX PR 17-SEP-2002; 2002US-0410961P.

XX PR 17-SEP-2002; 2002US-0410962P.

XX PR 17-SEP-2002; 2002US-0411019P.

XX PR 17-SEP-2002; 2002US-0411022P.

26	18	69.2	360	8 ADP31439	Adp31439 Human sec
27	18	69.2	390	8 ADP31218	Adp31218 Human sec
28	18	69.2	421	8 ADP31159	Adp31159 Human sec
29	18	69.2	426	8 ADP31495	Adp31495 Human sec
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31	18	69.2	453	8 ADP31465	Adp31465 Human sec
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33	18	69.2	525	8 ADP31227	Adp31227 Human sec
34	18	69.2	549	8 ADP30855	Adp30855 Human sec
35	18	69.2	555	8 ADP31416	Adp31416 Human sec
36	18	69.2	555	8 ADP31417	Adp31417 Human sec
37	18	69.2	588	8 ADP31699	Adp31699 Human sec
38	18	69.2	600	8 ADP30865	Adp30865 Human sec
39	18	69.2	604	8 ADP30940	Adp30940 Human sec
40	18	69.2	604	8 ADP30941	Adp30941 Human sec
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45	18	69.2	653	3 AAY94907	Aay94907 Human sec

PR	17-SEP-2002;	2002US-0411023P.	
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PR	17-SEP-2002;	2002US-0411046P.	
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PR	02-MAY-2003;	2003US-0467230P.	
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PR	08-AUG-2003;	2003US-0493577P.	
PA	(FIVE-) FIVE PRIME THERAPEUTICS INC.		
XX	Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;		
PI	Halenbeck RP, Huang WM, Kochakota S, Haishan L, Linnemann T;		
PI	Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;		
XX	WPI; 2004-348438/32.		
DR			
XX			
XX			
PT	New nucleic acid molecule for diagnosing, preventing or treating diseases		
PT	such as proliferative (e.g. cancer), inflammatory, immune, metabolic,		
PT	Genetic, bacterial and viral diseases.		
XX			
PS	Claim 1; SEQ ID NO 2531; 428pp; English.		
XX			
CC	The present invention relates to an isolated nucleic acid molecule		
CC	encoding a polypeptide which is believed to be cytostatic,		
CC	antiinflammatory, immunosuppressive, antibacterial and virucidal. The		
CC	composition and methods are useful for diagnosing, preventing and		
CC	treating diseases such as proliferative (e.g. cancer), inflammatory,		
CC	immune, metabolic, genetic, bacterial and viral diseases. The present		
CC	sequence represents a human secreted protein. The present sequence is		
CC	available on WIFOWEB and is not in the specification.		
XX			
SQ	Sequence 89 AA;		
Query Match 69.2%; Score 18; DB 8; Length 89;			
Best Local Similarity 20.0%; Pred. No. 2.6;			
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;			
Qy	1 CXXXXXXXC 10		

Db	24	CTTAAAAAAC 33
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ID	ADP30531	
XX	ADP30531 standard; protein; 89 AA.	
AC	ADP30531;	
XX		
DT	12-AUG-2004 (first entry)	
XX		
DE	Human secreted protein SEQ ID #1298.	
XX		
KW	Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;	
KW	cancer; inflammatory; immune; human secreted protein.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004035732-A2.	
XX		
PD	29-APR-2004.	
XX		
PF	28-AUG-2003; 2003WO-US026780.	
XX		
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 PR 08-AUG-2003; 2003US-0493573P.  
 PR 08-AUG-2003; 2003US-0493577P.  
 XX (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 XX Williams LT, Chu K, Lee E, Hestir K, Beurang PA, Behrens D;  
 PI Halenbeck RF, Huang MM, Kothakota S, Haisnan L, Linnemann T;  
 PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
 XX WPI; 2004-348438/32.  
 XX New nucleic acid molecule for diagnosing, preventing or treating diseases  
 PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
 PT genetic, bacterial and viral diseases.  
 XX Claim 1; SEQ ID NO 2529; 428pp; English.  
 PS The present invention relates to an isolated nucleic acid molecule  
 CC encoding a polypeptide which is believed to be cytostatic,  
 CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
 CC composition and methods are useful for diagnosing, preventing and  
 CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
 CC immune, metabolic, genetic, bacterial and viral diseases. The present  
 CC sequence represents a human secreted protein. The present sequence is  
 CC available on WIPWEB and is not in the specification.  
 XX SQ Sequence 89 AA;  
 Query Match 69.2%; Score 18; DB 8; Length 89;  
 Best Local Similarity 20.0%; Pred. No. 2.6;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 CXXXXXXXC 10  
 Db 24 CTTAAAAAC 33  
 RESULT 3  
 AAM93527  
 ID AAM93527 standard; protein; 109 AA.  
 XX  
 AC AAM93527;  
 XX  
 XX 06-NOV-2001 (first entry)  
 DT  
 DE Human polypeptide, SEQ ID NO: 3263.  
 XX Human; full length cDNA; cDNA synthesis; oligo-capping.  
 KW  
 XX Homo sapiens.  
 OS  
 PN EP1130094-A2.  
 XX  
 PD 05-SEP-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-00114089.

XX 08-JUL-1999; 99JP-00194486.  
 PR 11-JAN-2000; 2000JP-00118774.  
 PR 02-MAY-2000; 2000JP-00183765.  
 PA (HELI-) HELIX RES INST.  
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX WPI; 2001-524255/58.  
 DR N-PSDB; AAK94457.  
 XX 830 Primers useful for synthesizing full length cDNA clones and their use  
 PT in genetic manipulation.  
 XX Claim 8; SEQ ID NO 3263; 1380pp + Sequence Listing; English.  
 CC The invention relates to primers for synthesising full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have  
 CC been determined. Primers for synthesising the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesised by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a polypeptide encoded by a full length  
 CC human cDNA of the invention. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in CD-ROM  
 CC format directly from EPO  
 XX SQ Sequence 109 AA;  
 Query Match 69.2%; Score 18; DB 4; Length 109;  
 Best Local Similarity 20.0%; Pred. No. 2.7;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 CXXXXXXXC 10  
 Db 4 CXXXXXXXC 13  
 RESULT 4  
 ADL31230  
 ID ADL31230 standard; protein; 109 AA.  
 XX  
 AC ADL31230;  
 XX  
 DT 20-MAY-2004 (first entry)  
 XX  
 DE Human protein encoded by a full length cDNA clone SeqID 3263.  
 XX human; medicine; signal transduction; glycoprotein; transcription;  
 KW oligo-capping method.  
 XX Homo sapiens.  
 OS  
 PN EP1396543-A2.  
 XX  
 PD 10-MAR-2004.  
 XX  
 PF 07-JUL-2000; 2003EP-00025638.  
 XX  
 PR 08-JUL-1999; 99JP-00194486.  
 PR 11-JAN-2000; 2000JP-00118774.  
 PR 02-MAY-2000; 2000JP-00183865.  
 PR 07-JUL-2000; 2000EP-00114089.  
 XX  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX



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Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 CXXXXXXXC 10
Db 96 CTTTATATC 105

RESULT 6
ADP31474
ID ADP31474 standard; protein; 144 AA.
AC ADP31474;
XX
XX
DT 12-AUG-2004 (first entry)
DE
DE Human secreted protein SEQ ID #2241.
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX
OS Homo sapiens.
XX
XX WO2004035732-A2.
PN
XX
PD 29-APR-2004.
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PF 28-AUG-2003; 2003WO-US025780.
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PR 29-AUG-2002; 2002US-0406576P.
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PR 29-AUG-2002; 2002US-0406616P.
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PR 17-SEP-2002; 2002US-0411111P.
PR 18-APR-2003; 2003US-0463700P.
PR 18-APR-2003; 2003US-0463708P.
PR 18-APR-2003; 2003US-0463716P.

PR 18-APR-2003; 2003US-0463732P.
PR 02-MAY-2003; 2003US-0467199P.
PR 02-MAY-2003; 2003US-0467201P.
PR 02-MAY-2003; 2003US-0467203P.
PR 02-MAY-2003; 2003US-0467230P.
PR 19-MAY-2003; 2003US-0471306P.
PR 19-MAY-2003; 2003US-0471336P.
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PR 09-JUN-2003; 2003US-0476641P.
PR 08-JUL-2003; 2003US-0485218P.
PR 08-JUL-2003; 2003US-0485223P.
PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
PR 14-JUL-2003; 2003US-0486446P.
PR 14-JUL-2003; 2003US-0486480P.
PR 15-JUL-2003; 2003US-0486891P.
PR 15-JUL-2003; 2003US-0486960P.
PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA
XX
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MM, Kothakota S, Haighan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
XX WPI; 2004-348438/32.
XX
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
XX Claim 1; SEQ ID NO 3472; 428pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic.
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPOWEB and is not in the specification.
XX
XX Sequence 144 AA;
SQ
Query Match 69.2%; Score 18; DB 8; Length 144;
Best Local Similarity 20.0%; Pred. No. 2.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 CXXXXXXXC 10
Db 72 CAATAAATC 81

RESULT 7
ABO69151
ID ABO69151 standard; protein; 167 AA.
XX
XX ABO69151;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX Pseudomonas aeruginosa polypeptide #1326.
DE
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
KW
XX Pseudomonas aeruginosa.
OS
XX
XX US6551795-B1.
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XX 22-APR-2003.  
 XX PD  
 XX 18-FEB-1999; 99US-00252991.  
 PF  
 XX 18-FEB-1998; 98US-0074788P.  
 XX 27-JUL-1998; 98US-0094190P.  
 XX PR  
 XX (GENO-) GENOME THERAPEUTICS CORP.  
 PA  
 XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
 PI WPI; 2003-615309/58.  
 XX N-PSDB; ABD02722.  
 DR  
 XX Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,  
 PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
 PT pathological conditions resulting from bacterial infection.  
 XX  
 XX Disclosure; SEQ ID NO 17897; 455pp; English.  
 PS  
 XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the  
 CC polynucleotides encoding them. The sequences are useful in diagnosis and  
 CC therapy of pathological conditions, as molecular targets for diagnostics,  
 CC prophylaxis and treatment of pathological conditions resulting from a  
 CC bacterial infection, for evaluating a compound, such as a polypeptide,  
 CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of  
 CC effective antibacterial targets, as targets for antibacterial drugs,  
 CC including anti-*P. aeruginosa* drugs, as templates for recombinant  
 CC production of *P. aeruginosa*-derived peptides or polypeptides, as target  
 CC components for diagnosis and/or treatment of *P. aeruginosa*-caused  
 CC infection, and in detection of *P. aeruginosa* sequences or other sequences  
 CC of *Pseudomonas* species using biochip technology. Sequences AB067826-  
 CC AB084396 represent *P. aeruginosa* polypeptides of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 XX  
 XX Sequence 167 AA;  
 SQ

Query Match 69.2%; Score 18; DB 7; Length 167;  
 Best Local Similarity 20.0%; Pred. No. 2.9;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10  
 Db 60 CSTSTSTSC 69

RESULT 8  
 ID ADP30794 standard; protein; 171 AA.  
 XX AC  
 XX ADP30794;  
 XX  
 XX 12-AUG-2004 (first entry)  
 DT  
 XX Human secreted protein SEQ ID #1561.  
 DE  
 XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
 KW cancer; inflammatory; immune; human secreted protein.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO2004035732-A2.  
 PN  
 XX 29-APR-2004.  
 PD  
 XX 28-AUG-2003; 2003WO-US026780.  
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 XX 29-AUG-2002; 2002US-0406576P.  
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 17-SEP-2002; 2002US-0411101P.  
 17-SEP-2002; 2002US-0411111P.  
 18-APR-2003; 2003US-0463700P.  
 18-APR-2003; 2003US-0463708P.  
 18-APR-2003; 2003US-0463716P.  
 18-APR-2003; 2003US-0463732P.  
 02-MAY-2003; 2003US-0467199P.  
 02-MAY-2003; 2003US-0467201P.  
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 02-MAY-2003; 2003US-0467230P.  
 19-MAY-2003; 2003US-0471306P.  
 19-MAY-2003; 2003US-0471336P.  
 22-MAY-2003; 2003US-0472420P.  
 22-MAY-2003; 2003US-0472430P.  
 09-JUN-2003; 2003US-0476609P.  
 09-JUN-2003; 2003US-0476641P.  
 08-JUL-2003; 2003US-0485218P.  
 08-JUL-2003; 2003US-0485223P.  
 08-JUL-2003; 2003US-0485224P.  
 08-JUL-2003; 2003US-0485325P.  
 14-JUL-2003; 2003US-0486446P.  
 14-JUL-2003; 2003US-0486480P.  
 15-JUL-2003; 2003US-0486891P.  
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 08-AUG-2003; 2003US-0493341P.  
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 08-AUG-2003; 2003US-0493573P.  
 08-AUG-2003; 2003US-0493577P.  
 XX  
 XX (FIVE-) FIVE PRIME THERAPEUTICS INC.  
 PA Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
 PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
 PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
 XX WPI; 2004-348438/32.  
 DR

XX New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
PS Claim 1; SEQ ID NO 2792; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPWEB and is not in the specification.  
XX  
XX Sequence 171 AA;  
  
Query Match 69.2%; Score 18; DB 8; Length 171;  
Best Local Similarity 20.0%; Pred. No. 2.9;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXC 10  
DB 146 CAATAAACC 155  
  
RESULT 9  
ADP30793  
ID ADP30793 standard; protein; 171 AA.  
AC ADP30793;  
XX  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human secreted protein SEQ ID #1560.  
XX  
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
XX  
XX Homo sapiens.  
XX  
XX WO2004035732-A2.  
XX  
XX 29-APR-2004.  
XX  
XX 28-AUG-2003; 2003WO-US026780.  
XX  
XX 29-AUG-2002; 2002US-0406576P.  
XX 29-AUG-2002; 2002US-0406579P.  
XX 29-AUG-2002; 2002US-0406585P.  
XX 29-AUG-2002; 2002US-0406588P.  
XX 29-AUG-2002; 2002US-0406608P.  
XX 29-AUG-2002; 2002US-0406611P.  
XX 29-AUG-2002; 2002US-0406612P.  
XX 29-AUG-2002; 2002US-0406616P.  
XX 29-AUG-2002; 2002US-0406640P.  
XX 29-AUG-2002; 2002US-0406642P.  
XX 29-AUG-2002; 2002US-0406646P.  
XX 29-AUG-2002; 2002US-0406653P.  
XX 29-AUG-2002; 2002US-0406655P.  
XX 17-SEP-2002; 2002US-0406669P.  
XX 17-SEP-2002; 2002US-0410946P.  
XX 17-SEP-2002; 2002US-0410947P.  
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XX 17-SEP-2002; 2002US-0410949P.  
XX 17-SEP-2002; 2002US-0410953P.  
XX 17-SEP-2002; 2002US-0410957P.  
XX 17-SEP-2002; 2002US-0410958P.  
XX 17-SEP-2002; 2002US-0410959P.  
XX 17-SEP-2002; 2002US-0410960P.  
XX 17-SEP-2002; 2002US-0410961P.  
XX 17-SEP-2002; 2002US-0410962P.

PR 17-SEP-2002; 2002US-0411019P.  
PR 17-SEP-2002; 2002US-0411022P.  
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PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411035P.  
PR 17-SEP-2002; 2002US-0411037P.  
PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
PR 17-SEP-2002; 2002US-0411046P.  
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PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411053P.  
PR 17-SEP-2002; 2002US-0411073P.  
PR 17-SEP-2002; 2002US-0411082P.  
PR 17-SEP-2002; 2002US-0411101P.  
PR 17-SEP-2002; 2002US-0411111P.  
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PR 18-APR-2003; 2003US-0463708P.  
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PR 22-MAY-2003; 2003US-0472420P.  
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PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
PR 08-JUL-2003; 2003US-0485223P.  
PR 08-JUL-2003; 2003US-0485224P.  
PR 08-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486446P.  
PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.  
  
(FIVE-) FIVE PRIME THERAPEUTICS INC.  
PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX  
XX WPI; 2004-348438/32.  
XX  
XX New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
XX Claim 1; SEQ ID NO 2791; 428pp; English.  
XX  
XX The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPWEB and is not in the specification.  
XX  
XX Sequence 171 AA;  
  
Query Match 69.2%; Score 18; DB 8; Length 171;  
Best Local Similarity 20.0%; Pred. No. 2.9;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
SQ Sequence 171 AA;

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Qy      1 CXXXXXXXC 10
Db      146 CAAATAAAC 155

RESULT 10
ADP30806
ID ADP30806 standard; protein; 183 AA.
XX
AC ADP30806;
XX
DT      12-AUG-2004 (first entry)
XX
DE      Human secreted protein SEQ ID #1573.
XX
KW      Cytostatic; Antinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW      cancer; inflammatory; immune; human secreted protein.
XX
OS      Homo sapiens.
XX
PN      WO2004035732-A2.
XX
PD      29-APR-2004.
XX
PF      28-AUG-2003; 2003WO-US026780.
XX
PR      29-AUG-2002; 2002US-0406576P.
PR      29-AUG-2002; 2002US-0406579P.
PR      29-AUG-2002; 2002US-0406585P.
PR      29-AUG-2002; 2002US-0406588P.
PR      29-AUG-2002; 2002US-0406608P.
PR      29-AUG-2002; 2002US-0406611P.
PR      29-AUG-2002; 2002US-0406612P.
PR      29-AUG-2002; 2002US-0406616P.
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PR      29-AUG-2002; 2002US-0406642P.
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PR      17-SEP-2002; 2002US-0410953P.
PR      17-SEP-2002; 2002US-0410957P.
PR      17-SEP-2002; 2002US-0410958P.
PR      17-SEP-2002; 2002US-0410959P.
PR      17-SEP-2002; 2002US-0410960P.
PR      17-SEP-2002; 2002US-0410961P.
PR      17-SEP-2002; 2002US-0410962P.
PR      17-SEP-2002; 2002US-0411019P.
PR      17-SEP-2002; 2002US-0411022P.
PR      17-SEP-2002; 2002US-0411023P.
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PR      17-SEP-2002; 2002US-0411101P.
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PR      18-APR-2003; 2003US-0463700P.
PR      18-APR-2003; 2003US-0463708P.
PR      18-APR-2003; 2003US-0463716P.
PR      18-APR-2003; 2003US-0463732P.
PR      02-MAY-2003; 2003US-0467199P.

02-MAY-2003; 2003US-0467201P.
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02-MAY-2003; 2003US-0467230P.
13-MAY-2003; 2003US-0471306P.
19-MAY-2003; 2003US-0471336P.
22-MAY-2003; 2003US-0472420P.
09-JUN-2003; 2003US-0476609P.
09-JUN-2003; 2003US-0476641P.
08-JUL-2003; 2003US-0485218P.
08-JUL-2003; 2003US-0485223P.
08-JUL-2003; 2003US-0485224P.
08-JUL-2003; 2003US-0485325P.
14-JUL-2003; 2003US-0486446P.
14-JUL-2003; 2003US-0486480P.
15-JUL-2003; 2003US-0486891P.
15-JUL-2003; 2003US-0486960P.
08-AUG-2003; 2003US-0493341P.
08-AUG-2003; 2003US-0493370P.
08-AUG-2003; 2003US-0493573P.
08-AUG-2003; 2003US-0493577P.
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA
XX
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RF, Huang MW, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
DR WPI; 2004-348438/32.
XX
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
PS Claim 1; SEQ ID NO 2804; 428pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPOWEB and is not in the specification.
XX
SQ Sequence 183 AA;
XX
XX Query Match 69.2%; Score 18; DB 8; Length 183;
XX Best Local Similarity 20.0%; Pred. No. 3;
XX Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy      1 CXXXXXXXC 10
Db      36 CATTTTTC 45

RESULT 11
ABO76619
ID ABO76619 standard; protein; 191 AA.
XX
AC ABO76619;
XX
DT      29-JUL-2004 (first entry)
XX
DE      Pseudomonas aeruginosa polypeptide #8794.
XX
KW      Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS      Pseudomonas aeruginosa.
XX
PN      US6551795-B1.
XX
PD      22-APR-2003.
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XX 18-FEB-1999; 99US-00252991.  
XX 18-FEB-1998; 98US-0074788P.  
PR 27-JUL-1998; 98US-0094190P.  
XX (GENO-) GENOME THERAPEUTICS CORP.  
PA  
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
PI WPI; 2003-615309/58.  
DR N-PSDB; ABD10190.  
XX  
PT Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,  
PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
PT pathological conditions resulting from bacterial infection.  
XX  
XX Disclosure; SEQ ID NO 25365; 455pp; English.  
XX  
CC The invention relates to *Pseudomonas aeruginosa* polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-*P. aeruginosa* drugs, as templates for recombinant  
CC components of *P. aeruginosa*-derived peptides or polypeptides, as target  
CC infection, and in detection of *P. aeruginosa* sequences or other sequences  
CC of *Pseudomonas* species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC Seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 191 AA;  
  
Query Match 69.2%; Score 18; DB 7; Length 191;  
Best Local Similarity 20.0%; Pred. No. 3;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXHC 10  
Db 49 CSTAASATSC 58  
  
RESULT 12  
ADP30921  
ID ADP30921 standard; protein; 228 AA.  
XX  
XX  
AC ADP30921;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
XX Human secreted protein SEQ ID #1688.  
DE  
DE  
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
XX  
XX Homo sapiens.  
OS  
XX WO2004035732-A2.  
XX  
XX 29-APR-2004.  
PD  
XX  
PF 28-AUG-2003; 2003WO-US026780.  
XX  
XX 29-AUG-2002; 2002US-0406576P.  
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PR 29-AUG-2002; 2002US-0406611P.  
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PR 29-AUG-2002; 2002US-0406640P.  
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PR 29-AUG-2002; 2002US-0406646P.  
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PR 29-AUG-2002; 2002US-0406655P.  
PR 29-AUG-2002; 2002US-0406666P.  
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PR 17-SEP-2002; 2002US-0410948P.  
PR 17-SEP-2002; 2002US-0410949P.  
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PR 19-MAY-2003; 2003US-0471306P.  
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PR 09-JUN-2003; 2003US-0476609P.  
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PR 08-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486446P.  
PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.  
XX  
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.  
XX  
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kothakota S, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX  
XX WPI; 2004-348438/32.  
DR  
XX  
XX New nucleic acid molecule for diagnosing, preventing or treating diseases

PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
PS Claim 1; SEQ ID NO 2919; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPOWEB and is not in the specification.  
XX  
SQ Sequence 228 AA;  
  
Query Match 69.2%; Score 18; DB 8; Length 228;  
Best Local Similarity 20.0%; Pred. No. 3.1;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 CXXXXXXXC 10  
Db 54 CATAAATTAC 63  
  
RESULT 13  
ADP31485  
ID ADP31485 standard; protein; 252 AA.  
AC ADP31485;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human secreted protein SEQ ID #252.  
XX  
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
XX  
OS Homo sapiens.  
XX  
PN WO2004035732-A2.  
XX  
PD 29-APR-2004.  
XX  
PF 28-AUG-2003; 2003WO-US026780.  
XX  
PR 29-AUG-2002; 2002US-0406576P.  
PR 29-AUG-2002; 2002US-0406579P.  
PR 29-AUG-2002; 2002US-0406585P.  
PR 29-AUG-2002; 2002US-0406588P.  
PR 29-AUG-2002; 2002US-0406608P.  
PR 29-AUG-2002; 2002US-0406611P.  
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PR 29-AUG-2002; 2002US-0406640P.  
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PR 29-AUG-2002; 2002US-0406646P.  
PR 29-AUG-2002; 2002US-0406653P.  
PR 29-AUG-2002; 2002US-0406655P.  
PR 29-AUG-2002; 2002US-0406666P.  
PR 17-SEP-2002; 2002US-0410947P.  
PR 17-SEP-2002; 2002US-0410947P.  
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PR 17-SEP-2002; 2002US-0410961P.  
PR 17-SEP-2002; 2002US-0410962P.  
PR 17-SEP-2002; 2002US-0411019P.  
PR 17-SEP-2002; 2002US-0411022P.

PR 17-SEP-2002; 2002US-0411023P.  
PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411035P.  
PR 17-SEP-2002; 2002US-0411037P.  
PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
PR 17-SEP-2002; 2002US-0411046P.  
PR 17-SEP-2002; 2002US-0411048P.  
PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411055P.  
PR 17-SEP-2002; 2002US-0411073P.  
PR 17-SEP-2002; 2002US-0411082P.  
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PR 17-SEP-2002; 2002US-0411111P.  
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PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463716P.  
PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
PR 02-MAY-2003; 2003US-0467201P.  
PR 02-MAY-2003; 2003US-0467203P.  
PR 02-MAY-2003; 2003US-0467230P.  
PR 19-MAY-2003; 2003US-0471306P.  
PR 19-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 22-MAY-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
PR 09-JUN-2003; 2003US-0476641P.  
PR 08-JUL-2003; 2003US-0485218P.  
PR 08-JUL-2003; 2003US-0485223P.  
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PR 08-JUL-2003; 2003US-0485325P.  
PR 14-JUL-2003; 2003US-0486446P.  
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PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493573P.  
PR 08-AUG-2003; 2003US-0493577P.  
XX  
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.  
PA Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RP, Huang MM, Korhakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX  
XX WPI; 2004-348438/32.  
XX  
XX New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
XX Claim 1; SEQ ID NO 3483; 428pp; English.  
PS  
XX The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPOWEB and is not in the specification.  
XX  
SQ Sequence 252 AA;  
  
Query Match 69.2%; Score 18; DB 8; Length 252;  
Best Local Similarity 20.0%; Pred. No. 3.2;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
Qy 1 CXXXXXXXC 10  
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Db          210 CTTTTATAC 219
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ID ADP30479 standard; protein; 258 AA.
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AC ADP30479;
DT
DT 12-AUG-2004 (first entry)
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DE Human secreted protein SEQ ID #1246.
XX
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX
OS Homo sapiens.
XX
XX WO2004035732-A2.
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PD 29-APR-2004.
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XX 28-AUG-2003; 2003WO-US026780.
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XX 29-AUG-2002; 2002US-0406576P.
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XX 17-SEP-2002; 2002US-0411035P.
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XX 17-SEP-2002; 2002US-0411055P.
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XX 17-SEP-2002; 2002US-0411111P.
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XX 18-APR-2003; 2003US-0463700P.
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XX 18-APR-2003; 2003US-0463716P.
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XX 18-APR-2003; 2003US-0463732P.
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XX 02-MAY-2003; 2003US-0467199P.
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XX 02-MAY-2003; 2003US-0467201P.
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XX 02-MAY-2003; 2003US-0467203P.
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PR 08-JUL-2003; 2003US-0485224P.
PR 08-JUL-2003; 2003US-0485325P.
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PR 08-AUG-2003; 2003US-0493341P.
PR 08-AUG-2003; 2003US-0493370P.
PR 08-AUG-2003; 2003US-0493573P.
PR 08-AUG-2003; 2003US-0493577P.
XX
XX (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA
XX
XX Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;
PI Halenbeck RP, Huang MM, Kothakota S, Haishan L, Linnemann T;
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
XX
XX WPI; 2004-348438/32.
XX
XX New nucleic acid molecule for diagnosing, preventing or treating diseases
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,
PT genetic, bacterial and viral diseases.
XX
XX Claim 1; SEQ ID NO 2477; 428pp; English.
XX
XX The present invention relates to an isolated nucleic acid molecule
CC encoding a polypeptide which is believed to be cytostatic,
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The
CC composition and methods are useful for diagnosing, preventing and
CC treating diseases such as proliferative (e.g. cancer), inflammatory,
CC immune, metabolic, genetic, bacterial and viral diseases. The present
CC sequence represents a human secreted protein. The present sequence is
CC available on WIPOWEB and is not in the specification.
XX
XX Sequence 258 AA;
SQ
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Best Local Similarity 20.0%; Pred No. 3.2;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 CXXXXXXXC 10
Db 237 CTTTTATAC 246
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ID ADP31412 standard; protein; 264 AA.
XX
XX ADP31412;
AC ADP31412;
XX
DT 12-AUG-2004 (first entry)
DE
DE Human secreted protein SEQ ID #2179.
XX
XX Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
KW cancer; inflammatory; immune; human secreted protein.
XX
XX Homo sapiens.
XX
XX WO2004035732-A2.
XX
XX 29-APR-2004.
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PF 28-AUG-2003; 2003WO-US026780.  
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PR 29-AUG-2002; 2002US-0406555P.  
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PR 17-SEP-2002; 2002US-0411024P.  
PR 17-SEP-2002; 2002US-0411032P.  
PR 17-SEP-2002; 2002US-0411035P.  
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PR 17-SEP-2002; 2002US-0411041P.  
PR 17-SEP-2002; 2002US-0411045P.  
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PR 17-SEP-2002; 2002US-0411052P.  
PR 17-SEP-2002; 2002US-0411055P.  
PR 17-SEP-2002; 2002US-0411073P.  
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PR 18-APR-2003; 2003US-0463700P.  
PR 18-APR-2003; 2003US-0463708P.  
PR 18-APR-2003; 2003US-0463716P.  
PR 18-APR-2003; 2003US-0463732P.  
PR 02-MAY-2003; 2003US-0467199P.  
PR 02-MAY-2003; 2003US-0467201P.  
PR 02-MAY-2003; 2003US-0467203P.  
PR 02-MAY-2003; 2003US-0467230P.  
PR 19-MAY-2003; 2003US-0471306P.  
PR 22-MAY-2003; 2003US-0471336P.  
PR 22-MAY-2003; 2003US-0472420P.  
PR 09-JUN-2003; 2003US-0472430P.  
PR 09-JUN-2003; 2003US-0476609P.  
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PR 08-JUL-2003; 2003US-0485218P.  
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PR 14-JUL-2003; 2003US-0486480P.  
PR 15-JUL-2003; 2003US-0486891P.  
PR 15-JUL-2003; 2003US-0486960P.  
PR 08-AUG-2003; 2003US-0493341P.  
PR 08-AUG-2003; 2003US-0493370P.  
PR 08-AUG-2003; 2003US-0493572P.  
PR 08-AUG-2003; 2003US-0493577P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

XX  
PA  
XX

PI Williams LT, Chu K, Lee E, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kothakota S, Haishan L, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX WPI; 2004-348438/32.  
XX New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX Claim 1; SEQ ID NO 3410; 428pp; English.  
XX The present invention relates to an isolated nucleic acid molecule  
CC encoding a polypeptide which is believed to be cytostatic,  
CC antiinflammatory, immunosuppressive, antibacterial and virucidal. The  
CC composition and methods are useful for diagnosing, preventing and  
CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
CC immune, metabolic, genetic, bacterial and viral diseases. The present  
CC sequence represents a human secreted protein. The present sequence is  
CC available on WIPOWEB and is not in the specification.  
XX Sequence 264 AA;  
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Query Match 69.2%; Score 18; DB 8; Length 264;  
Best Local Similarity 20.0%; Pred. NO. 3.2;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXC 10  
DB 186 CATAAATTC 195

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Job time : 71.6226 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

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Listing first 45 summaries

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2	18	69.2	167	4	US-09-252-991A-17897
3	18	69.2	191	4	US-09-252-991A-25365
4	18	69.2	438	4	US-09-252-991A-31307
5	18	69.2	777	4	US-09-270-767-44409
6	18	69.2	801	1	US-07-906-349A-6
7	18	69.2	1388	4	US-09-463-048A-6
8	18	69.2	1497	4	US-09-060-854B-2
9	18	69.2	1917	4	US-09-627-650B-5
10	18	69.2	1917	4	US-09-436-063C-5
11	17	65.4	45	2	US-08-824-379-3
12	17	65.4	48	5	PCUS-996-01720-9
13	17	65.4	150	4	US-09-252-991A-31728
14	17	65.4	156	4	US-09-252-991A-20612
15	17	65.4	169	4	US-09-252-991A-20344
16	17	65.4	169	4	US-09-252-991A-24301
17	17	65.4	172	4	US-09-252-991A-23050
18	17	65.4	191	4	US-09-252-991A-19331
19	17	65.4	200	4	US-09-252-991A-22497
20	17	65.4	204	4	US-09-252-991A-31049
21	17	65.4	222	4	US-09-252-991A-26487
22	17	65.4	229	4	US-09-252-991A-25247
23	17	65.4	243	4	US-09-252-991A-25814
24	17	65.4	281	4	US-09-252-991A-23199
25	17	65.4	314	4	US-09-252-991A-31368
26	17	65.4	341	2	US-08-209-521-11
27	17	65.4	414	4	US-09-252-991A-25096

28	17	65.4	908	4	US-08-714-741-44	Sequence 44, Appl
29	17	65.4	1076	4	US-10-140-002-219	Sequence 219, Appl
30	17	65.4	1400	3	US-08-630-915A-37	Sequence 37, Appl
31	17	65.4	1400	4	US-09-879-957-37	Sequence 37, Appl
32	17	65.4	1461	4	US-10-142-231-86	Sequence 86, Appl
33	17	65.4	1652	4	US-09-627-650B-1	Sequence 1, Appl
34	17	65.4	1652	4	US-09-436-063C-1	Sequence 1, Appl
35	17	65.4	2508	4	US-09-627-650B-7	Sequence 7, Appl
36	17	65.4	2508	4	US-09-436-063C-7	Sequence 7, Appl
37	17	65.4	2544	4	US-09-627-650B-3	Sequence 3, Appl
38	17	65.4	2544	4	US-09-436-063C-3	Sequence 3, Appl
39	17	65.4	2601	4	US-09-627-650B-9	Sequence 9, Appl
40	17	65.4	2601	4	US-09-436-063C-9	Sequence 9, Appl
41	17	65.4	2732	4	US-09-086-436-30	Sequence 30, Appl
42	16	61.5	12	4	US-10-029-212-1	Sequence 1, Appl
43	16	61.5	20	4	US-09-419-381-115	Sequence 115, Appl
44	16	61.5	24	3	US-08-482-085B-92	Sequence 92, Appl
45	16	61.5	24	3	US-08-900-230-27	Sequence 27, Appl

## ALIGNMENTS

## RESULT 1

US-08-727-688-23

; Sequence 23, Application US/08727688

; Patent No. 5919638

; GENERAL INFORMATION:

; APPLICANT: Russell, John C.

; TITLE OF INVENTION: Reagents and Methods for Detecting Prostate Tumors

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Road D377/AP6D

; CITY: Abbott Park

; STATE: IL

; COUNTRY: USA

; ZIP: 60064

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/727,688

; FILING DATE:

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Porembski, Priscilla E.

; REGISTRATION NUMBER: 33,207

; REFERENCE/DOCKET NUMBER: 5967.US.01

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (847) 937-0378

; TELEFAX: (847) 938-2623

; TELEX:

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLESCALE TYPE: No. 5919638e

; US-08-727-688-23

Query Match 69.2%; Score 18; DB 2; Length 14;

Best Local Similarity 20.0%; Pred. No. 0.17;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXC 10

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Db          3 C$SSSSSSAC 12

RESULT 2
US-09-252-991A-17897
; Sequence 17897, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17897
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17897

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Qy      1 CXXXXXXXC 10
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Db      60 CSTSTSTTSC 69

RESULT 3
US-09-252-991A-25365
; Sequence 25365, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25365
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25365

Query Match          69.2%; Score 18; DB 4; Length 191;
Best Local Similarity 20.0%; Pred. No. 0.29;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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RESULT 4
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; Sequence 31307, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
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; LENGTH: 438
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31307

Query Match          69.2%; Score 18; DB 4; Length 438;
Best Local Similarity 20.0%; Pred. No. 0.34;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31307
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31307

Query Match          69.2%; Score 18; DB 4; Length 438;
Best Local Similarity 20.0%; Pred. No. 0.34;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1 CXXXXXXXC 10
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Db      56 CSAATATSTC 65

RESULT 5
US-09-270-767-44409
; Sequence 44409, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44409
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44409

Query Match          69.2%; Score 18; DB 4; Length 777;
Best Local Similarity 20.0%; Pred. No. 0.39;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy      1 CXXXXXXXC 10
      |
Db      729 CSTSSSSSSC 738

RESULT 6
US-07-906-349A-6
; Sequence 6, Application US/07906349A
; Patent No. 5434064
; GENERAL INFORMATION:
; APPLICANT: Schlessinger, Joseph
; APPLICANT: Skolnik, Edward Y.
; APPLICANT: Margolis, Benjamin L.
; TITLE OF INVENTION: A NOVEL EXPRESSION-CLONING METHOD FOR
; IDENTIFYING TARGET PROTEINS FOR EUKARYOTIC TYROSINE KINASES AND
; TARGET PROTEINS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/906,349A
/ FILING DATE: 30-JUN-1992
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/643,237
/ FILING DATE: 18-JAN-1991
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 801 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-07-906-349A-6

Query Match          69.2%; Score 18; DB 1; Length 801;
Best Local Similarity 20.0%; Pred. No. 0.39;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
DB      608 CTTTTTTC 617

RESULT 7
US-09-463-048A-6
/ Sequence 6, Application US/09463048A
/ Patent No. 6630619
/ GENERAL INFORMATION:
/ APPLICANT: Commonwealth Scientific and Industrial Research Organisation
/ TITLE OF INVENTION: Toxin Genes from the Bacteria Xenorhabdus nematophilus and Photoc
/ FILE OF INVENTION: luminescens
/ FILE REFERENCE: 050179-0076
/ CURRENT APPLICATION NUMBER: US/09/463,048A
/ CURRENT FILING DATE: 2002-12-13
/ PRIOR APPLICATION NUMBER: PCT/AU98/00562
/ PRIOR FILING DATE: 1998-07-17
/ PRIOR APPLICATION NUMBER: PO 8088
/ PRIOR FILING DATE: 1997-07-17
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 6
/ LENGTH: 1388
/ TYPE: PRT
/ ORGANISM: Photorhabdus luminescens
/ US-09-463-048A-6

Query Match          69.2%; Score 18; DB 4; Length 1388;
Best Local Similarity 20.0%; Pred. No. 0.43;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
DB      8 CTAATAATTC 17

RESULT 8
US-09-060-854B-2
/ Sequence 2, Application US/09060854B
/ Patent No. 6642011
/ GENERAL INFORMATION:
/ APPLICANT: Retell, David Aaron
/ TITLE OF INVENTION: Human Protease and Use of Such Protease for Pharmaceutical
/ TITLE OF INVENTION: Applications and for Reducing the Allergenicity of No. 6642011-H
/ TITLE OF INVENTION: Proteins
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/ FILE REFERENCE: GC532
/ CURRENT APPLICATION NUMBER: US/09/060,854B
/ CURRENT FILING DATE: 1998-04-15
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSEQ for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 1497
/ TYPE: PRT
/ ORGANISM: B. amyloliquefaciens
/ US-09-060-854B-2

Query Match          69.2%; Score 18; DB 4; Length 1497;
Best Local Similarity 20.0%; Pred. No. 0.44;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
DB      30 CAATTAATAC 39

RESULT 9
US-09-627-650B-5
/ Sequence 5, Application US/09627650B
/ Patent No. 6406872
/ GENERAL INFORMATION:
/ APPLICANT: Bamber, Bruce
/ TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
/ TITLE OF INVENTION: Methods Related Thereto
/ FILE REFERENCE: 21101.0009U3
/ CURRENT APPLICATION NUMBER: US/09/627,650B
/ CURRENT FILING DATE: 2000-07-28
/ PRIOR APPLICATION NUMBER: 09/436,063
/ PRIOR FILING DATE: 1999-11-08
/ PRIOR APPLICATION NUMBER: 60/107,727
/ PRIOR FILING DATE: 1998-11-09
/ NUMBER OF SEQ ID NOS: 50
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 1917
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
/ US-09-627-650B-5

Query Match          69.2%; Score 18; DB 4; Length 1917;
Best Local Similarity 20.0%; Pred. No. 0.46;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      1 CXXXXXXXXC 10
DB      1049 CAATATATC 1058

RESULT 10
US-09-436-063C-5
/ Sequence 5, Application US/09436063C
/ Patent No. 6407210
/ GENERAL INFORMATION:
/ APPLICANT: Bamber, Bruce
/ TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
/ TITLE OF INVENTION: Methods Related Thereto
/ FILE REFERENCE: P-1095corrected
/ CURRENT APPLICATION NUMBER: US/09/436,063C
/ CURRENT FILING DATE: 1999-11-08
/ PRIOR APPLICATION NUMBER: 60/107727
/ PRIOR FILING DATE: 1998-11-09
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 1917
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
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US-09-436-063C-5

Query Match 69.2%; Score 18; DB 4; Length 1917;  
 Best Local Similarity 20.0%; Pred. No. 0.46;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
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 Db 1049 CAAATATATC 1058

RESULT 11  
 US-08-824-379-3  
 ; Sequence 3, Application US/08824379  
 ; Patent No. 5885801  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rao, A. Gururaj  
 ; TITLE OF INVENTION: High Threonine Derivatives of  
 ; MOLECULE TYPE: Alpha-Hordothionin  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pioneer Hi-Bred International, Inc.  
 ; STREET: 700 Capital Square, 400 Locust Street  
 ; CITY: Des Moines  
 ; STATE: Iowa  
 ; COUNTRY: United States of America  
 ; ZIP: 50309  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/824,379  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/459,180  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Simon, Soma G.  
 ; REGISTRATION NUMBER: 37,444  
 ; REFERENCE/DOCKET NUMBER: 354-US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 515-248-4896  
 ; TELEFAX: 515-248-4844  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 45 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; US-08-824-379-3

Query Match 65.4%; Score 17; DB 2; Length 45;  
 Best Local Similarity 20.0%; Pred. No. 0.99;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
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 Db 16 CTTTATTTC 25

RESULT 12  
 PCT-US96-01720-9  
 ; Sequence 9, Application PC/TUS9601720  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN  
 ; NUMBER OF SEQUENCES: 11  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

US-09-436-063C-5

Query Match 69.2%; Score 18; DB 4; Length 1917;  
 Best Local Similarity 20.0%; Pred. No. 0.46;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
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 Db 1049 CAAATATATC 1058

RESULT 11  
 US-08-824-379-3  
 ; Sequence 3, Application US/08824379  
 ; Patent No. 5885801  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rao, A. Gururaj  
 ; TITLE OF INVENTION: High Threonine Derivatives of  
 ; MOLECULE TYPE: Alpha-Hordothionin  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pioneer Hi-Bred International, Inc.  
 ; STREET: 700 Capital Square, 400 Locust Street  
 ; CITY: Des Moines  
 ; STATE: Iowa  
 ; COUNTRY: United States of America  
 ; ZIP: 50309  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/824,379  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/459,180  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Simon, Soma G.  
 ; REGISTRATION NUMBER: 37,444  
 ; REFERENCE/DOCKET NUMBER: 354-US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 515-248-4896  
 ; TELEFAX: 515-248-4844  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 45 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; US-08-824-379-3

Query Match 65.4%; Score 17; DB 2; Length 45;  
 Best Local Similarity 20.0%; Pred. No. 0.99;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
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 Db 16 CTTTATTTC 25

RESULT 12  
 PCT-US96-01720-9  
 ; Sequence 9, Application PC/TUS9601720  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: MODIFIED-AFFINITY STREPTAVIDIN  
 ; NUMBER OF SEQUENCES: 11  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

US-09-252-991A-20612

Query Match 65.4%; Score 17; DB 4; Length 150;  
 Best Local Similarity 20.0%; Pred. No. 1.3;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
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 Db 35 CASAAAISSC 44

RESULT 14  
 US-09-252-991A-20612  
 ; Sequence 20612, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 31728  
 ; LENGTH: 150  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 ; US-09-252-991A-31728

Query Match 65.4%; Score 17; DB 5; Length 48;  
 Best Local Similarity 20.0%; Pred. No. 1;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
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 Db 3 CGTTTAAATC 12

RESULT 13  
 US-09-252-991A-31728  
 ; Sequence 31728, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 31728  
 ; LENGTH: 150  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 ; US-09-252-991A-31728

Query Match 65.4%; Score 17; DB 5; Length 48;  
 Best Local Similarity 20.0%; Pred. No. 1;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
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 Db 3 CGTTTAAATC 12

; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20612  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20612

Query Match 65.4%; Score 17; DB 4; Length 156;  
Best Local Similarity 20.0%; Pred. No. 1.3;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
DB 78 CSTTAGSTSC 87

RESULT 15  
US-09-252-991A-20344  
; Sequence 20344, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 20344  
; LENGTH: 169  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-20344

Query Match 65.4%; Score 17; DB 4; Length 169;  
Best Local Similarity 20.0%; Pred. No. 1.3;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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DB 17 CSTSSARATC 26

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 13:08:04 ; Search time 74.5283 Seconds  
(without alignments)  
48.267 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62

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Searched: 1599051 seqs, 359727711 residues

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Maximum Match 100%  
Listing first 45 summaries

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- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
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- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
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- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	69.2	33	16	US-10-697-399-10 Sequence 10, Appl
2	18	69.2	37	16	US-10-380-927-7 Sequence 7, Appl
3	18	69.2	328	15	US-10-296-115-800 Sequence 800, App
4	18	69.2	429	15	US-10-424-955A-28 Sequence 28, Appl
5	18	69.2	598	16	US-10-437-963-162631 Sequence 162631, Sequence 86, Appl
6	18	69.2	630	10	US-09-791-279-86 Sequence 539, App
7	18	69.2	647	14	US-10-184-644-539 Sequence 539, App
8	18	69.2	647	14	US-10-184-634-539 Sequence 539, App
9	18	69.2	653	10	US-09-374-046A-20 Sequence 20, Appl
10	18	69.2	653	14	US-10-102-524-1851 Sequence 1851, Ap
11	18	69.2	653	14	US-10-331-496A-81 Sequence 81, Appl
12	18	69.2	653	14	US-10-616-263-20 Sequence 20, Appl
13	18	69.2	693	14	US-10-123-155-499 Sequence 499, App

14	18	69.2	693	14	US-10-146-731-499	Sequence 499, App
15	18	69.2	693	14	US-10-140-472-499	Sequence 499, App
16	18	69.2	693	14	US-10-141-761-499	Sequence 499, App
17	18	69.2	693	14	US-10-142-885-499	Sequence 499, App
18	18	69.2	693	14	US-10-158-790-499	Sequence 499, App
19	18	69.2	693	14	US-10-137-871-499	Sequence 499, App
20	18	69.2	693	14	US-10-140-923-499	Sequence 499, App
21	18	69.2	693	14	US-10-141-756-499	Sequence 499, App
22	18	69.2	693	14	US-10-141-759-499	Sequence 499, App
23	18	69.2	693	14	US-10-140-805-499	Sequence 499, App
24	18	69.2	693	14	US-10-140-864-499	Sequence 499, App
25	18	69.2	693	15	US-10-142-426-499	Sequence 499, App
26	18	69.2	733	16	US-10-437-963-129702	Sequence 129702,
27	18	69.2	735	14	US-10-184-644-167	Sequence 167, App
28	18	69.2	735	14	US-10-184-634-167	Sequence 167, App
29	18	69.2	755	14	US-10-123-155-153	Sequence 153, App
30	18	69.2	755	14	US-10-146-731-153	Sequence 153, App
31	18	69.2	755	14	US-10-140-472-153	Sequence 153, App
32	18	69.2	755	14	US-10-141-761-153	Sequence 153, App
33	18	69.2	755	14	US-10-142-885-153	Sequence 153, App
34	18	69.2	755	14	US-10-158-790-153	Sequence 153, App
35	18	69.2	755	14	US-10-137-871-153	Sequence 153, App
36	18	69.2	755	14	US-10-140-923-153	Sequence 153, App
37	18	69.2	755	14	US-10-141-756-153	Sequence 153, App
38	18	69.2	755	14	US-10-141-759-153	Sequence 153, App
39	18	69.2	755	14	US-10-140-805-153	Sequence 153, App
40	18	69.2	755	14	US-10-140-864-153	Sequence 153, App
41	18	69.2	755	15	US-10-142-426-153	Sequence 153, App
42	18	69.2	823	14	US-10-123-155-379	Sequence 379, App
43	18	69.2	823	14	US-10-146-731-379	Sequence 379, App
44	18	69.2	823	14	US-10-140-472-379	Sequence 379, App
45	18	69.2	823	14	US-10-141-761-379	Sequence 379, App

ALIGNMENTS

RESULT 1

US-10-697-399-10  
; Sequence 10, Application US/10697399  
; Publication No. US20040162413A1  
; GENERAL INFORMATION:  
; APPLICANT: Watkins, Jeffrey D.  
; APPLICANT: Huse, William D.  
; APPLICANT: Vasserot, Alain P.  
; APPLICANT: Marquis, David P.  
; APPLICANT: Smith, Eric P.  
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity  
; FILE REFERENCE: AME-08122  
; CURRENT APPLICATION NUMBER: US/10/697,399  
; CURRENT FILING DATE: 2003-10-30  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 33  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-697-399-10

Query Match 69.2%; Score 18; DB 16; Length 33;  
Best Local Similarity 20.0%; Pred. No. 2;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10

Db 24 CTATTAAAC 33

RESULT 2

US-10-380-927-7  
; Sequence 7, Application US/10380927

; Publication No. US20040110165A1  
; GENERAL INFORMATION:  
; APPLICANT: Larry W. Kwak  
; APPLICANT: Arya Biragyn  
; TITLE OF INVENTION: VIRAL CHEMOKINE-ANTIGEN FUSION PROTEINS  
; FILE REFERENCE: 14014.0381U2  
; CURRENT APPLICATION NUMBER: US/10/380,927  
; CURRENT FILING DATE: 2003-12-04  
; PRIOR APPLICATION NUMBER: PCT/US01/29075  
; PRIOR FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: 60/233,067  
; PRIOR FILING DATE: 2000-09-15  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence = Note  
; OTHER INFORMATION: Synthetic Construct  
US-10-380-927-7

Query Match 69.2%; Score 18; DB 16; Length 37;  
Best Local Similarity 20.0%; Pred. No. 2.1;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10  
Db 7 CTTTATTTC 16

## RESULT 3

; Sequence 800, Application US/10296115  
; Publication No. US20040053248A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq Inc  
; TITLE OF INVENTION: No. US20040053248A1el Nucleic Acids and Polypeptides  
; FILE REFERENCE: 784PCT  
; CURRENT APPLICATION NUMBER: US/10/296,115  
; CURRENT FILING DATE: 2002-11-18  
; PRIOR APPLICATION NUMBER: US09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 1478  
; SEQ ID NO 800  
; LENGTH: 328  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(328)  
; OTHER INFORMATION: Xaa = any amino acid or other as shown in Table 3  
US-10-296-115-800

Query Match 69.2%; Score 18; DB 15; Length 328;  
Best Local Similarity 20.0%; Pred. No. 3.1;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10  
Db 63 CAAAAAAAC 72

## RESULT 4

; Sequence 28, Application US/10424955A  
; Publication No. US20040014658A1  
; GENERAL INFORMATION:  
; APPLICANT: PROCHON BIOTECH LTD  
; APPLICANT: Bogen, Oren

; APPLICANT: Yavon, Avner  
; APPLICANT: Adar, Rivka  
; TITLE OF INVENTION: ACTIVE VARIANTS OF FGF WITH IMPROVED SPECIFICITY  
; FILE REFERENCE: 139380 IL  
; CURRENT APPLICATION NUMBER: US/10/424,955A  
; CURRENT FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: 139380 IL  
; PRIOR FILING DATE: 2000-10-31  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 28  
; LENGTH: 429  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-424-955A-28

Query Match 69.2%; Score 18; DB 15; Length 429;  
Best Local Similarity 20.0%; Pred. No. 3.2;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10  
Db 397 CATTTTTAC 406

## RESULT 5

; Sequence 162631, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 162631  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_61704C.1.pep  
US-10-437-963-162631

Query Match 69.2%; Score 18; DB 16; Length 598;  
Best Local Similarity 20.0%; Pred. No. 3.4;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10  
Db 148 CTASSSSSSC 157

## RESULT 6

; Sequence 86, Application US/09791279  
; Publication No. US20030050456A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogeli, Gabriel  
; APPLICANT: Wood, Linda S.  
; APPLICANT: Parodi, Luis  
; APPLICANT: Lind, Peter  
; TITLE OF INVENTION: No. US20030050456A1el G Protein-Coupled Receptors  
; FILE REFERENCE: 00048.US1  
; CURRENT APPLICATION NUMBER: US/09/791,279

; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/184,715  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184725  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,712  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,606  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,602  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,604  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,822  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,710  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,689  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,690  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/184,716  
; PRIOR FILING DATE: 2000-02-24  
; NUMBER OF SEQ ID NOS: 220  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 86  
; LENGTH: 630  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
US-09-791-273-86

Query Match 69.2%; Score 18; DB 10; Length 630;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
DB 128 CTTTTTAAC 137

RESULT 7  
US-10-184-644-539  
; Sequence 539, Application US/10184644  
; Publication No. US2003004930A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC227  
; CURRENT APPLICATION NUMBER: US/10/184,644  
; CURRENT FILING DATE: 2002-06-28  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 539  
; LENGTH: 647  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-184-644-539

Query Match 69.2%; Score 18; DB 14; Length 647;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
DB 288 CTTAAAAAAC 297

RESULT 8  
US-10-184-634-539  
; Sequence 539, Application US/10184634  
; Publication No. US2003006864A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430RIC217  
; CURRENT APPLICATION NUMBER: US/10/184,634  
; CURRENT FILING DATE: 2002-06-28  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 539  
; LENGTH: 647  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-184-634-539

Query Match 69.2%; Score 18; DB 14; Length 647;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
DB 288 CTTAAAAAAC 297

RESULT 9  
US-09-374-046A-20  
; Sequence 20, Application US/09374046A  
; Publication No. US20030096951A1  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: McCoy, John M.  
; APPLICANT: Lavallie, Edward R.  
; APPLICANT: Collins-Racie, Lisa A.  
; APPLICANT: Evans, Cheryl  
; APPLICANT: Merberg, David  
; APPLICANT: Treacy, Maurice  
; APPLICANT: Agostino, Michael J.  
; APPLICANT: Steining, Robert J.  
; APPLICANT: Spaulding, Vikki  
; APPLICANT: Wong, Gordon G.  
; APPLICANT: Clark, Hilary  
; APPLICANT: Fechtel, Kim  
; APPLICANT: Genetics Institute, Inc.  
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
; FILE REFERENCE: GI 6075-83A  
; CURRENT APPLICATION NUMBER: US/09/374,046A  
; CURRENT FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 240  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20  
; LENGTH: 653  
; TYPE: PRF  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: UNSURE  
 ; LOCATION: (114)  
 ; FEATURE:  
 ; NAME/KEY: UNSURE  
 ; LOCATION: (247)  
 ; FEATURE:  
 ; NAME/KEY: UNSURE  
 ; LOCATION: (290)  
 ; FEATURE:  
 ; NAME/KEY: UNSURE  
 ; LOCATION: (601)  
 ; FEATURE:  
 ; NAME/KEY: UNSURE  
 ; LOCATION: (604)  
 ; US-09-374-046A-20

Query Match 69.2%; Score 18; DB 10; Length 653;  
 Best Local Similarity 20.0%; Pred. No. 3.5;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10  
 Db 173 CAAAAAAAC 182

## RESULT 10

US-10-102-524-1851  
 ; Sequence 1851, Application US/10102524  
 ; Publication No. US20030109434A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mannion, Paul A.  
 ; APPLICANT: Algate, Paul A.  
 ; APPLICANT: Gaiger, Alexander  
 ; APPLICANT: Gordon, Brian  
 ; APPLICANT: Harlocker, Susan L.  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
 ; FILE REFERENCE: 210121.572  
 ; CURRENT APPLICATION NUMBER: US/10/102,524  
 ; CURRENT FILING DATE: 2002-03-19  
 ; NUMBER OF SEQ ID NOS: 1863  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1851  
 ; LENGTH: 653  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: variant  
 ; LOCATION: 114,247,290,601,604  
 ; OTHER INFORMATION: Xaa = Any amino acid  
 US-10-102-524-1851

Query Match 69.2%; Score 18; DB 14; Length 653;  
 Best Local Similarity 20.0%; Pred. No. 3.5;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10  
 Db 173 CAAAAAAAC 182

## RESULT 11

US-10-331-496A-81  
 ; Sequence 81, Application US/10331496A  
 ; Publication No. US20030228305A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FRANTZ, GRETCHEN  
 ; APPLICANT: HILLAN, KENNETH J.  
 ; APPLICANT: PHILLIPS, HEIDI S.  
 ; APPLICANT: POLAKIS, PAUL  
 ; APPLICANT: SMITH, VICTORIA  
 ; APPLICANT: SPENCER, SUSAN D.  
 ; APPLICANT: WILLIAMS, P. MICKEY

; APPLICANT: WU, THOMAS D.  
 ; APPLICANT: ZHANG, ZEMIN  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
 ; TITLE OF INVENTION: TREATMENT OF TUMOR  
 ; FILE REFERENCE: P5014R1-PCT  
 ; CURRENT APPLICATION NUMBER: US/10/331,496A  
 ; CURRENT FILING DATE: 2002-12-30  
 ; PRIOR APPLICATION NUMBER: US 60/345,444  
 ; PRIOR FILING DATE: 2002-01-02  
 ; PRIOR APPLICATION NUMBER: US 60/351,885  
 ; PRIOR FILING DATE: 2002-01-25  
 ; PRIOR APPLICATION NUMBER: US 60/360,066  
 ; PRIOR FILING DATE: 2002-02-25  
 ; PRIOR APPLICATION NUMBER: US 60/362,004  
 ; PRIOR FILING DATE: 2002-03-05  
 ; PRIOR APPLICATION NUMBER: US 60/366,869  
 ; PRIOR FILING DATE: 2002-03-20  
 ; PRIOR APPLICATION NUMBER: US 60/366,284  
 ; PRIOR FILING DATE: 2002-03-21  
 ; PRIOR APPLICATION NUMBER: US 60/368,679  
 ; PRIOR FILING DATE: 2002-03-28  
 ; PRIOR APPLICATION NUMBER: US 60/404,809  
 ; PRIOR FILING DATE: 2002-08-19  
 ; PRIOR APPLICATION NUMBER: US 60/405,645  
 ; PRIOR FILING DATE: 2002-08-21  
 ; NUMBER OF SEQ ID NOS: 95  
 ; SEQ ID NO 81  
 ; LENGTH: 653  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapien  
 ; FEATURE:  
 ; NAME/KEY: X  
 ; LOCATION: 114, 247, 290, 601, 604  
 ; OTHER INFORMATION: Unknown base  
 US-10-331-496A-81

Query Match 69.2%; Score 18; DB 14; Length 653;  
 Best Local Similarity 20.0%; Pred. No. 3.5;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10  
 Db 173 CAAAAAAAC 182

## RESULT 12

US-10-616-263-20  
 ; Sequence 20, Application US/10616263  
 ; Publication No. US20040038276A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jacobs, Kenneth  
 ; APPLICANT: McCoy, John M.  
 ; APPLICANT: Lavallie, Edward R.  
 ; APPLICANT: Collins-Racie, Lisa A.  
 ; APPLICANT: Evans, Cheryl  
 ; APPLICANT: Merberg, David  
 ; APPLICANT: Treacy, Maurice  
 ; APPLICANT: Agostino, Michael J.  
 ; APPLICANT: Steinhinger II, Robert J.  
 ; APPLICANT: Spaulding, Vikki  
 ; APPLICANT: Wong, Gordon G.  
 ; APPLICANT: Clark, Hilary  
 ; APPLICANT: Rehtel, Kim  
 ; APPLICANT: Genetics Institute, Inc.

; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
 ; FILE REFERENCE: 00766.000103.5  
 ; CURRENT APPLICATION NUMBER: US/10/616,263  
 ; CURRENT FILING DATE: 2003-07-08  
 ; NUMBER OF SEQ ID NOS: 240  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 20  
 ; LENGTH: 653  
 ; TYPE: PRT

; ORGANISM: Homo sapiens  
; FEATURE: NAME/KEY: UNSURE  
; LOCATION: (114)  
; FEATURE: NAME/KEY: UNSURE  
; LOCATION: (247)  
; FEATURE: NAME/KEY: UNSURE  
; LOCATION: (290)  
; FEATURE: NAME/KEY: UNSURE  
; LOCATION: (601)  
; FEATURE: NAME/KEY: UNSURE  
; LOCATION: (604)  
US-10-616-263-20

Query Match 69.2%; Score 18; DB 15; Length 653;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
DB 173 CAAAAAAAC 182

## RESULT 13

US-10-123-155-499  
; Sequence 499, Application US/10123155  
; Publication No. US20030068794A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C30  
; CURRENT APPLICATION NUMBER: US/10/123,155  
; CURRENT FILING DATE: 2002-04-15

; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 499  
; LENGTH: 693

; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-123-155-499

Query Match 69.2%; Score 18; DB 14; Length 693;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
DB 613 CAATAAAATC 622

## RESULT 14

US-10-146-731-499

; Sequence 499, Application US/10146731  
; Publication No. US20030129692A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C323  
; CURRENT APPLICATION NUMBER: US/10/146,731

; CURRENT FILING DATE: 2002-05-15  
; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 499

; LENGTH: 693  
; TYPE: DNA

; ORGANISM: Homo Sapien  
US-10-146-731-499

Query Match 69.2%; Score 18; DB 14; Length 693;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
DB 613 CAATAAAATC 622

## RESULT 15

US-10-140-472-499

; Sequence 499, Application US/10140472  
; Publication No. US20030138888A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C168  
; CURRENT APPLICATION NUMBER: US/10/140,472

; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 499

; LENGTH: 693

; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-140-472-499

Query Match 69.2%; Score 18; DB 14; Length 693;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXXC 10  
|  
Db 613 CAATAAAATC 622

Search completed: December 30, 2004, 13:49:59  
Job time : 75.5283 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:59:17 ; Search time 11.5094 Seconds  
(without alignments)  
83.598 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXXC 10  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	69.2	313	2 S59448	hypothetical prote
2	18	69.2	480	2 E75433	hypothetical prote
3	17	65.4	194	2 JQ1560	hypothetical 20.6K
4	17	65.4	220	2 JC4082	coat protein - Cym
5	17	65.4	376	2 AB2920	cobalamin biosynth
6	17	65.4	388	2 C97694	cobalamin biosynth
7	17	65.4	389	2 T23167	hypothetical prote
8	17	65.4	570	2 T37314	probable texin (EC
9	17	65.4	634	2 S33575	dnaK-type molecula
10	17	65.4	942	2 D87803	protein bli-4D [im
11	17	65.4	2704	2 S09118	G surface protein
12	16	61.5	71	2 F84312	hypothetical prote
13	16	61.5	85	2 E70531	hypothetical prote
14	16	61.5	104	2 S51479	drought-induced pr
15	16	61.5	105	2 A71249	hypothetical prote
16	16	61.5	108	2 D72549	hypothetical prote
17	16	61.5	126	2 A23473	chymotrypsin-like
18	16	61.5	129	2 T9498	hypothetical prote
19	16	61.5	133	2 A96746	hypothetical prote
20	16	61.5	147	2 S09762	hypothetical prote
21	16	61.5	153	2 P0103	hypothetical 17K p
22	16	61.5	161	2 T28088	hypothetical prote
23	16	61.5	164	2 JQ1252	hypothetical 16.7K
24	16	61.5	229	2 T34277	hypothetical prote
25	16	61.5	242	2 A45724	pectate lyase (EC
26	16	61.5	244	2 S72219	chymotrypsin B - A
27	16	61.5	251	2 A55035	cysteine-rich prot
28	16	61.5	262	1 JQ1724	E1 membrane glycop
29	16	61.5	263	2 S47537	chymotrypsin (EC 3

30	16	61.5	275	2 G91011	probable elongatio
31	16	61.5	275	2 A85856	probable elongatio
32	16	61.5	275	2 B64986	hypothetical 30.9
33	16	61.5	294	2 T23682	hypothetical prote
34	16	61.5	306	2 C71498	probable yop trans
35	16	61.5	317	2 T00500	probable elicitor
36	16	61.5	321	2 A84792	hypothetical prote
37	16	61.5	349	2 JE0202	paired-box-contain
38	16	61.5	380	2 T04007	hypothetical prote
39	16	61.5	397	2 T26077	hypothetical prote
40	16	61.5	422	2 S41514	RAD52 protein homo
41	16	61.5	473	2 C81039	lipopolysaccharide
42	16	61.5	473	2 C81984	probable lipopolys
43	16	61.5	475	2 T36342	probable glutamate
44	16	61.5	486	2 B86460	hypothetical prote
45	16	61.5	510	2 A55207	glycerol-3-phospha

RESULT 1

S59448  
hypothetical protein YMR206w - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein YM8325.07  
C:Species: Saccharomyces cerevisiae  
C:Date: 30-Nov-1995 #sequence\_revision 23-Feb-1996 #text\_change 09-Jul-2004  
C:Accession: S59448  
R:Odell, C.; Bowman, S.  
submitted to the EMBL Data Library, March 1995  
A:Reference number: S59448  
A:Accession: S59448  
A:Molecule type: DNA  
A:Residues: 1-313 <ODS>  
A:Cross-references: UNIPROT:Q03695; EMBL:Z48755; NID:g736296; PIDN:CAA88648.1; PID:g73631  
C:Experimental source: strain AB972  
C:Genetics:  
A:Gene: MIPS:YMR206w  
A:Cross-references: SGD:S0004819  
A:Map position: 13R

Query Match 69.2%; Score 18; DB 2; Length 313;  
Best Local Similarity 20.0%; Pred. No. 0.49;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy	1	CXXXXXXXXC	10
Db	245	CSSSSSSSSAC	254

RESULT 2

E75433  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: E75433  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; T  
M.; Shen, M.; Vanathean, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: E75433  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-480 <WHI>  
A:Cross-references: UNIPROT:Q9RV87; GB:AE001963; GB:AE000513; NID:g6458869; PIDN:AAF1071  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR1142  
A:Map position: 1  
C:Superfamily: Deinococcus radiodurans hypothetical protein DR1142

Query Match 69.2%; Score 18; DB 2; Length 480;  
Best Local Similarity 20.0%; Pred. No. 0.56;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXC 10  
Db 464 CAAATAAAC 473

RESULT 3  
JQ1560  
hypothetical 20.6K protein - Lymantria dispar nuclear polyhedrosis virus  
N;Alternate names: hypothetical protein 4  
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdNPV  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: JQ1560  
R;Bjornson, R.M.; Rohrmann, G.F.  
J. Gen. Virol. 73, 1499-1504, 1992  
A;Title: Nucleotide sequence of the polyhedron envelope protein gene region of the Lymantria dispar nuclear polyhedrosis virus, LdNPV  
A;Reference number: PQ0339; MUID:92300345; PMID:1607868  
A;Accession: JQ1560  
A;Molecule type: DNA  
A;Residues: 1-194 <BJO>  
A;Cross-references: UNIPROT:P36868; DDBJ:D10836

Query Match 65.4%; Score 17; DB 2; Length 194;  
Best Local Similarity 20.0%; Pred. No. 1.7;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXC 10  
Db 74 CSAATSSSC 83

RESULT 4  
JC4082  
coat protein - Cymbidium mosaic virus  
C;Species: Cymbidium mosaic virus  
C;Date: 21-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C;Accession: JC4082  
R;Ryu, K.H.; Yoon, K.E.; Park, W.M.  
Gene 156, 303-304, 1995  
A;Title: Cloning and sequencing of a cDNA encoding the coat protein of a Korean isolate of Cymbidium mosaic virus  
A;Reference number: JC4082; MUID:95278762; PMID:7758973  
A;Accession: JC4082  
A;Molecule type: mRNA  
A;Residues: 1-220 <RYU>  
A;Cross-references: UNIPROT:Q66152; EMBL:X81051; NID:G897718; PIDN:CAA56941.1; PID:G897718  
A;Note: The authors translated the codon GTG for residue 161 as Leu  
C;Superfamily: potato virus coat protein  
C;Keywords: coat protein

Query Match 65.4%; Score 17; DB 2; Length 220;  
Best Local Similarity 20.0%; Pred. No. 1.8;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXC 10  
Db 166 CSAATLTATC 175

RESULT 5  
AB2920  
cobalamin biosynthetic protein [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C;Species: Agrobacterium tumefaciens  
C;Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C;Accession: AB2920  
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, F.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, A.; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A.; ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A;Reference number: AB2577; MUID:21608550; PMID:11743193  
A;Accession: AB2920  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-376 <KUR>  
A;Cross-references: UNIPROT:Q8UBQ6; GB:AE008688; PIDN:AAL43776.1; PID:G17741313; GSPDB:GN000020; CESP:K01C8  
A;Experimental source: strain C58 (Dupont)  
C;Genetics:  
A;Gene: cbid  
A;Map position: circular chromosome  
C;Superfamily: Methanobacterium cobalamin biosynthesis protein D

Query Match 65.4%; Score 17; DB 2; Length 376;  
Best Local Similarity 20.0%; Pred. No. 2.2;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXC 10  
Db 17 CAAATKAAC 26

RESULT 6  
C97694  
cobalamin biosynthetic protein cbid (PA2908) [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C;Species: Agrobacterium tumefaciens  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: C97694  
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurolo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58  
A;Reference number: A97359; MUID:21608551; PMID:11743194  
A;Accession: C97694  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-388 <KUR>  
A;Cross-references: UNIPROT:Q8UBQ6; GB:AE007869; PIDN:AAK88508.1; PID:G15158019; GSPDB:GN000020; CESP:K01C8  
A;Gene: AGR\_C\_5073  
A;Map position: circular chromosome  
C;Superfamily: Methanobacterium cobalamin biosynthesis protein D

Query Match 65.4%; Score 17; DB 2; Length 388;  
Best Local Similarity 20.0%; Pred. No. 2.2;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXC 10  
Db 29 CAAATKAAC 38

RESULT 7  
T23167  
hypothetical protein K01C8.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T23167  
R;Sims, M.  
submitted to the EMBL Data Library, April 1995  
A;Reference number: Z19702  
A;Accession: T23167  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-389 <MIL>  
A;Cross-references: UNIPROT:Q21081; EMBL:Z49068; PIDN:CAA8855.1; GSPDB:GN000020; CESP:K01C8  
A;Experimental source: clone K01C8  
C;Genetics:  
A;Gene: CESP:K01C8.2  
A;Map position: 2  
A;Introns: 54/2; 146/3; 208/3; 283/1; 379/3

Query Match 65.4%; Score 17; DB 2; Length 389;

Best Local Similarity 20.0%; Pred. No. 2.2; Mismatches 0; Indels 8; Gaps 0;  
Matches 2; Conservative 0

QY 1 CXXXXXXXC 10  
DB 123 CSSSISTSSC 132

RESULT 8  
T37314  
probable kexin (EC 3.4.21.61) - Caenorhabditis elegans (fragment)  
N:Alternate names: blisterase 4  
C:Species: Caenorhabditis elegans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C:Accession: T37314  
R:Thacker, C.; Peters, K.; Strayko, M.; Rose, A.M.  
Genes Dev. 9, 956-971, 1995  
A:Title: The bli-4 locus of Caenorhabditis elegans encodes structurally distinct kex2/su  
A:Reference number: T37314  
A:Accession: T37314  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-570 <THA>  
A:Cross-references: EMBL:L29440; NID:G459702; PIDN:AAA98752.1; PID:G459703  
C:Genetics:  
A:Gene: bli-4  
A:Map position: I  
C:Keywords: alternative splicing; hydrolase; serine proteinase

Query Match 65.4%; Score 17; DB 2; Length 570;  
Best Local Similarity 20.0%; Pred. No. 2.5; Mismatches 0; Indels 8; Gaps 0;  
Matches 2; Conservative 0

QY 1 CXXXXXXXC 10  
DB 311 CTESSSATSC 320

RESULT 9  
S33575  
dnaK-type molecular chaperone precursor, mitochondrial - Leishmania major  
N:Alternate names: heat shock protein 70-related protein; mitochondrial stress protein  
C:Species: Leishmania major  
C:Date: 09-Dec-1997 #sequence\_revision 09-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: S33575; S78090; S05438  
R:Searle, S.; McCrossan, M.V.; Smith, D.F.  
J. Cell Sci. 104, 1091-1100, 1993  
A:Title: Expression of a mitochondrial stress protein in the protozoan parasite Leishman  
A:Reference number: S33575; MUID:93300981; PMID:8314893  
A:Accession: S33575  
A:Molecule type: DNA  
A:Residues: 1-634 <SEA>  
A:Cross-references: UNIPROT:P12076; EMBL:X64137  
R:Smith, D.F.  
submitted to the EMBL Data Library, January 1992  
A:Reference number: S78090  
A:Accession: S78090  
A:Molecule type: DNA  
A:Residues: 1-460,481-500 'OGREBTASENQIRGEFDLSG' 501-634 <SMI>  
A:Cross-references: EMBL:X64137; NID:9311289; PIDN:CAA45498.1; PID:G311290  
R:Searle, S.; Campos, A.J.R.; Coulson, R.M.R.; Spithill, T.W.; Smith, D.F.  
Nucleic Acids Res. 17, 5081-5095, 1989  
A:Title: A family of heat shock protein 70-related genes are expressed in the promastig  
A:Reference number: S05438; MUID:89345072; PMID:2762121  
A:Accession: S05438  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-249 <SEF>  
A:Cross-references: EMBL:X14574; NID:G9561; PIDN:CAA32713.1; PID:G9562  
C:Genetics:  
A:Gene: Lmhp70.1  
A:Genome: nuclear  
C:Function:

A:Description: involved in protein folding and assembling/disassembling of protein comple  
C:Superfamily: heat shock protein 70  
C:Keywords: ATP; mitochondrion; molecular chaperone; stress-induced protein  
F:1-23/Domain: transit peptide (mitochondrion) #status predicted <TNP>  
F:24-634/Product: heat shock protein 70, mitochondrial #status predicted <MAT>

Query Match 65.4%; Score 17; DB 2; Length 634;  
Best Local Similarity 20.0%; Pred. No. 2.6; Mismatches 0; Indels 8; Gaps 0;  
Matches 2; Conservative 0

QY 1 CXXXXXXXC 10  
DB 7 CGSAAASAAC 16

RESULT 10  
D87803  
protein bli-4D [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 21-Jun-2002  
C:Accession: D87803  
R:Anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_eleg  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A:Accession: D87803  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-942 <STO>  
A:Cross-references: GB:chr\_I; PIDN:AAB96754.1; PID:G2773243; GSPDB:GN00019  
C:Genetics:  
A:Gene: bli-4D  
A:Map position: 1  
C:Superfamily: kexin; subtilisin homology

Query Match 65.4%; Score 17; DB 2; Length 942;  
Best Local Similarity 20.0%; Pred. No. 3; Mismatches 0; Indels 8; Gaps 0;  
Matches 2; Conservative 0

QY 1 CXXXXXXXC 10  
DB 683 CTESSSATSC 692

RESULT 11  
S09118  
G surface protein 168 - Paramaecium primaurelia  
C:Species: Paramaecium primaurelia  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004  
C:Accession: S09118  
R:Prat, A.  
J. Mol. Biol. 211, 521-535, 1990  
A:Title: Conserved sequences flank variable tandem repeats in two alleles of the G surfac  
A:Reference number: S09118; MUID:90172419; PMID:2308165  
A:Accession: S09118  
A:Molecule type: DNA  
A:Residues: 1-2704 <PRA>  
A:Cross-references: UNIPROT:P17053; EMBL:X52133; NID:G10049; PIDN:CAA36378.1; PID:G57847;  
C:Genetics:  
A:Genetic code: SGC5  
C:Superfamily: G surface protein

Query Match 65.4%; Score 17; DB 2; Length 2704;  
Best Local Similarity 20.0%; Pred. No. 4.3; Mismatches 0; Indels 8; Gaps 0;  
Matches 2; Conservative 0

QY 1 CXXXXXXXC 10  
DB 1632 CVAATAATTC 1641

## RESULT 12

F84312  
hypothetical protein Vng1598h [imported] - Halobacterium sp. NRC-1  
C;Species: Halobacterium sp. NRC-1  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: F84312  
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo  
Jung, K.H.; Alam, M.; Freitas, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li  
A;Title: Genome sequence of Halobacterium species NRC-1.  
A;Reference number: A84160; MUID:20504483; PMID:11016950  
A;Accession: F84312  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-71 <STO>  
A;Cross-references: UNIPROT:Q9HPK1; GB:AE004437; NID:g10581076; PIDN:AAG19866.1; GSPDB:G  
C;Genetics:  
A;Gene: VNG1598H

Query Match 61.5%; Score 16; DB 2; Length 71;  
Best Local Similarity 20.0%; Pred. No. 5.1;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
DB 30 CSRSVSTSTC 39

## RESULT 13

E70531  
hypothetical protein Rv2706c - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: E70531  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtrold, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998  
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: E70531  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-85 <COL>  
A;Cross-references: UNIPROT:O07207; GB:Z96072; GB:AL123456; NID:g3261793; PIDN:CAB09466.  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: Rv2706c

Query Match 61.5%; Score 16; DB 2; Length 85;  
Best Local Similarity 20.0%; Pred. No. 5.4;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
DB 24 CSATAVAAC 33

## RESULT 14

S51479  
drought-induced protein Di21 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 15-Jul-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S51479; S43176  
R;Gosti, F.; Bertauche, N.; Vartanian, N.; Giraudat, J.  
Mol. Gen. Genet. 246, 10-18, 1995  
A;Title: Abscissic acid-dependent and -independent regulation of gene expression by progra  
A;Reference number: S51478; MUID:95124290; PMID:7823904  
A;Accession: S51479  
A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 1-104 <GOS>

A;Cross-references: UNIPROT:Q39084; EMBL:X78598; NID:g469111; PIDN:CAA55322.1; PID:g46911

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994

C;Genetics:

A;Gene: Di21

C;Superfamily: late embryogenesis-abundant protein leas

Query Match 61.5%; Score 16; DB 2; Length 104;  
Best Local Similarity 20.0%; Pred. No. 5.8;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
DB 14 CSNAGSLSC 23

## RESULT 15

A71249  
hypothetical protein PH0248 - Pyrococcus horikoshii  
C;Species: Pyrococcus horikoshii  
C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 12-Jul-2004  
C;Accession: A71249  
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine, M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi, DNA Res. 5, 55-76, 1998  
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic an  
A;Reference number: A71000; MUID:98344137; PMID:9679194  
A;Accession: A71249  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-105 <KAW>  
A;Cross-references: UNIPROT:O57986; GB:AP000001; NID:g3236128; PIDN:BAA29320.1; PID:g3256  
A;Experimental source: strain OT3  
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C;Genetics:  
A;Gene: PH0248

Query Match 61.5%; Score 16; DB 2; Length 105;  
Best Local Similarity 20.0%; Pred. No. 5.8;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
|  
DB 35 CFTASASLAC 44

Search completed: December 30, 2004, 13:17:10  
Job time : 14.6761 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:57:52 ; Search time 92.2641 Seconds  
(without alignments)  
62.362 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	69.2	213	2 Q96KM3	Q96KM3 homo sapien
2	18	69.2	283	2 Q7PRQ7	Q7PRQ7 anopheles g
3	18	69.2	313	1 YMS8 YEAST	Q03695 saccharomyc
4	18	69.2	357	2 Q6ZDR4	Q6ZDR4 oryza sativ
5	18	69.2	357	2 BA009322	Bad09322 oryza sat
6	18	69.2	480	2 Q9RV87	Q9RV87 deinococcus
7	18	69.2	653	2 Q8IXM8	Q8IXM8 homo sapien
8	17	65.4	52	2 Q8LPD6	Q8LPD6 hordeum vul
9	17	65.4	128	2 Q96LJ4	Q96LJ4 homo sapien
10	17	65.4	139	2 Q6ZKM7	Q6ZKM7 oryza sativ
11	17	65.4	139	2 BA008805	Bad08805 oryza sat
12	17	65.4	155	2 Q6H482	Q6H482 oryza sativ
13	17	65.4	219	2 Q825E8	Q825E8 streptomyce
14	17	65.4	220	2 Q66152	Q66152 cymbidium m
15	17	65.4	256	2 Q6VTS2	Q6VTS2 oryza sativ
16	17	65.4	256	2 Q6ZKM7	Q6ZKM7 oryza sativ
17	17	65.4	260	2 Q850Z3	Q850Z3 oryza sativ
18	17	65.4	368	2 Q70RD3	Q70RD3 gerbera hyb
19	17	65.4	368	2 CAD87007	Cad87007 gerbera h
20	17	65.4	376	1 CBID AGRT5	Q8ubq6 agrobacteri
21	17	65.4	388	2 Q7PV13	Q7PV13 anopheles g
22	17	65.4	389	2 Q21081	Q21081 caenorhabdi
23	17	65.4	471	2 Q9VMG7	Q9VMG7 drosophila
24	17	65.4	475	2 Q7X7A4	Q7X7A4 oryza sativ
25	17	65.4	475	2 CAE04361	Cae04361 oryza sat
26	17	65.4	475	2 CAE04825	Cae04825 oryza sat
27	17	65.4	556	2 Q803D5	Q803D5 brachydanio
28	17	65.4	634	1 HS71 LEIMA	P12076 leishmania
29	17	65.4	699	2 Q819F8	Q819F8 corbicula f
30	17	65.4	699	2 AA017927	AA017927 corbicula
31	17	65.4	734	2 Q9NKE3	Q9NKE3 drosophila

32	17	65.4	843	2 Q80GV2	Q80GV2 hepatitis b
33	17	65.4	943	1 BLI4 CAEEL	P51559 caenorhabdi
34	17	65.4	1056	2 Q7QE80	Q7QE80 anopheles g
35	17	65.4	1130	2 Q9H1V5	Q9H1V5 homo sapien
36	17	65.4	1137	2 Q6CCI6	Q6CCI6 varowia li
37	17	65.4	2704	1 G168_PARPR	P17053 paramecium
38	17	65.4	2717	2 Q94710	Q94710 paramecium
39	17	65.4	2721	2 Q76973	Q76973 paramecium
40	17	65.4	2729	2 Q6PQK6	Q6PQK6 paramecium
41	17	65.4	2729	2 AAS94225	AAS94225 parameciu
42	16	61.5	68	2 Q6TL92	Q6TL92 neisseria g
43	16	61.5	68	2 AAS16526	AAS16526 neisseria
44	16	61.5	71	2 Q9HPK1	Q9HPK1 halobacteri
45	16	61.5	80	2 Q6IGD0	Q6IGD0 drosophila

ALIGNMENTS

RESULT 1  
Q96KM3 PRELIMINARY; PRT; 213 AA.  
AC Q96KM3;  
DT 01-DEC-2001 (TRENBLrel. 19, Created)  
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)  
DE ABERANT WM domain-containing oxidoreductase.  
GN Name=WMOX;  
OS Homo sapiens (Human);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21457335; PubMed=11572989;  
RA Page A.J.W., Taylor K.J., Taylor C., Hallier S.G., Farrington S.,  
RA Scott D., Porteous D.J., Smyth J.F., Gabra H., Watson J.E.V.;  
RT "WMOX: a candidate tumor suppressor gene involved in multiple tumor  
RT types.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:11417-11422(2001).  
DR EMBL; AF325432; AAL05451.1;  
DR EMBL; AF325423; AAL05451.1; JOINED.  
DR EMBL; AF325424; AAL05451.1; JOINED.  
DR EMBL; AF325426; AAL05451.1; JOINED.  
DR EMBL; AF325433; AAL05451.1; JOINED.  
DR EMBL; AF325425; AAL05451.1; JOINED.  
DR HSSP; Q13526; 1PIN.  
DR InterPro; IPR001202; WW\_Rsp5\_WWP.  
DR Pfam; PF00397; WW; 2.  
DR SMART; SM00456; WW; 2.  
DR PROSITE; PS01159; WW DOMAIN 1; 2.  
DR PROSITE; PS00020; WW DOMAIN 2; 2.  
SQ SEQUENCE 213 AA; 23868 MW; A21054FF8214CC7C CRC64;

Query Match 69.2%; Score 18; DB 2; Length 213;  
Best Local Similarity 20.0%; Pred. No. 0.66;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10

DB 184 CTSTTAAAC 193

RESULT 2

Q7PRQ7 PRELIMINARY; PRT; 283 AA.  
ID Q7PRQ7;  
AC Q7PRQ7;  
DT 01-MAR-2004 (TRENBLrel. 26, Created)  
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
DE ENSANGP0000001657 (Fragment).  
GN Name=ENSANGG00000001387;  
OS Anopheles gambiae str. PEST.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.  
 OX NCBI\_TaxID=180454;  
 RN [1]  
 RC STRAIN=PEST;  
 RP SEQUENCE FROM N.A.  
 RA Anopheles Genome Sequencing Consortium;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AAB01008847; EAA06779.2; -.  
 DR InterPro; IPR000877; Prot.inh.BBI.  
 DR PROSITE; PS00281; BOWMAN\_EIRK; UNKNOWN\_2.  
 FT NON\_TER 1 283  
 FT TER 283 283  
 SQ SEQUENCE 283 AA; 25479 MW; EF5695E19584D5F2 CRC64;

Query Match 69.2%; Score 18; DB 2; Length 283;  
 Best Local Similarity 20.0%; Pred. No. 0.74;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
 DB 163 CASSSTTSC 172

RESULT 3  
 YMS8 YEAST  
 ID YMS8 YEAST STANDARD; PRT; 313 AA.  
 AC Q0365;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Hypothetical 35.0 kDa protein in PFK2-HFA1 intergenic region.  
 GN OrderedLocusNames=YMR306W; ORFNames=YMR325.07;  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288c / AB972;  
 RX MEDLINE=97313268; PubMed=9169872;  
 RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,  
 RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,  
 RA Jagels K., Iye G., Moule S., Odell C., Pearson D., Rajandream M.A.,  
 RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;  
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome  
 XIII.";  
 RL Nature 387:90-93(1997).  
 CC -1- SIMILARITY: SOME, TO YEAST YNR014W.

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DR EMBL; Z48755; CA88648.1; -.  
 DR PIR; S59448; S59448.  
 DR Germline; 142881; -.  
 DR SGD; S0004819; YMR206W.  
 KW Hypothetical protein.  
 FT DOMAIN 3 6 Poly-Ser.  
 FT DOMAIN 146 149 Poly-Gln.  
 FT DOMAIN 246 252 Poly-Ser.  
 SQ SEQUENCE 313 AA; 35017 MW; 9D92BFDE982577F0 CRC64;

Query Match 69.2%; Score 18; DB 1; Length 313;  
 Best Local Similarity 20.0%; Pred. No. 0.77;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 CXXXXXXXC 10  
 DB 245 CSSSSSSSSAC 254

RESULT 4  
 Q6ZDR4  
 ID Q6ZDR4 PRELIMINARY; PRT; 357 AA.  
 AC Q6ZDR4;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Putative transcription factor Myb protein.  
 GN Name=P0481F05.20;  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -1- SIMILARITY: Contains 2 Myb-like domains.

DR EMBL; AP004376; BAD09322.1; -.  
 DR InterPro; IPR009057; Homeodomain like.  
 DR InterPro; IPR001005; Myb DNA binding.  
 DR Pfam; PF00249; Myb DNA-binding; 2.  
 DR SMART; SM00717; SANT; 2. UNKNOWN\_1.  
 DR PROSITE; PS00037; MYB\_1; UNKNOWN\_1.  
 DR PROSITE; PS00334; MYB\_2; 1.  
 DR PROSITE; PS00090; MYB\_3; 2.  
 KW Nuclear protein.  
 SQ SEQUENCE 357 AA; 36754 MW; 3F4F56860D3B4E22 CRC64;

Query Match 69.2%; Score 18; DB 2; Length 357;  
 Best Local Similarity 20.0%; Pred. No. 0.81;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
 DB 322 CSATASASSC 331

RESULT 5  
 BAD09322  
 ID BAD09322 PRELIMINARY; PRT; 357 AA.  
 AC BAD09322;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Putative transcription factor Myb protein.  
 GN P0481F05.20  
 OS Oryza sativa (japonica cultivar-group).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzaceae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Nipponbare;  
 RA Sasaki T., Matsumoto T., Yamamoto K.;  
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, PAC  
 clone:P0481F05.";  
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AP004376; BAD09322.1; -.  
 SQ SEQUENCE 357 AA; 36754 MW; 3F4F56860D3B4E22 CRC64;

Query Match 69.2%; Score 18; DB 2; Length 357;  
 Best Local Similarity 20.0%; Pred. No. 0.81;

Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
Db 322 CSATASASC 331

RESULT 6

Q9RV87 ID Q9RV87 PRELIMINARY; PRT; 480 AA.

AC Q9RV87

DT 01-MAY-2000 (TReMBLrel. 13, Created)

DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Hypothetical protein DR1142.

GN OrderedLocusNames=DR1142;

OS Deinococcus radiodurans

OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;

OC Deinococcaceae; Deinococcus.

OX NCBI\_TaxID=1299;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=E1 / ATCC 13939 / DSM 20539 / NCIB 9279;

RX MEDLINE=20036896; PubMed=10567266;

RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonack L.A., Utterback T.R., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.C., Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

RA "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";

RL Science 286:1571-1577 (1999).

DR EMBL: AE001963; RAF10716.1; --

DR FICR; E75433; E75433.

DR TIGR; DR1142; --

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 480 AA; 49364 MW; 18B962ADA5CA24AE CRC64;

Query Match 69.2%; Score 18; DB 2; Length 480;  
Best Local Similarity 20.0%; Pred. No. 0.91;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
Db 464 CASAAATAC 473

RESULT 7

Q8IXM8 ID Q8IXM8 PRELIMINARY; PRT; 653 AA.

AC Q8IXM8

DT 01-MAR-2003 (TReMBLrel. 23, Created)

DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)

DE KIAA0779 protein.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NCMMalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Skin;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udlin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Skin;

RA Strausberg R.;

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC039859; AAH39859.1; -- 18807D171E874205 CRC64;

SQ SEQUENCE 653 AA; 72052 MW; 18807D171E874205 CRC64;

Query Match 69.2%; Score 18; DB 2; Length 653;  
Best Local Similarity 20.0%; Pred. No. 1;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
Db 173 CAAAAAAAC 182

RESULT 8

Q8LDP6 ID Q8LDP6 PRELIMINARY; PRT; 52 AA.

AC Q8LDP6;

DT 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Putative glutathione-S-transferase (Fragment).

GN Name=bar2;

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticaceae; Hordeum.

OX NCBI\_TaxID=4513;

RN [1]

RP SEQUENCE FROM N.A.

RA Baldwin A.;

RT "The effect of thiocarbamate herbicides and the safener dichlorimid in barley and wild oats.";

RL Thesis (2001), Department of Cardiff School of Biosciences, Cardiff University, Cardiff, United Kingdom.

RN [2]

RP SEQUENCE FROM N.A.

RA Baldwin A., Harwood J.L., Machray G.C., Francis D., Rogers H.J.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ419772; CAD11963.1; --

DR HSSP; P12653; 1AXD.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR InterPro; IPR002197; HTH\_Fis.

DR PRINTS; PRO1590; HTHFIS.

KW Transferase.

FT NON\_TER 1 1

FT NON\_TER 52 52

SQ SEQUENCE 52 AA; 5750 MW; 7392EB72A3C70B9B CRC64;

Query Match 65.4%; Score 17; DB 2; Length 52;  
Best Local Similarity 20.0%; Pred. No. 1.9;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXXXXXXC 10  
Db 18 CTSASSTRSC 27

```

us-10-046-922-33.rup

RESULT 9
Q96LJ4 PRELIMINARY; PRT; 128 AA.
AC Q96LJ4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ25437.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
RA Sugano S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK058166; BAB71697.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR00719; Prot_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD00001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding.
SQ SEQUENCE 128 AA; 14115 MW; D30AC8C668621B0C CRC64;

Query Match 65.4%; Score 17; DB 2; Length 128;
Best Local Similarity 20.0%; Pred. No. 2.6;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 118 CTATSSAKT 127

RESULT 10
Q6ZKM7 PRELIMINARY; PRT; 139 AA.
AC Q6ZKM7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OJ1118_A06.7-1.
GN Name=OJ1118_A06.7-1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003873; BAD08805.1; -.
KW Hypothetical protein.
SQ SEQUENCE 139 AA; 14109 MW; E281360370FB63C9 CRC64;

Query Match 65.4%; Score 17; DB 2; Length 139;
Best Local Similarity 20.0%; Pred. No. 2.7;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 77 CAAITSSSC 86

RESULT 11
BAD08805 PRELIMINARY; PRT; 139 AA.
AC BAD08805;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OJ1118_A06.7-1.
GN OJ1118_A06.7-1.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC
RT clone:OJ1118_A06.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003873; BAD08805.1; -.
KW Hypothetical protein.
SQ SEQUENCE 139 AA; 14109 MW; E281360370FB63C9 CRC64;

Query Match 65.4%; Score 17; DB 2; Length 139;
Best Local Similarity 20.0%; Pred. No. 2.7;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 77 CAAITSSSC 86

RESULT 12
Q6H482 PRELIMINARY; PRT; 155 AA.
AC Q6H482;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein OJ1119_C03.6.
GN Name=OJ1119_C03.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Hattori M., Sasaki Y., Katayose Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005969; BAD26467.1; -.
KW Hypothetical protein.
SQ SEQUENCE 155 AA; 16233 MW; 02D8365E58C77B52 CRC64;

Query Match 65.4%; Score 17; DB 2; Length 155;
Best Local Similarity 20.0%; Pred. No. 2.8;
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 CXXXXXXXC 10
Db 25 CSTTSAADC 34

RESULT 13
Q825E8 PRELIMINARY; PRT; 219 AA.
ID Q825E8
AC Q825E8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)

```

01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
01-NOV-2004 (TrEMBLrel. 26, Last annotation update)  
Putative TetR-family transcriptional regulator.  
OrderedLocusNames=SAV7510;  
Streptomyces avermitilis.  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptomycineae; Streptomycetaceae; Streptomycetes.  
NCBI\_TaxID=33903;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=NA-4680;  
RC MEDLINE=21477403; PubMed=11572948;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,  
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
"Genome sequence of an industrial microorganism Streptomyces  
avermitilis: deducing the ability of producing secondary  
metabolites.";   
Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).  
[2]  
SEQUENCE FROM N.A.  
RC STRAIN=NA-4680;  
RC MEDLINE=22608306; PubMed=12692562;  
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,  
Sakaki Y., Hattori M., Omura S.;  
"Complete genome sequence and comparative analysis of the industrial  
microorganism Streptomyces avermitilis.";   
Nat. Biotechnol. 21:526-531(2003).  
DR EMBL; AP005050; BAC75221.1; -;  
DR GO; GO:0003700; F:transcription factor activity; IEA.  
DR InterPro; IPR006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR009057; Homeodomain\_like.  
DR Pfam; PF00440; TetR\_N; 1.  
KW Complete proteome.  
SQ SEQUENCE 219 AA; 24066 MW; 5C59ADF39430F304 CRC64;  
  
Query Match 65.4%; Score 17; DB 2; Length 219;  
Best Local Similarity 20.0%; Pred. No. 3.3;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXC 10  
DB 151 CAEAAAAAAC 160  
  
RESULT 14  
Q66152 PRELIMINARY; PRT; 220 AA.  
AC Q66152;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Coat protein.  
OS Cymbidium mosaic virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae;  
OC Potexvirus.  
OC NCBI\_TaxID=12178;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Korean isolate;  
RX MEDLINE=95278762; PubMed=7758973;  
RA Ryu K.H., Yoon K.E., Park W.M.;  
"Nucleotide sequence of coat protein gene of cymbidium mosaic  
potexvirus genomic RNA, the Korean isolate.";   
Gene 156:303-304(1995).  
CC -!- SIMILARITY: Belongs to the potexviruses coat protein family.  
DR EMBL; X81051; CAAS56941.1; -;  
DR PIR; JC4082; JC4082.  
DR GO; GO:0015028; C:viral capsid; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000052; P1tvir\_coat.  
DR Pfam; PF00286; Virus\_P-coat; 1.

DR PRINTS; PR00232; POTXCARLCOAT.  
DR ProDom; PD000603; P1tvir\_coat; 1.  
KW Coat protein.  
SQ SEQUENCE 220 AA; 23719 MW; 1F40C6E7CDCCF3B8 CRC64;  
  
Query Match 65.4%; Score 17; DB 2; Length 220;  
Best Local Similarity 20.0%; Pred. No. 3.3;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXC 10  
DB 166 CSAATLTATC 175  
  
RESULT 15  
Q6YTS2 PRELIMINARY; PRT; 256 AA.  
AC Q6YTS2;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein P0419H09.29.  
GN Name=P0419H09.29;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T., Matsumoto T., Katayose Y.;  
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP005918; BAD10719.1; -;  
KW Hypothetical protein.  
SQ SEQUENCE 256 AA; 26591 MW; 63BFCAF53D2D40EA CRC64;  
  
Query Match 65.4%; Score 17; DB 2; Length 256;  
Best Local Similarity 20.0%; Pred. No. 3.5;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
  
QY 1 CXXXXXXXC 10  
DB 203 CSASASARC 212  
  
Search completed: December 30, 2004, 13:16:04  
Job time : 95.2641 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:19:46 ; Search time 94 Seconds  
(without alignments)  
38.163 Million cell updates/sec

Title: US-10-046-922-34

Perfect score: 56

Sequence: 1 XGYWLTWGX 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 444336

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	96.4	10	5	ABP53931
2	54	96.4	10	5	ABP53932
3	33	58.9	7	5	ABP53964
4	33	58.9	8	5	ABP53965
5	33	58.9	10	5	ABP53968
6	32	57.1	7	3	AAY76794 Somatost
7	32	57.1	7	5	ABP53418
8	31	55.4	8	2	AAW97529 Antigenic
9	31	55.4	9	5	ABP53933
10	31	55.4	9	8	ADN64476 HLA bindi
11	31	55.4	10	4	AAW95260 Human com
12	30.5	54.5	10	2	AAK14709 Labaditin
13	30	53.6	9	4	AAU02369 HLA bindi
14	30	53.6	9	4	AAU02282 HLA bindi
15	30	53.6	10	4	AAW99759 Rhesus D
16	30	53.6	10	8	ADG94728 Human JAM
17	30	53.6	10	8	ADI47102 Permeabil
18	30	53.6	10	8	ADP87303 Human cla
19	29	51.8	5	2	AAK29452 Endotheli
20	29	51.8	5	2	AAW56531 Antigenic
21	29	51.8	5	2	AAW56531 Tyrosine
22	29	51.8	7	8	ADJ25834
23	29	51.8	8	4	ABP22594 HIV All m
24	29	51.8	8	4	ABP14287 HIV A03 s
25	29	51.8	8	4	ABP18686 HIV B62 s

26	29	51.8	8	4	ABP20292	Abp20292 HIV A03 m
27	29	51.8	8	4	ABP19992	Abp19992 HIV A03 m
28	29	51.8	8	4	ABP12050	Abp12050 HIV A02 s
29	29	51.8	8	4	ABP14288	Abp14288 HIV A03 s
30	29	51.8	8	4	ABP16999	Abp16999 HIV B27 s
31	29	51.8	8	4	ABP22402	Abp22402 HIV All m
32	29	51.8	8	7	ADL17320	ADL17320 DENGIN-18
33	29	51.8	8	8	ADH62133	ADH62133 Cyclic an
34	29	51.8	8	8	ADH62029	ADH62029 Cyclic an
35	29	51.8	8	8	ADH62062	ADH62062 Cyclic an
36	29	51.8	8	8	ADP67844	ADP67844 Anti-micr
37	29	51.8	8	8	ADP67877	ADP67877 Anti-micr
38	29	51.8	8	8	ADP67948	ADP67948 Anti-micr
39	29	51.8	8	8	ADQ28160	ADQ28160 Excluded
40	29	51.8	8	8	ADQ28097	ADQ28097 Excluded
41	29	51.8	8	8	ADQ28067	ADQ28067 Excluded
42	29	51.8	9	2	AAK37115	AAK37115 HIV envel
43	29	51.8	9	2	AAK37113	AAK37113 HIV envel
44	29	51.8	9	2	AAW73059	AAW73059 Antigen f
45	29	51.8	9	2	AAW43338	AAW43338 Immunogen

#### ALIGNMENTS

RESULT 1  
ABP53931  
ID ABP53931 standard; peptide; 10 AA.  
XX AC ABP53931;  
XX DT 09-JAN-2003 (first entry)  
XX DE VEGFR-3 binding peptide SEQ ID NO:34.  
XX KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnary; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX OS Homo sapiens.  
OS Synthetic.

XX EH Key Location/Qualifiers  
FT Misc-difference 1 /note= "any amino acid"  
FT Misc-difference 10 /note= "any amino acid"  
WO200257299-A2.  
XX PD 25-JUL-2002.  
XX PF 16-JAN-2002; 2002WO-IB000099.  
XX PR 17-JAN-2001; 2001US-0262476P.  
XX PA (LUDW-) LUDWIG INST CANCER RES.  
XX PA (LICN ) LICENTIA LTD.  
XX PI Alitalo K, Koivunen E, Kubo H;  
XX DR WPI; 2002-691521/74.  
XX PA New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX PS Claim 12; Page 80; 149pp; English.  
XX CC The present invention describes an isolated peptide (I) that binds to and

CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
 CC antidiabetic and vulnerary activities, and can be used in gene therapy.  
 CC Compositions and methods from the present invention are useful for  
 CC diagnosing, evaluating and treating disorders mediated by the activity of  
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
 CC represents a specifically claimed VEGFR-3 binding peptide from the  
 CC present invention  
 XX  
 SQ Sequence 10 AA;  
 Query Match 96.4%; Score 54; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.091;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GYWLTIWG 9  
 Db 2 GYWLTIWG 9  
 RESULT 2  
 ABP53932  
 ID ABP53932 standard; peptide; 10 AA.  
 XX  
 AC ABP53932;  
 XX  
 DT 09-JAN-2003 (first entry)  
 XX  
 DE VEGFR-3 binding peptide SEQ ID NO:35.  
 XX  
 KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
 KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
 KW vulnerary; cell surface receptor; cancer; neovascularisation;  
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
 KW diabetes; PDGF; platelet derived growth factor.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FN WO200257299-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 16-JAN-2002; 2002WO-IB000099.  
 XX  
 PR 17-JAN-2001; 2001US-0262476P.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 PA (LICN ) LICENTIA LTD.  
 XX  
 PI Alitalo K, Koivunen E, Kubo H;  
 XX  
 DR WPI; 2002-691521/74.  
 XX  
 PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
 XX diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
 PT such as cancer and diseases of neovascularization.  
 XX  
 PS Claim 13; Page 80; 149pp; English.  
 XX  
 CC The present invention describes an isolated peptide (I) that binds to and  
 CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
 CC antidiabetic and vulnerary activities, and can be used in gene therapy.  
 CC Compositions and methods from the present invention are useful for  
 CC diagnosing, evaluating and treating disorders mediated by the activity of  
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
 CC represents a specifically claimed VEGFR-3 binding peptide from the  
 CC present invention  
 XX  
 SQ Sequence 10 AA;  
 Query Match 96.4%; Score 54; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.091;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GYWLTIWG 9  
 Db 2 GYWLTIWG 9  
 RESULT 3  
 ABP53964  
 ID ABP53964 standard; peptide; 7 AA.  
 XX  
 AC ABP53964;  
 XX  
 DT 09-JAN-2003 (first entry)  
 XX  
 DE VEGFR-3 binding peptide SEQ ID NO:67.  
 XX  
 KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
 KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
 KW vulnerary; cell surface receptor; cancer; neovascularisation;  
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
 KW diabetes; PDGF; platelet derived growth factor.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 FN Key Location/Qualifiers  
 FT Misc-difference 4. .6  
 FT /note= "X is any amino acid"  
 XX  
 PN WO200257299-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 16-JAN-2002; 2002WO-IB000099.  
 XX  
 PR 17-JAN-2001; 2001US-0262476P.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 PA (LICN ) LICENTIA LTD.  
 XX  
 PI Alitalo K, Koivunen E, Kubo H;  
 XX  
 DR WPI; 2002-691521/74.  
 XX  
 PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
 XX diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
 PT such as cancer and diseases of neovascularization.  
 XX  
 PS Claim 21; Page 81; 149pp; English.  
 XX  
 CC The present invention describes an isolated peptide (I) that binds to and  
 CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
 CC antidiabetic and vulnerary activities, and can be used in gene therapy.  
 CC Compositions and methods from the present invention are useful for  
 CC diagnosing, evaluating and treating disorders mediated by the activity of  
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,

CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a specifically claimed VEGFR-3 binding peptide from the  
CC present invention  
XX  
SQ Sequence 7 AA;  
Query Match 58.9%; Score 33; DB 5; Length 7;  
Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GYWLTIW 8  
DB 1 GYWXXXW 7  
RESULT 4  
ABP53965  
ID ABP53965 standard; peptide; 8 AA.  
XX  
AC ABP53965;  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:68.  
XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnary; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 4..6  
FT /note= "X is any amino acid"  
FT  
FT Misc-difference 8  
FT /note= "any amino acid"  
XX  
PN WO200257299-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB0000099.  
XX  
PR 17-JAN-2001; 2001US-0262476P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
XX  
PI Alitalo K, Koivunen E, Kubo H;  
XX  
DR WPI; 2002-691521/74.  
XX  
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX  
PS Claim 22; Page 81; 149pp; English.  
XX  
CC The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,

CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
CC represents a specifically claimed VEGFR-3 binding peptide from the  
CC present invention  
XX  
SQ Sequence 8 AA;  
Query Match 58.9%; Score 33; DB 5; Length 8;  
Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GYWLTIW 8  
DB 1 GYWXXXW 7  
RESULT 5  
ABP53968  
ID ABP53968 standard; peptide; 10 AA.  
XX  
AC ABP53968;  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:73.  
XX  
KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnary; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 5..7  
FT /note= "X is any amino acid"  
FT  
FT Misc-difference 9  
FT /note= "X is any amino acid"  
XX  
PN WO200257299-A2.  
XX  
PD 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB0000099.  
XX  
PR 17-JAN-2001; 2001US-0262476P.  
XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN ) LICENTIA LTD.  
XX  
PI Alitalo K, Koivunen E, Kubo H;  
XX  
DR WPI; 2002-691521/74.  
XX  
PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX  
PS Disclosure; Page 147; 149pp; English.  
XX  
CC The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,

CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
 CC represents a VEGFR-3 binding peptide, which is given in the  
 CC exemplification of the present invention

XX SQ Sequence 10 AA;

Query Match 58.9%; Score 33; DB 5; Length 10;  
 Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8  
 |||||  
 Db 2 GYWXW 8

RESULT 6  
 AAY76794  
 ID AAY76794 standard; peptide; 7 AA.

XX AC AAY76794;

XX 20-APR-2000 (first entry)

XX Somatostatin analogue peptide 3181.

XX Somatostatin analogue; therapy; cyclic peptide; autoimmune disease;  
 KW endocrine disorder; cancer; diabetic-associated complication; diagnosis;  
 KW gastrointestinal disorder; inflammatory disease; pancreatitis;  
 KW atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor;  
 KW hormone-secreting tumour; hormone-dependent tumour; diarrhoea;  
 KW vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.

XX OS Synthetic.

XX Key Location/Qualifiers  
 FH Misc-difference 3 /note= "D-form residue"  
 FT Modified-site 7 /note= "Trp-NH2"  
 FT

XX WO9965508-A1.

XX 23-DEC-1999.

XX 15-JUN-1999; 99WO-IL000329.

XX 19-JUN-1998; 98US-00100360.

XX 02-DEC-1998; 98US-00203389.

XX (PEPT-) PEPTOR LTD.

XX Hornik V, Afargan MM, Gellerman G;

XX WPI; 2000-136888/12.

XX Cyclized somatostatin analogs for inhibiting growth hormone secretion  
 FT from anterior pituitary and as antiproliferative agents for the treatment  
 FT of tumors.

XX Example 11; Page 61; 82pp; English.

XX This sequence represents a somatostatin analogue of the invention. The  
 CC invention relates to a backbone cyclised somatostatin analogue that has  
 CC one building unit containing a nitrogen atom of the peptide backbone  
 CC connected to a bridging group comprising an amide, thioether, thioester  
 CC or disulphide. At least one building unit is connected via a bridging  
 CC group to form a cyclic structure with a moiety selected from a second  
 CC building unit, side chain of or N-terminal amino acid residue. A  
 CC composition containing the analogue may be used for preventing disorders  
 CC such as cancers, autoimmune diseases, endocrine disorders, diabetic-  
 CC associated complications, gastrointestinal disorders, inflammatory

CC diseases, pancreatitis, atherosclerosis, restenosis and post-surgical  
 CC pain. It may also be used for diagnosing cancer. The backbone cyclic  
 CC analogue is used for imaging the existence of metastases. Somatostatin  
 CC analogues can be used for the treatment patients with hormone-secreting  
 CC and hormone-dependent tumours. They reduce diarrhoea through the  
 CC inhibition of vasoactive intestinal peptide (VIP) secretion and by direct  
 CC effect on intestinal secretion. Somatostatin analogues selective to type  
 CC 2 and 5 receptors may be used for treatment of non-insulin dependent  
 CC diabetes mellitus. They are useful for the prevention of atherosclerosis  
 CC and restenosis. The analogues are metabolically stable, selective in  
 CC their in-vivo activities and safe

XX SQ Sequence 7 AA;

Query Match 57.1%; Score 32; DB 3; Length 7;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8  
 |||||  
 Db 1 GYWKVCW 7

RESULT 7  
 ABP53418

ID ABP53418 standard; peptide; 7 AA.

XX AC ABP53418;

XX 19-NOV-2002 (first entry)

XX Backbone cyclised somatostatin analogue PTR 3181.

XX Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;  
 KW somatotropin release inhibiting factor; somatostatin receptor subtype;  
 KW synthesis; antiatherosclerotic; immunosuppressive; cytostatic; cancer;  
 KW antidiabetic; antiinflammatory; somatostatin receptor ligand;  
 KW atherosclerosis; autoimmune disease; diabetic-associated complication;  
 KW endocrine disorder; inflammation; gastrointestinal disorder; restenosis;  
 KW pancreatitis; post-surgical pain.

XX OS Synthetic.

XX Key Location/Qualifiers  
 FH Modified-site 1 /note= "N-terminally modified with Fmoc  
 (fluorenylmethoxycarbonyl)"  
 FT Misc-difference 3 /note= "D form residue"  
 FT Modified-site 7 /note= "amidated"

XX US2002052315-A1.

XX 02-MAY-2002.

XX 13-DEC-2000; 2000US-00734583.

XX 19-JUN-1998; 98US-00100360.

XX 02-DEC-1998; 98US-00203389.

XX 15-JUN-1999; 99WO-IL000329.

XX (HORN/) HORNIK V.

XX (AFAR/) AFARGAN M M.

XX (GELL/) GELLERMAN G.

XX Hornik V, Afargan MM, Gellerman G;

XX WPI; 2002-681319/73.

XX New backbone cyclized somatostatin analogs are e.g. useful in the  
 FT treatment of atherosclerosis, autoimmune diseases and cancers.

XX

PS Example 12; Page 21; 30pp; English.

XX The present invention describes backbone cyclised somatostatin analogues  
 CC (I) that incorporates at least one building unit containing one nitrogen  
 CC atom of the peptide backbone connected to a bridging group (comprising an  
 CC amide, thioether, thioester or disulfide) where at least one building  
 CC unit is connected via the bridging group to form a cyclic structure with  
 CC a moiety selected from the group consisting of a second building unit,  
 CC the side chain of an amino acid residue of the sequence or the N-terminal  
 CC amino acid residue. (I) has antiarteriosclerotic, immunosuppressive,  
 CC cytostatic, antidiabetic, antiinflammatory and analgesic activities, and  
 CC can be used as a somatostatin receptor ligand. (I) are useful in the  
 CC treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-  
 CC associated complications, endocrine disorders, inflammation,  
 CC gastrointestinal disorders, pancreatitis, post-surgical pain, and  
 CC restenosis. (I) can also be used in the diagnosis of cancer, by imaging  
 CC the existence of metastases, it being labeled with a detectable probe.  
 CC The present sequence represents a backbone cyclised somatostatin analogue  
 CC from the present invention

XX Sequence 7 AA;

Query Match 57.1%; Score 32; DB 5; Length 7;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
 |||||  
 Db 1 GYWKVCW 7

RESULT 8

AAW97529  
 ID AAW97529 standard; peptide; 8 AA.

XX AAW97529;

XX 19-MAY-1999 (first entry)

XX Antigenic site of HN protein loop beta-4L23.

XX Antigenic site; haemagglutinin-neuraminidase; HN; paramyxoviridae;  
 KW virus epitope; attachment protein; vaccine; immunodominant epitope.

XX Measles virus.

XX WO9902695-A2.

XX 21-JAN-1999.

XX 08-JUL-1998; 98WO-NL000390.

XX 08-JUL-1997; 97BP-00202100.

XX (DIER-) STICHTING INST DIERHOUDERIJ EN DIERGEZON.

XX Langedijk JPM, Van Oirschot JT;

XX WPI; 1999-120896/10.

XX Isolated proteinaceous substance - comprising at least one virus epitope  
 PT derived from an attachment protein of a paramyxovirus.

XX Disclosure; Page 48; 63pp; English.

XX AAW97452-571 represent antigenic sites derived from the haemagglutinin-  
 CC neuraminidase (HN) protein of the paramyxoviridae. The specification  
 CC describes 3-D models identifying a proteinaceous substance comprising at  
 CC least one virus epitope derived from the attachment protein, which  
 CC corresponds to an antigenic site present on one of the loops of HN. The  
 CC antigenic sites can be used to produce vaccines, to detect the viruses,  
 CC and to select the immunodominant epitope

SQ Sequence 8 AA;

Query Match 55.4%; Score 31; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YWLTI 7  
 |||||  
 Db 4 YWLTI 8

RESULT 9

ABP53933

ID ABP53933 standard; peptide; 9 AA.

XX AC ABP53933;

XX 09-JAN-2003 (first entry)

XX VEGFR-3 binding peptide SEQ ID NO:36.

XX Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
 KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
 KW vulnary; cell surface receptor; cancer; neovascularisation;  
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
 KW diabetes; PDGF; platelet derived growth factor.

XX Homo sapiens.

XX Synthetic.

XX WO200257299-A2.

XX 25-JUL-2002.

XX 16-JAN-2002; 2002WO-IB0000099.

XX 17-JAN-2001; 2001US-0262476P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (LICN) LICENTIA LTD.

XX Alitalo K, Koivunen E, Kubo H;

XX WPI; 2002-691521/74.

XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
 PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
 PT such as cancer and diseases of neovascularization.

XX Claim 14; Page 80; 149pp; English.

XX The present invention describes an isolated peptide (I) that binds to and  
 CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
 CC antidiabetic and vulnary activities, and can be used in gene therapy.  
 CC Compositions and methods from the present invention are useful for  
 CC diagnosing, evaluating and treating disorders mediated by the activity of  
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
 CC represents a specifically claimed VEGFR-3 binding peptide from the  
 CC present invention

XX Sequence 9 AA;

Query Match 55.4%; Score 31; DB 5; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

QY      2 GYWLTIW 8
Db      2 GYWDWTW 8

RESULT 10
ID      ADN64476
XX      ADN64476 standard; peptide; 9 AA.
AC      ADN64476;
XX
XX      01-JUL-2004 (first entry)
XX
XX      HLA binding peptide #1076.
XX
XX      cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
KW      gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;
KW      prostate specific antigen; prostate specific membrane antigen;
KW      hepatitis B virus antigen; hepatitis C virus antigen;
KW      malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;
KW      prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
KW      chondyoma acuminatum.
XX
XX      Unidentified.
XX      OS
XX      WO2004031211-A2.
XX      PN
XX      15-APR-2004.
XX      PD
XX      03-OCT-2003; 2003WO-US031308.
XX      PF
XX      03-OCT-2002; 2002US-0416207P.
XX      PR
XX      08-OCT-2002; 2002US-0417269P.
XX      XX
XX      (EPIM-) EPIMMUNE INC.
XX      PA
XX      Sidney J, Southwood S, Sette A;
XX      PI
XX      WPI; 2004-347953/32.
XX      DR
XX      New composition of peptides and nucleic acids capable of binding Major
PT      Histocompatibility Complex molecules, useful for diagnosing, preventing
PT      or treating viral infections or cancer, such as prostate cancer,
PT      hepatitis B or AIDS.
XX
XX      Claim 1; SEQ ID NO 1076; 186pp; English.
XX
XX      The invention relates to a novel composition comprising one or more
CC      peptides or nucleic acids encoding an HLA binding peptide. The
CC      composition further comprises an HTL epitope. It also comprises a spacer
CC      molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
CC      are incorporated as part of a liposome. The peptide is from an antigen
CC      selected from prostate specific antigen (PSA), prostate specific membrane
CC      antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
CC      antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
CC      immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
CC      Papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53,
CC      murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein
CC      (TKP). The composition is useful for preventing or treating viral
CC      infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
CC      AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyoma
CC      acuminatum. The composition is also be used for diagnosing such diseases.
CC      This sequence represents a peptide of the invention.
XX
XX      Sequence 9 AA;
XX      Query Match      55.4%; Score 31; DB 8; Length 9;
XX      Best Local Similarity 60.0%; Pred. No. 1.7e+06;
XX      Matches      3; Conservative      2; Mismatches      0; Indels      0; Gaps      0;

QY      4 WLTIW 8
Db      5 WVTWV 9

us-10-046-922-34.10max.rag
Page 6

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XX 23-APR-1990; 90US-00512796.  
 XX 23-APR-1990; 90US-00512796.  
 XX (UYUT-) RIJKSUNIV UTRECHT.  
 XX Labadie RP;  
 XX WPI; 1991-339755/46.  
 XX New cyclic peptide(s) e.g. labaditin, having IGG binding properties -  
 PT used for IGG binding in mammals including humans and for treating  
 PT inflammatory diseases including rheumatic and autoimmune diseases.  
 XX  
 XX Claim 11; Page 12; 15pp; English.  
 XX  
 CC The peptide is isolated from plants of the Euphorbiaceae family (see PBBS  
 CC Letters 256, 1-2, 1989). It selectively inhibits the classical activation  
 CC pathway of the complement system by binding to IgG. It can be used to  
 CC treat autoimmune disorders e.g. rheu- matic and other inflammatory  
 CC disorders, and immuno-complex-related diseases, e.g. extrinsic allergic  
 CC alveolitis. It may also be used to isolate IgG from blood plasma or serum  
 CC to reduce the level of IgG, or as immunoassay reagent to determine IgG  
 CC levels in body fluids. See also AAK14710. (Updated on 25-MAR-2003 to  
 CC correct PA field.)  
 XX  
 XX Sequence 10 AA;  
 SQ  
 Query Match 54.5%; Score 30.5; DB 2; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 3e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
 QY 2 GYWLTIWG 9  
 | | | | |  
 Db 2 GYW-TVWG 8  
 | | | | |  
 RESULT 13  
 AAU02369  
 ID AAU02369 standard; peptide; 9 AA.  
 XX  
 AC AAU02369;  
 XX  
 DT 29-AUG-2001 (first entry)  
 XX  
 DE HLA binding TADG-16 peptide #145.  
 XX  
 KW Human; extracellular serine protease; tumour antigen derived gene-16;  
 KW TADG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;  
 KW prostate cancer; HLA type.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200127257-A1.  
 XX  
 PD 19-APR-2001.  
 XX  
 PF 13-OCT-2000; 2000WO-US028558.  
 XX  
 PR 14-OCT-1999; 99US-00418527.  
 XX  
 PA (UYAR-) UNIV ARKANSAS.  
 XX  
 PI O'Brien TJ, Underwood LJ, Shigemasa K;  
 XX WPI; 2001-273769/28.  
 XX  
 PT New tumor antigen-derived gene-16 protein, useful for diagnosis and  
 PT treatment of ovarian, breast, lung, colon and prostate cancer.  
 XX  
 PS Example 8; Page 55; 124pp; English.  
 XX

CC AAU02225-AAU02384 represent TADG-16 peptides which are tested for their  
 CC binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A1, HLA  
 CC A24, HLA B7, HLA B8, HLA B2702, and HLA B403. Tumour antigen derived  
 CC gene-16 protein, TADG-16 (AAU02223), is a novel human extracellular  
 CC serine protease. TADG-16 is expressed in normal ovaries and testes and in  
 CC certain ovarian carcinomas. TADG-16 contains the conserved catalytic  
 CC triad, His-Asp-Ser, and a signal secretion sequence characteristic of the  
 CC serine protease family. An antisense oligonucleotide having a  
 CC complementary sequence to the TADG-16 nucleic acid is useful for treating  
 CC various cancers, including ovarian, breast, lung, colon and prostate. The  
 CC TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16  
 CC are useful for the diagnosis of cancer. TADG-16 protein or its fragments  
 CC are useful for vaccinating an individual against TADG-16  
 XX  
 XX Sequence 9 AA;  
 SQ  
 Query Match 53.6%; Score 30; DB 4; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 WLTIWG 9  
 | | | | |  
 Db 3 WVTGWG 8  
 | | | | |  
 RESULT 14  
 AAU02282  
 ID AAU02282 standard; peptide; 9 AA.  
 XX  
 AC AAU02282;  
 XX  
 DT 29-AUG-2001 (first entry)  
 XX  
 DE HLA binding TADG-16 peptide #58.  
 XX  
 KW Human; extracellular serine protease; tumour antigen derived gene-16;  
 KW TADG-16; ovarian carcinoma; breast cancer; lung cancer; colon cancer;  
 KW prostate cancer; HLA type.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200127257-A1.  
 XX  
 PD 19-APR-2001.  
 XX  
 PF 13-OCT-2000; 2000WO-US028558.  
 XX  
 PR 14-OCT-1999; 99US-00418527.  
 XX  
 PA (UYAR-) UNIV ARKANSAS.  
 XX  
 PI O'Brien TJ, Underwood LJ, Shigemasa K;  
 XX WPI; 2001-273769/28.  
 XX  
 PT New tumor antigen-derived gene-16 protein, useful for diagnosis and  
 PT treatment of ovarian, breast, lung, colon and prostate cancer.  
 XX  
 PS Example 8; Page 53; 124pp; English.  
 XX  
 CC AAU02225-AAU02384 represent TADG-16 peptides which are tested for their  
 CC binding affinity to the 8 haplotypes HLA A0201, HLA A0205, HLA A1, HLA  
 CC A24, HLA B7, HLA B8, HLA B2702, and HLA B403. Tumour antigen derived  
 CC gene-16 protein, TADG-16 (AAU02223), is a novel human extracellular  
 CC serine protease. TADG-16 is expressed in normal ovaries and testes and in  
 CC certain ovarian carcinomas. TADG-16 contains the conserved catalytic  
 CC triad, His-Asp-Ser, and a signal secretion sequence characteristic of the  
 CC serine protease family. An antisense oligonucleotide having a  
 CC complementary sequence to the TADG-16 nucleic acid is useful for treating  
 CC various cancers, including ovarian, breast, lung, colon and prostate. The  
 CC TADG-16 nucleic acid, TADG-16 protein and antibodies specific to TADG-16  
 CC are useful for the diagnosis of cancer. TADG-16 protein or its fragments  
 CC are useful for vaccinating an individual against TADG-16

XX SQ Sequence 9 AA;  
Query Match 53.6%; Score 30; DB 4; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 4 WLTWIG 9  
|:|:|  
Db 1 WVTGWG 6

Query Match 53.6%; Score 30; DB 4; Length 10;  
Best Local Similarity 57.1%; Pred. No. 3.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 GYWLTIW 8  
|:|:|  
Db 1 GYWSAKW 7

Search completed: December 29, 2004, 21:35:31  
Job time : 97.3333 secs

RESULT 15  
AAB99759  
ID AAB99759 standard; peptide; 10 AA.  
XX AC AAB99759;  
XX DT 21-SEP-2001 (first entry)  
XX DE Rhesus D antibody binding peptide SEQ ID NO:4.  
XX KW Rhesus D antibody binding peptide; Rhesus D; RhD; identification;  
XX KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;  
XX KW prophylaxis; haemolytic disease of the newborn; HDN; ITP;  
XX KW idiopathic thrombocytopenic purpura; immunoglobulin.  
XX OS Homo sapiens.  
XX PN EP1106625-A1.  
XX PD 13-JUN-2001.  
XX PF 17-NOV-1999; 99EP-00122858.  
XX PR 17-NOV-1999; 99EP-00122858.  
XX PA (ZLBB-) ZLB BIOPLASMA AG.  
XX PI Miescher S, Hofmann A, Fisch I;  
XX DR WPI; 2001-383568/41.  
XX PT Novel peptides capable of binding Rhesus D antibodies are used to  
PT manufacture an agent for the diagnosis, therapy or prophylaxis of  
PT diseases associated with Rhesus D antigen, e.g. hemolytic disease of the  
PT newborn (HDN).  
XX PS Claim 1; Page 12; 19pp; English.  
XX CC The present sequence represents a peptide capable of binding Rhesus D  
CC antibodies (I). Also described in the present invention are: (1) a  
CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more  
CC (II) operably linked to an expression control system; (3) a cell (IV)  
CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)  
CC peptides having immunologic properties of Rhesus D protein epitopes  
CC comprising subjecting an antibody/antibody fragment recognising an  
CC epitope of Rhesus D protein to several panning rounds with a phage  
CC display library, and identifying immunogenic peptide sequences which are  
CC mimotopes which differ in their amino acid sequence from the amino acid  
CC sequences of Rhesus D protein; and (6) peptides (V) with immunological  
CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to  
CC manufacture an agent for the diagnosis, therapy or prophylaxis of  
CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the  
CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the  
CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified  
CC or removed from body fluids or immunoglobulin preparations. Using (I) as  
CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation  
CC with foreign erythrocytes thereby avoiding the risk of transmission of  
CC viral diseases like AIDS and hepatitis B  
XX SQ Sequence 10 AA;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:20:27 ; Search time 23.6667 Seconds  
(without alignments)  
28.022 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 110780

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/prodata/1/1aa/5B-COMB.pep:\*  
3: /cgn2\_6/prodata/1/1aa/6A-COMB.pep:\*  
4: /cgn2\_6/prodata/1/1aa/6B-COMB.pep:\*  
5: /cgn2\_6/prodata/1/1aa/PCTUS-COMB.pep:\*  
6: /cgn2\_6/prodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	51.8	7	4	US-09-069-827A-94
2	29	51.8	9	4	US-09-311-784A-348
3	29	51.8	10	2	US-08-735-253-8
4	29	51.8	10	2	US-08-735-253-13
5	28	50.0	8	3	US-09-315-304B-1649
6	28	50.0	10	4	US-09-125-641-3
7	27.5	49.1	6	1	US-08-191-571-12
8	27.5	49.1	6	5	PCT-US95-00296-12
9	27	48.2	8	3	US-08-586-670A-17
10	27	48.2	8	3	US-09-082-279B-1495
11	27	48.2	8	4	US-09-834-784-1495
12	27	48.2	8	4	US-09-350-641C-1650
13	27	48.2	10	3	US-09-315-304B-1587
14	27	48.2	10	4	US-09-350-323-47
15	27	48.2	10	4	US-09-350-641C-1587
16	27	48.2	10	4	US-09-239-043D-2474
17	27	48.2	10	4	US-09-620-091-28
18	26	46.4	5	1	US-08-353-400-27
19	26	46.4	6	1	US-08-415-099A-3
20	26	46.4	8	1	US-08-415-099A-4
21	26	46.4	8	3	US-08-467-472C-5
22	26	46.4	8	3	US-08-467-472C-6
23	26	46.4	8	3	US-09-082-279B-1500
24	26	46.4	8	3	US-09-384-061-5
25	26	46.4	8	3	US-09-384-061-6
26	26	46.4	8	4	US-09-834-784-1500
27	26	46.4	8	4	US-08-632-444B-9

28	26	46.4	8	4	US-09-350-641C-1655	Sequence 1655, Ap
29	26	46.4	8	4	US-09-852-870A-5	Sequence 5, Appl
30	26	46.4	9	1	US-08-024-253-18	Sequence 18, Appl
31	26	46.4	9	3	US-08-985-526-13	Sequence 13, Appl
32	26	46.4	10	4	US-08-632-444B-10	Sequence 10, Appl
33	26	46.4	10	4	US-09-852-870A-6	Sequence 6, Appl
34	26	46.4	10	4	US-09-620-091-41	Sequence 41, Appl
35	25.5	45.5	8	1	US-08-191-571-21	Sequence 21, Appl
36	25.5	45.5	8	5	PCT-US95-00296-21	Sequence 21, Appl
37	25	44.6	5	4	US-09-155-106-1	Sequence 1, Appl
38	25	44.6	6	2	US-08-660-747-56	Sequence 56, Appl
39	25	44.6	8	4	US-09-125-641-1	Sequence 1, Appl
40	25	44.6	8	4	US-09-125-641-2	Sequence 2, Appl
41	25	44.6	9	4	US-09-125-641-9	Sequence 29, Appl
42	25	44.6	10	1	US-08-208-886C-83	Sequence 83, Appl
43	25	44.6	10	1	US-08-208-886C-87	Sequence 87, Appl
44	25	44.6	10	1	US-08-704-744-85	Sequence 85, Appl
45	25	44.6	10	1	US-08-704-744-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1  
US-09-069-827A-94  
; Sequence 94, Application US/09069827A  
; Patent No. 6617114  
; GENERAL INFORMATION:  
; APPLICANT: FOWLKES, Dana M  
; KAY, Brian K  
; FRELINGER, Jeffrey A  
; HYDE-DERUYSCHE, Robin P  
; TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING  
; COMPLEMENTARY COMBINATORIAL LIBRARIES  
; NUMBER OF SEQUENCES: 178  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 624 Ninth Street N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/09/069,827A  
; FILING DATE: 30-Apr-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/050,359  
; FILING DATE: 31-MAR-1998  
; APPLICATION NUMBER: PCT/US97/19638  
; FILING DATE: 31-OCT-1997  
; APPLICATION NUMBER: US 08/740,671  
; FILING DATE: 31-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, Iver P  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/POCKET NUMBER: FOWLKES=4C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 94:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 94:

## US-09-069-827A-94

Query Match 51.8%; Score 29; DB 4; Length 7;  
Best Local Similarity 57.1%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 YWLTIWG 9  
|||  
Db 1 YWPDWG 7

## RESULT 2

US-09-311-784A-348

Sequence 348, Application US/09311784A

Patent No. 6534482

GENERAL INFORMATION:

APPLICANT: Fikes, John D.

APPLICANT: Hermanson, Gary G.

APPLICANT: Sette, Alessandro

APPLICANT: Ishioka, Glenn Y.

APPLICANT: Livingston, Brian

APPLICANT: Chesnut, Robert W.

APPLICANT: Epimmune Inc.

TITLE OF INVENTION: Expression Vectors for Stimulating an Immune Response and Methods of Using the Same

FILE REFERENCE: 39963-20022.01

CURRENT APPLICATION NUMBER: US/09/311,784A

CURRENT FILING DATE: 1999-05-13

PRIOR APPLICATION NUMBER: US 60/085,751

PRIOR FILING DATE: 1998-05-15

NUMBER OF SEQ ID NOS: 463

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 348

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: HIV1 ENV 61 (peptide 25.0032)

US-09-311-784A-348

Query Match 51.8%; Score 29; DB 4; Length 9;  
Best Local Similarity 80.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LTIWG 9  
|||  
Db 4 LTVWG 8

## RESULT 3

US-08-735-253-8

Sequence 8, Application US/08735253

Patent No. 5942491

GENERAL INFORMATION:

APPLICANT: Root-Bernstein, Robert S.

TITLE OF INVENTION: Methods and Compositions for Treating

TITLE OF INVENTION: Arthritis

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Goldsmith, Milnamow &amp; Katz, Ltd.

STREET: 180 N. Stetson

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/735,253

FILING DATE:

CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5942491thrup, Thomas E.  
REGISTRATION NUMBER: 33,268  
REFERENCE/DOCKET NUMBER: MIC3302P0010US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 616-5400  
TELEFAX: (312) 616-5460  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-735-253-8

Query Match 51.8%; Score 29; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YWLTIWG 9  
:||  
Db 1 FWRFLWG 7

## RESULT 4

US-08-735-253-13

Sequence 13, Application US/08735253

Patent No. 5942491

GENERAL INFORMATION:

APPLICANT: Root-Bernstein, Robert S.

TITLE OF INVENTION: Methods and Compositions for Treating

TITLE OF INVENTION: Arthritis

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Goldsmith, Milnamow &amp; Katz, Ltd.

STREET: 180 N. Stetson

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/735,253

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: No. 5942491thrup, Thomas E.

REGISTRATION NUMBER: 33,268

REFERENCE/DOCKET NUMBER: MIC3302P0010US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 616-5400

TELEFAX: (312) 616-5460

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-735-253-13

Query Match 51.8%; Score 29; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 1.6e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 YWLTIWG 9  
:||  
Db 1 FWRFLWG 7

Db 1 FWRFLWG 7

RESULT 5

US-09-315-304B-1649

Sequence 1649, Application US/09315304B

Patent No. 6348568

GENERAL INFORMATION:

APPLICANT: Barney, S.

APPLICANT: Guthrie, K.

APPLICANT: Merutka, G.

APPLICANT: Anwer, M.

APPLICANT: Lambert, D.

TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

FILE REFERENCE: 7872-052

CURRENT APPLICATION NUMBER: US/09/315,304B

CURRENT FILING DATE: 1999-05-20

PRIOR APPLICATION NUMBER: 09/082,279

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 1667

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1649

LENGTH: 8

TYPE: PRT

ORGANISM: HIV-1

US-09-315-304B-1649

Query Match 50.0%; Score 28; DB 3; Length 8;

Best Local Similarity 50.0%; Pred. No. 3.8e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTLWG 9

Db 1 WNSLWG 6

RESULT 6

US-09-125-641-3

Sequence 3, Application US/09125641

Patent No. 6610297

GENERAL INFORMATION:

APPLICANT: Kricek, Franz

APPLICANT: Stadler, Benda

TITLE OF INVENTION: Peptide Immunogens For Vaccination

TITLE OF INVENTION: Against and Treatment of Allergy

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6610297artis Corporation

STREET: 564 Morris Avenue

CITY: Summit

STATE: New Jersey

COUNTRY: U.S.A.

ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/125,641

FILING DATE: 21-AUG-1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/EP97/01013

FILING DATE: 28-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9604412.8

FILING DATE: 01-MAR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9617702.7

FILING DATE: 22-AUG-1996

ATTORNEY/AGENT INFORMATION:

NAME: Boudreaux, William R

REGISTRATION NUMBER: 35,796

REFERENCE/DOCKET NUMBER: M01718

TELECOMMUNICATION INFORMATION:

TELEPHONE: 513-948-6566

TELEFAX: 513-948-7961 or 4681

TELEX: 214320

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

TOPOLOGY: circular

MOLECULE TYPE: peptide

US-08-191-571-12

Query Match 49.1%; Score 27.5; DB 1; Length 6;

Best Local Similarity 71.4%; Pred. No. 3.8e+05;

Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

NAME: Ferraro, Gregory D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 4-900-9862/A/NFI/PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 522-6923

TELEFAX: (908) 522-6923

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: YES

ANTI-SENSE: NO

FRAGMENT TYPE: internal

US-09-125-641-3

Query Match 50.0%; Score 28; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWL 5

Db 6 GYWL 9

RESULT 7

US-08-191-571-12

Sequence 12, Application US/08191571

Patent No. 5521156

GENERAL INFORMATION:

APPLICANT: Owen, Thomas J.

APPLICANT: Kudlacz, Elizabeth M

APPLICANT: Buck, Stephen H

APPLICANT: Harbeson, Scott L

TITLE OF INVENTION: Cyclic Neurokinin A Antagonists

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marion Merrell Dow Inc.

STREET: P. O. Box 156300 2110 E. Galbraith Rd.

CITY: Cincinnati

STATE: Ohio

COUNTRY: United States

ZIP: 45215-6300

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/191,571

FILING DATE: 03-FEB-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Boudreaux, William R

REGISTRATION NUMBER: 35,796

REFERENCE/DOCKET NUMBER: M01718

TELECOMMUNICATION INFORMATION:

TELEPHONE: 513-948-6566

TELEFAX: 513-948-7961 or 4681

TELEX: 214320

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

TOPOLOGY: circular

MOLECULE TYPE: peptide

US-08-191-571-12

Qy 3 YWLTIWG 9  
Db 1 YWLR-WG 6

RESULT 8  
PCT-US95-00296-12  
; Sequence 12, Application PC/TUS9500296  
; GENERAL INFORMATION:  
; APPLICANT: Merrell Dow Pharmaceuticals Inc.  
; TITLE OF INVENTION: Cyclic Neurokinin A Antagonists  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marion Merrell Dow Inc., P.O. Box 156300  
; STREET: 2110 East Galbraith Road, P.O. Box 156300  
; CITY: Cincinnati  
; STATE: OH  
; COUNTRY: USA  
; ZIP: 45215-6300  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/00296  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Boudreaux, William R  
; REGISTRATION NUMBER: 35,796  
; REFERENCE/DOCKET NUMBER: M01718A WO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 513-948-6566  
; TELEFAX: 513-948-7961 or 4681  
; TELEX: 214320  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: circular  
; MOLECULE TYPE: peptide  
; PCT-US95-00296-12

Query Match 49.1%; Score 27.5; DB 5; Length 6;  
Best Local Similarity 71.4%; Pred. No. 3.8e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 3 YWLTIWG 9  
Db 1 YWLR-WG 6

RESULT 9  
US-08-586-670A-17  
; Sequence 17, Application US/08586670A  
; Patent No. 6241965  
; GENERAL INFORMATION:  
; APPLICANT: McBride, William  
; APPLICANT: Dean, Richard T.  
; TITLE OF INVENTION: Somatostatin Derivatives  
; TITLE OF INVENTION: And their Radiolabeled Products  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff, Ltd.  
; STREET: 10 South Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/586,670A  
FILING DATE: 22-APR-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6241965nan, Kevin E  
REGISTRATION NUMBER: 35,303  
REFERENCE/DOCKET NUMBER: 92,385-DD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312-715-1000  
TELEFAX: 312-715-1234  
TELEX: 910-221-5317  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 8 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1.1.2  
OTHER INFORMATION: /label= Variant residues  
OTHER INFORMATION: /note= "Phe is in the D conformation and is linked to DTPA;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 1.4  
OTHER INFORMATION: /label= Variant residues  
OTHER INFORMATION: /note= "The Phe is in the D conformation; Xaa  
OTHER INFORMATION: is L-4-chlorophenylalanine; the Trp is in the D conformation;  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 7..8  
OTHER INFORMATION: /label= Variant residues  
OTHER INFORMATION: /note= "The carboxyl group of the C-terminal  
OTHER INFORMATION: Thr is reduced to an alcohol;  
US-08-586-670A-17

Query Match 48.2%; Score 27; DB 3; Length 8;  
Best Local Similarity 80.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTL 6  
Db 2 GYWK 6

RESULT 10  
US-09-082-279B-1495  
; Sequence 1495, Application US/09082279B  
; Patent No. 6258782  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohmed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/082,279B  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1495  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: HIV-1  
US-09-082-279B-1495

Query Match 48.2%; Score 27; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTIWG 9  
| : : : :  
DB 1 WDSLWG 6

RESULT 11  
US-09-834-784-1495  
; Sequence 1495, Application US/09834784  
; Patent No. 6562787  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohamed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/834,784  
; CURRENT FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1495  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: HIV-1  
US-09-834-784-1495

Query Match 48.2%; Score 27; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTIWG 9  
| : : : :  
DB 1 WDSLWG 6

RESULT 12  
US-09-350-641C-1650  
; Sequence 1650, Application US/09350641C  
; Patent No. 6656906  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-067  
; CURRENT APPLICATION NUMBER: US/09/350,641C  
; CURRENT FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/315,304  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1757  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1650  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: HIV-1  
US-09-350-641C-1650

Query Match 48.2%; Score 27; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 4 WLTIWG 9  
| : : : :  
DB 1 WDSLWG 6

RESULT 13  
US-09-315-304B-1587  
; Sequence 1587, Application US/09315304B  
; Patent No. 6348568  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-052  
; CURRENT APPLICATION NUMBER: US/09/315,304B  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1667  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1587  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-315-304B-1587

Query Match 48.2%; Score 27; DB 3; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.1e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
| : : : :  
DB 1 GGWASLW 7

RESULT 14  
US-09-350-325-47  
; Sequence 47, Application US/09350325  
; Patent No. 6541020  
; GENERAL INFORMATION:  
; APPLICANT: Ding, S.  
; APPLICANT: Kang, M.  
; APPLICANT: Venetta, T.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ADMINISTRATION OF THERAPEUTIC REAGENTS  
; FILE REFERENCE: 7872-062  
; CURRENT APPLICATION NUMBER: US/09/350,325  
; CURRENT FILING DATE: 1999-07-09  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 47  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: enhancer peptide  
US-09-350-325-47

Query Match 48.2%; Score 27; DB 4; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.1e+02;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
| : : : :  
DB 1 GGWASLW 7

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RESULT 15
US-09-350-641C-1587
; Sequence 1587, Application US/09350641C
; Patent No. 6656906
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-067
; CURRENT APPLICATION NUMBER: US/09/350,641C
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1587
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-641C-1587

Query Match      48.2%; Score 27; DB 4; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.1e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GYWLTIW 8
Db      1 GSWASLW 7

Search completed: December 29, 2004, 21:36:44
Job time : 24.6667 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 21:36:53 ; Search time 82 Seconds  
(without alignments)  
43.869 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 182644

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*

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- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
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- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
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- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	96.4	10	13	US-10-046-922-34 Sequence 34, Appl
2	54	96.4	10	13	US-10-046-922-35 Sequence 35, Appl
3	33	58.9	7	13	US-10-046-922-67 Sequence 67, Appl
4	33	58.9	8	13	US-10-046-922-68 Sequence 68, Appl
5	33	58.9	10	13	US-10-046-922-73 Sequence 73, Appl
6	31	55.4	9	13	US-10-046-922-36 Sequence 36, Appl
7	31	55.4	10	15	US-09-572-404B-1454 Sequence 1454, Ap
8	30	53.6	10	15	US-10-462-452-707 Sequence 707, App
9	30	53.6	10	15	US-10-601-953-812 Sequence 812, App
10	30	53.6	10	16	US-10-322-266-708 Sequence 708, App
11	29	51.8	9	9	US-09-894-018-154 Sequence 154, App
12	29	51.8	9	14	US-10-133-210-8 Sequence 8, Appli
13	29	51.8	9	14	US-10-371-525-348 Sequence 348, App

14	29	51.8	9	14	US-10-371-069-348	Sequence 348, App
15	29	51.8	9	14	US-10-371-645-348	Sequence 348, App
16	29	51.8	9	14	US-10-371-360-348	Sequence 348, App
17	29	51.8	9	15	US-10-182-252A-180	Sequence 180, App
18	29	51.8	9	15	US-10-182-252A-181	Sequence 181, App
19	29	51.8	9	15	US-10-182-252A-305	Sequence 305, App
20	29	51.8	9	15	US-10-182-252A-792	Sequence 792, App
21	29	51.8	9	15	US-10-182-252A-793	Sequence 793, App
22	29	51.8	9	15	US-10-182-252A-837	Sequence 837, App
23	29	51.8	9	15	US-10-182-252A-838	Sequence 838, App
24	29	51.8	9	15	US-10-182-252A-1271	Sequence 1271, Ap
25	29	51.8	9	17	US-10-474-960A-154	Sequence 154, App
26	29	51.8	10	8	US-08-821-739A-52	Sequence 92, Appl
27	29	51.8	10	14	US-10-133-210-7	Sequence 7, Appli
28	29	51.8	10	14	US-10-133-210-40	Sequence 40, Appl
29	29	51.8	10	14	US-10-133-210-70	Sequence 70, Appl
30	29	51.8	10	14	US-10-200-708-355	Sequence 355, App
31	29	51.8	10	14	US-10-200-708-581	Sequence 581, App
32	28	50.0	10	10	US-09-793-451-69	Sequence 69, Appl
33	28	50.0	10	14	US-10-050-902-181	Sequence 181, App
34	28	50.0	10	14	US-10-050-998-181	Sequence 181, App
35	28	50.0	10	14	US-10-283-722-69	Sequence 69, Appl
36	28	50.0	10	14	US-10-283-903-69	Sequence 69, Appl
37	28	50.0	10	15	US-10-617-876-33	Sequence 33, Appl
38	27	48.2	8	14	US-10-351-641-1650	Sequence 1650, Ap
39	27	48.2	9	15	US-10-239-656-11	Sequence 11, Appl
40	27	48.2	10	14	US-10-347-562-47	Sequence 47, Appl
41	27	48.2	10	14	US-10-351-641-1587	Sequence 1587, Ap
42	27	48.2	10	15	US-10-239-656-34	Sequence 34, Appl
43	27	48.2	10	15	US-10-239-656-44	Sequence 44, Appl
44	27	48.2	10	16	US-10-327-598-450	Sequence 450, Appl
45	26	46.4	7	9	US-09-884-767A-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1  
US-10-046-922-34  
; Sequence 34, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 34  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Isolated peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (10)..(10)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-34

Query Match 96.4% ; Score 54; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.22; 0; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 GYWLTIWG 9  
DB 2 GYWLTIWG 9

```
RESULT 2
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35
Query Match          96.4%; Score 54; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GYWLTIWG 9
Db      2 GYWLTIWG 9
|||||||

RESULT 3
US-10-046-922-67
; Sequence 67, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 67
; LENGTH: 7
; TYPE: PRT
; ORGANISM: peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)..(6)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-67
Query Match          58.9%; Score 33; DB 13; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches      4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GYWLTIW 8
Db      1 GYWXXXW 7
|||||

RESULT 4
US-10-046-922-68
; Sequence 68, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
```

```
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 8
; TYPE: PRT
; ORGANISM: peptide
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (4)..(6)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (8)..(8)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-68
Query Match          58.9%; Score 33; DB 13; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches      4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GYWLTIW 8
Db      1 GYWXXXW 7
|||||

RESULT 5
US-10-046-922-73
; Sequence 73, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 10
; TYPE: PRT
; ORGANISM: peptide library
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)..(7)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (9)..(9)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-73
Query Match          58.9%; Score 33; DB 13; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.2e+02;
Matches      4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      2 GYWLTIW 8
Db      2 GYWXXXW 8
|||||

RESULT 6
US-10-046-922-36
; Sequence 36, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
```

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; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: peptide
US-10-046-922-36

Query Match      55.4%; Score 31; DB 13; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8
DB 2 GYWDWTW 8

RESULT 7
US-09-572-404B-1454
; Sequence 1454, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; PRIOR FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1454
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in P2RY5 at 139-148 and may interact with Sequen
; OTHER INFORMATION: in this patent.
US-09-572-404B-1454

Query Match      55.4%; Score 31; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIW 9
DB 1 GYWLTVIG 8

RESULT 8
US-10-462-452-707
; Sequence 707, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; FILE REFERENCE: Mucosal-Delivery of Interferon Beta
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 707
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-707

Query Match      53.6%; Score 30; DB 15; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
```

```
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YWLTIW 8
DB 5 YWANLW 10

RESULT 9
US-10-601-953-812
; Sequence 812, Application US/10601953
; Publication No. US20040077540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
; FILE REFERENCE: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; CURRENT APPLICATION NUMBER: US/10/601,953
; CURRENT FILING DATE: 2003-06-24
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 812
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-812

Query Match      53.6%; Score 30; DB 15; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YWLTIW 8
DB 5 YWANLW 10

RESULT 10
US-10-322-266-708
; Sequence 708, Application US/10322266
; Publication No. US20040115135A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide
; FILE REFERENCE: YY And Methods For Treating And Preventing Obesity
; CURRENT APPLICATION NUMBER: US/10/322,266
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 797
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 708
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-322-266-708

Query Match      53.6%; Score 30; DB 16; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YWLTIW 8
DB 5 YWANLW 10

RESULT 11
US-09-894-018-154
; Sequence 154, Application US/09894018
```

; Patent No. US20020119127A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMUNE, Inc.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Chestnut, Robert  
; APPLICANT: Livingston, Brian  
; APPLICANT: Baker, Denisw  
; APPLICANT: Newman, Mark  
; APPLICANT: Brown, David  
; TITLE OF INVENTION: METODS AND SYSTEM FOR OPTIMIZING  
; FILE REFERENCE: 39963-20033.00  
; CURRENT APPLICATION NUMBER: US/09/894,018  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/173,390  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 60/284,221  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 368  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 154  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Transgenic mouse  
US-09-894-018-154

Query Match 51.8%; Score 29; DB 9; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.5e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LTIWG 9  
Db 4 LTVWG 8

RESULT 12  
US-10-133-210-8  
; Sequence 8, Application US/10133210  
; Publication No. US20030103964A1  
; GENERAL INFORMATION:  
; APPLICANT: Delisi, Charles  
; APPLICANT: Berzofsky, Jay  
; APPLICANT: Gulukota, Kanalakar  
; APPLICANT: Vaccaro, Dennis  
; APPLICANT: Weng, Ziping  
; APPLICANT: Zhang, Chao  
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND  
; FILE REFERENCE: BU-035AX  
; CURRENT APPLICATION NUMBER: US/10/133,210  
; CURRENT FILING DATE: 2002-04-26  
; NUMBER OF SEQ ID NOS: 281  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-133-210-8

Query Match 51.8%; Score 29; DB 14; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.5e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LTIWG 9  
Db 4 LTVWG 8

RESULT 13

US-10-371-525-348  
; Sequence 348, Application US/10371525  
; Publication No. US20030203869A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; FILE REFERENCE: 39963-20022.01  
; CURRENT APPLICATION NUMBER: US/10/371,525  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR FILING DATE: US 09/311,784  
; PRIOR APPLICATION NUMBER: US 60/085,751  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 348  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV1 ENV 61 (peptide 25.0032)  
US-10-371-525-348

Query Match 51.8%; Score 29; DB 14; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.5e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LTIWG 9  
Db 4 LTVWG 8

RESULT 14  
US-10-371-069-348  
; Sequence 348, Application US/10371069  
; Publication No. US20030216342A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMUNE Inc.  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; FILE REFERENCE: 39963-20022.10  
; CURRENT APPLICATION NUMBER: US/10/371,069  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR FILING DATE: US 09/078,904  
; PRIOR APPLICATION NUMBER: US 60/085,751  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 348  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV1 ENV 61 (peptide 25.0032)  
US-10-371-069-348

Query Match 51.8%; Score 29; DB 14; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.5e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LTIWG 9  
||:|  
Db 4 LTVWG 8

RESULT 15  
US-10-371-645-348  
; Sequence 348, Application US/10371645  
; Publication No. US20030216343A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMMUNE Inc.  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 39963-20022.11  
; CURRENT APPLICATION NUMBER: US/10/371,645  
; CURRENT FILING DATE: 2003-06-20  
; PRIOR APPLICATION NUMBER: US 09/078,904  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: US 60/085,751  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 348  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV1 ENV 61 (peptide 25.0032)  
US-10-371-645-348

Query Match 51.8%; Score 29; DB 14; Length 9;  
Best Local Similarity 80.0%; Pred. No. 1.5e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LTIWG 9  
||:|  
Db 4 LTVWG 8

Search completed: December 29, 2004, 22:01:39  
Job time : 83 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:30:17 ; Search time 19 Seconds  
(without alignments)  
50.640 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	42.9	10	S71868	glutathione transf
2	22	39.3	7	PT0586	T-cell receptor be
3	22	39.3	10	T17075	cytochrome-c oxida
4	20	35.7	5	JH0253	gut pentapeptide -
5	19	33.9	9	PT0324	Ig heavy chain CRD
6	19	33.9	10	PT0289	Ig heavy chain CRD
7	18	32.1	8	JS0315	leucokinin V - Mad
8	18	32.1	10	PT0230	Ig heavy chain CDR
9	18	32.1	10	F31932	Ig mu chain J regi
10	17	30.4	4	B53284	T-cell receptor be
11	17	30.4	6	PT0629	T-cell receptor be
12	17	30.4	6	PT0637	T-cell receptor be
13	17	30.4	6	A61068	locustakinin - mig
14	17	30.4	7	PT0628	T-cell receptor be
15	17	30.4	7	PT0642	T-cell receptor be
16	17	30.4	7	PT0722	T-cell receptor be
17	17	30.4	7	PT0728	T-cell receptor be
18	17	30.4	7	PX0008	glucuronosyltransf
19	17	30.4	7	B48394	major fat-globule
20	17	30.4	7	PD0029	pev-kinin I - pena
21	17	30.4	7	S57274	triacylglycerol li
22	17	30.4	7	S33244	neuromodulatory pe
23	17	30.4	7	S33245	neuromodulatory pe
24	17	30.4	7	S33246	neuromodulatory pe
25	17	30.4	8	PT0724	T-cell receptor be
26	17	30.4	8	JS0316	leucokinin VI - Ma
27	17	30.4	8	JS0317	leucokinin VII - M
28	17	30.4	8	JS0318	leucokinin VIII -
29	17	30.4	8	A31570	angiotensin-conver

30	17	30.4	9	2	A24244	adipokinetic hormo
31	17	30.4	9	2	PT0634	T-cell receptor be
32	17	30.4	9	2	PT0562	T-cell receptor be
33	17	30.4	9	2	A60522	sperm-activating p
34	17	30.4	10	2	B33995	hypertrehalosemic h
35	17	30.4	10	2	S08997	hypertrehalosemic
36	17	30.4	10	2	A60421	hypertrehalosemic
37	17	30.4	10	2	S08998	hypertrehalosemic
38	17	30.4	10	2	A26381	hypertrehalosemic
39	17	30.4	10	2	JC1416	hypertrehalosemic
40	17	30.4	10	2	S09138	hypertrehalosemic
41	17	30.4	10	2	A31571	hypertrehalosemic/
42	17	30.4	10	2	A49187	gonadotropin-relea
43	17	30.4	10	2	PH1344	Ig heavy chain DJ
44	17	30.4	10	2	PH0923	T-cell receptor be
45	17	30.4	10	2	A40753	aldehyde ferredoxi

ALIGNMENTS

RESULT 1

S71868  
glutathione transferase (EC 2.5.1.18) class mu 4 - pig (fragment)  
N:Alternate names: glutathione S-transferase class mu 4  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 19-Mar-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004  
C:Accession: S71868  
R:Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.  
Biochem. J. 317, 879-884, 1996  
A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospray  
A:Reference number: S71864; MUID:96332484; PMID:8760377  
A:Accession: S71868  
A:Molecule type: protein  
A:Residues: 1-10 <ROU>  
A:Cross-references: UNIPROT:Q7M3E8  
C:Comment: At least five species-independent classes of cytosolic glutathion transferases  
s mitochondrial form are known.  
C:Complex: dimer  
C:Function:  
A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a v  
A:Pathway: detoxification; xenobiotics metabolism  
A>Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism  
es of damage  
C:Superfamily: glutathione transferase  
C:Keywords: dimer; transferase

Query Match 42.9%; Score 24; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 5.1e+02;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GW 4  
|||  
Db 4 GW 6

RESULT 2

PT0586  
T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0586; PT0592  
R:Peeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0586  
A>Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-7 <FEE>  
A:Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)  
C:Keywords: T-cell receptor

Query Match 39.3%; Score 22; DB 2; Length 7;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TIWG 9  
 :|||  
 Db 3 SIWG 6

RESULT 3  
 T17075  
 cytochrome-c oxidase (EC 1.9.3.1) chain I - Chamaeleo fischeri mitochondrion (fragment)  
 C;Species: mitochondrion Chamaeleo fischeri  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T17075  
 R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.  
 J. Mol. Evol. 44, 660-674, 1997  
 A;Title: Evolutionary shifts in three major structural features of the mitochondrial gene  
 A;Reference number: Z18674; MUID:97315309; PMID:9169559  
 A;Accession: T17075  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-10 <YAM>  
 A;Cross-references: UNIPROT:O79912; EMBL:U82688; NID:G3603112; PIDN:AAC622  
 C;Genetics:  
 A;Genome: mitochondrion  
 A;Note: COI  
 C;Keywords: mitochondrion; oxidoreductase

Query Match 39.3%; Score 22; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 1e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WLTIW 8  
 :|||  
 Db 2 WLLRW 6

RESULT 4  
 JH0253  
 gut pentapeptide - Japanese eel  
 C;Species: Anguilla japonica (Japanese eel)  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
 C;Accession: JH0253  
 R;Uesaka, T.; Ikeda, T.; Kubota, I.; Munesaka, Y.; Ando, M.  
 Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
 A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
 A;Reference number: JH0253; MUID:92062113; PMID:1953755  
 A;Accession: JH0253  
 A;Molecule type: protein  
 A;Residues: 1-5 <UES>  
 A;Experimental source: gut  
 C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric  
 , and of the circular muscle of the gastro-intestinal junction.

Query Match 35.7%; Score 20; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYW 4  
 :|||  
 Db 1 GFW 3

RESULT 5  
 PT0324  
 Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C;Accession: PT0324  
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j

A;Reference number: PT0222; MUID:91108337; PMID:1899102  
 A;Accession: PT0324  
 A;Molecule type: DNA  
 A;Residues: 1-9 <YAM>  
 A;Experimental source: B lymphocyte  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 33.9%; Score 19; DB 2; Length 9;  
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8  
 :|||  
 Db 3 GYGESYW 9

RESULT 6  
 PT0289  
 Ig heavy chain CRD3 region (clone 4-109) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
 C;Accession: PT0289  
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 395-407, 1991  
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j  
 A;Reference number: PT0222; MUID:91108337; PMID:1899102  
 A;Accession: PT0289  
 A;Molecule type: DNA  
 A;Residues: 1-10 <YAM>  
 A;Experimental source: B lymphocyte  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 33.9%; Score 19; DB 2; Length 10;  
 Best Local Similarity 33.3%; Pred. No. 3e+03;  
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 WLTIWG 9  
 :|||  
 Db 4 WISWGG 9

RESULT 7  
 JS0315  
 leucokinin V - Madeira cockroach  
 C;Species: Leucophaea maderae (Madeira cockroach)  
 C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 C;Accession: JS0315  
 R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
 Comp. Biochem. Physiol. C 88, 27-30, 1987  
 A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic  
 A;Reference number: JS0315  
 A;Accession: JS0315  
 A;Molecule type: protein  
 A;Residues: 1-8 <HOL>  
 A;Cross-references: UNIPROT:P19987  
 C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile acti  
 C;Keywords: amidated carboxyl end; cephalomyotropic peptide  
 F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 32.1%; Score 18; DB 2; Length 8;  
 Best Local Similarity 37.5%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9  
 :|||  
 Db 1 GSGFSSWG 8

RESULT 8  
 PT0230  
 Ig heavy chain CDR3 region (clone 1-118A) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C:Accession: PT0230  
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0230  
A:Molecule type: DNA  
A:Residues: 1-10 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 32.1%; Score 18; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 LTIWG 9  
DB 3 ITIFG 7

RESULT 9  
F33932  
IG mu chain J region (E7) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 09-Jul-2004  
C:Accession: F33932  
R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.  
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989  
A:Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-1  
A:Reference number: A33932; MUID:89282823; PMID:2499887  
A:Accession: F33932  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-10 <BAC>  
A:Cross-references: UNIPROT:Q92406; UNIPROT:Q92409; UNIPROT:Q924Q1; UNIP  
PROT:Q9DCD9; UNIPROT:Q924R0; UNIPROT:Q8K172; UNIPROT:Q99LA6; UNIPROT:Q91X92; GB:M27106  
C:Keywords: immunoglobulin

Query Match 32.1%; Score 18; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.2e+03;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 YW 4  
DB 4 YW 5

RESULT 10  
B53284  
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: B53284  
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 881-888, 1991  
A:Title: Evolutionarily conserved organization and sequences of germline diversity and J  
A:Reference number: A53284; MUID:91342695; PMID:1678859  
A:Accession: B53284  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-4 <HAR>  
A:Cross-references: GB:S60737; NID:Q233916; PIDN:AAB19518.1; PID:Q233918  
A:Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIIP:60738)  
C:Keywords: T-cell receptor

Query Match 30.4%; Score 17; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 WG 9  
DB 2 WG 3

RESULT 11  
PT0629  
T-cell receptor beta chain V-D-J region (100-2AH) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0629; PT0528  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0629  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FEE>  
A:Experimental source: newborn thymus, strain BALB/c, clone 100-2AH  
A:Accession: PT0528  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FE2>  
A:Experimental source: adult thymus, strain BALB/c, clone 100-4AB  
C:Keywords: T-cell receptor

Query Match 30.4%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 WG 9  
DB 5 WG 6

RESULT 12  
PT0637  
T-cell receptor beta chain V-D-J region (111-1K) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0637  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0637  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FEE>  
A:Experimental source: newborn thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 30.4%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 WG 9  
DB 5 WG 6

RESULT 13  
A61068  
locustakinin - migratory locust  
C:Species: Locusta migratoria (migratory locust)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: A61068  
R:Schoofs, L.; Holman, G.M.; Proost, P.; Van Damme, J.; Hayes, T.K.; De Loof, A.  
Regul. Pept. 37, 43-57, 1992  
A:Title: Locustakinin, a novel myotropic peptide from Locusta migratoria, isolation, prin  
A:Reference number: A61068; MUID:92262851; PMID:1585017  
A:Accession: A61068  
A:Molecule type: protein  
A:Residues: 1-6 <SCH>  
A:Cross-references: UNIPROT:P41491  
C:Keywords: amidated carboxyl end; cephalomylotropic peptide; neuropeptide

F;6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 30.4%; Score 17; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 WG 9  
||  
Db 5 WG 6

## RESULT 14

PT0628

T-cell receptor beta chain V-D-J region (111-1AG) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0628

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0628

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <PEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 30.4%; Score 17; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 WG 9  
||  
Db 6 WG 7

## RESULT 15

PT0642

T-cell receptor beta chain V-D-J region (111-1H) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0642

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID:91277601; PMID:1711558

A;Accession: PT0642

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-7 <PEE>

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 30.4%; Score 17; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 WG 9  
||  
Db 5 WG 6

Search completed: December 29, 2004, 21:42:54

Job time : 20 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:27:57 ; Search time 100 Seconds  
(without alignments)  
57.537 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 2971

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	30.5	54.5	10	1 LABA_JATMU	P13270 jatropha mu
2	27	48.2	10	2 Q8SHF6	Q8shf6 chamealeo m
3	26	46.4	8	2 Q70Y57	Q70y57 fuerstia af
4	26	46.4	8	2 CAD45547	Cad45547 fuerstia
5	24	42.9	10	2 Q7M3E8	Q7m3e8 sus scrofa
6	24	42.9	10	2 Q8SHN1	Q8shn1 bradypodion
7	24	42.9	10	2 Q6JL97	Q6jl97 neisseria g
8	24	42.9	10	2 AAS16521	Aas16521 neisseria
9	23.5	42.0	9	2 Q85DB0	Q85db0 lepitemur s
10	23.5	42.0	9	2 Q85DB8	Q85db8 lepitemur e
11	23.5	42.0	9	2 Q94NA9	Q94na9 daubentonla
12	23.5	42.0	9	2 Q94NB0	Q94nb0 microcebus
13	23.5	42.0	9	2 Q94NB1	Q94nb1 microcebus
14	23.5	42.0	9	2 Q94NB2	Q94nb2 microcebus
15	23.5	42.0	9	2 Q94XE6	Q94xe6 tectocoris
16	23	41.1	10	2 Q8SHC6	Q8shc6 furcifer be
17	22	39.3	10	2 Q79912	Q79912 chamealeo f
18	22	39.3	10	2 Q9G897	Q9g897 chamealeo d
19	22	39.3	10	2 Q8SH83	Q8sh83 brookesia t
20	22	39.3	10	2 Q8SH85	Q8sh85 brookesia t
21	22	39.3	10	2 Q8SH88	Q8sh88 brookesia t
22	22	39.3	10	2 Q8SH90	Q8sh90 brookesia t
23	22	39.3	10	2 Q8SH96	Q8sh96 brookesia p
24	22	39.3	10	2 Q8SHA2	Q8sha2 brookesia b
25	22	39.3	10	2 Q8SHAS	Q8sha5 brookesia a
26	22	39.3	10	2 Q8SHC9	Q8shc9 furcifer ba
27	22	39.3	10	2 Q8SHD2	Q8shd2 chamealeo w
28	22	39.3	10	2 Q8SHD5	Q8shd5 chamealeo s
29	22	39.3	10	2 Q8SHD8	Q8shd8 chamealeo r
30	22	39.3	10	2 Q8SHS1	Q8she1 chamealeo q
31	22	39.3	10	2 Q8SHE4	Q8she4 chamealeo q

32	22	39.3	10	2 Q8SHE7	Q8she7 chamealeo p
33	22	39.3	10	2 Q8SHF3	Q8shf3 chamealeo m
34	22	39.3	10	2 Q8SHF9	Q8shf9 chamealeo j
35	22	39.3	10	2 Q8SHG5	Q8shg5 chamealeo h
36	22	39.3	10	2 Q8SHG8	Q8shg8 chamealeo g
37	22	39.3	10	2 Q8SHH1	Q8shh1 chamealeo i
38	22	39.3	10	2 Q8SHH4	Q8shh4 chamealeo f
39	22	39.3	10	2 Q8SHH7	Q8shh7 chamealeo e
40	22	39.3	10	2 Q8SHI0	Q8shi0 chamealeo d
41	22	39.3	10	2 Q8SHI3	Q8shi3 chamealeo c
42	22	39.3	10	2 Q8SHI6	Q8shi6 chamealeo c
43	22	39.3	10	2 Q8SHI9	Q8shi9 chamealeo c
44	22	39.3	10	2 Q8SHJ2	Q8shj2 chamealeo a
45	22	39.3	10	2 Q8SHJ5	Q8shj5 calumma par

ALIGNMENTS

RESULT 1  
LABA\_JATMU  
ID LABA\_JATMU STANDARD; PRT; 10 AA.  
AC P13270;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Labaditin.  
OS Jatropha multifida (Physic nut).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosid1; Malpighiales; Euphorbiaceae; Crotonoideae; Jatrophaeae;  
OC Jatropha.  
OX NCBI\_TaxID=3996;  
RN [1] \_TaxID=3996;  
RP SEQUENCE.  
RC TISSUE=latex;  
RA Kosai S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;  
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha  
RT multifida L. (Euphorbiaceae). Isolation and sequence determination by  
RT means of two-dimensional NMR.";  
RL FEBS Lett. 256:91-96(1989).  
CC -!- FUNCTION: Labaditin is an active peptide which inhibits the  
CC classical pathway of complement activation in vitro. Activity  
CC seems to be based on an interaction with C1.  
CC -!- PTM: This is a cyclic peptide.  
CC -!- MISCELLANEOUS: Latex of this plant is used in folkloric medicine  
CC for treatment of infected wounds, skins infections and scabies.  
KW Direct protein sequencing.  
SQ SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;

Query Match 54.5%; Score 30.5; DB 1; Length 10;  
Best Local Similarity 62.5%; Pred. No. 3.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 GYWLTWGX 9  
| | | | |  
Db 2 GYW-TWGX 8

RESULT 2  
Q8SHF6 PRELIMINARY; PRT; 10 AA.  
ID Q8SHF6;  
AC Q8SHF6;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Chamealeo melleri (Meller's chameleon).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.  
OX NCBI\_TaxID=179915;

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RN  SEQUENCE FROM N.A.
RP  MEDLINE=22169767; PubMed=12182400;
RX  Townsend T., Larson A.;
RT  "Molecular phylogenetics and mitochondrial genomic evolution in the
RL  chamaeleonidae (Reptilia, Squamata).";
RN  Mol. Phylogenet. Evol. 23:22-36(2002).
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Townsend T.M., Larson A.L.;
RL  Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF48755; AAL90547.1; -
DR  GO; GO:0005739; C:mitochondrion; IEA.
KW  Mitochondrion.
FT  NON TER 10 10
SQ  SEQUENCE 10 AA; 1276 MW; 5E218E2733772727 CRC64;

Query Match 48.2%; Score 27; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 WLTW 8
Db 2 WLLW 6

RESULT 3
Q70Y57 PRELIMINARY; PRT; 8 AA.
AC Q70Y57;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN Name=tps16;
OS Fuerstia africana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fierstia.
OX NCBI_TaxID=204226;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15019625;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 46.4%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TIWG 9
Db 2 TIWG 5

RESULT 4
CAD45547 PRELIMINARY; PRT; 8 AA.
AC CAD45547;
DT 14-MAR-2004 (TrEMBLrel. 27, Created)
DT 14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).

```

```

GN RPS16.
OS Fuerstia africana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fierstia.
OX NCBI_TaxID=204226;
RN [1]
RP SEQUENCE FROM N.A.
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -
KW Chloroplast; Ribosomal protein.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 46.4%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TIWG 9
Db 2 TIWG 5

RESULT 5
Q7M3E8 PRELIMINARY; PRT; 10 AA.
AC Q7M3E8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glutathione transferase (EC 2.5.1.18) class mu 4 (Fragment).
OS Sus scrofa domestica (domestic pig)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9825;
RN [1]
RP SEQUENCE.
RA Rouimi P., Anglade P., Debrauwer L., Tulliez J.;
RT "Characterization of pig liver glutathione S-transferases using HPLC-
RT electrospray-ionization mass spectrometry.";
RL Biochem. J. 317:879-884(1996).
DR PIR; S71868; S71868.
DR GO; GO:0004364; F:glutathione transferase activity; IEA.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1223 MW; 5E16395AB36B5877 CRC64;

Query Match 42.9%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYW 4
Db 4 GYW 6

RESULT 6
Q8SHN1 PRELIMINARY; PRT; 10 AA.
AC Q8SHN1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Bradypodion tavetanum (Dwarf Fischer's chameleon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

RESULT 10

Q85DB8  
ID Q85DB8 PRELIMINARY; PRT; 9 AA.  
AC Q85DB8  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Lepilemur edwardsi (Milne-Edwards's sportive lemur).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.  
OX NCBI\_TaxID=122230;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).  
DR EMBL; AF224595; AAK33644.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1 1  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
Query Match 42.0%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
QY 3 YWLTWG 9  
DB 5 YW---WG 8  
RESULT 11  
Q94NA9  
ID Q94NA9 PRELIMINARY; PRT; 9 AA.  
AC Q94NA9  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Daubentonia madagascariensis (Aye-aye).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirhini; Daubentonidae;  
OX NCBI\_TaxID=31869;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184272; PubMed=11286490;  
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
RT "Molecular phylogeny of the lemur family Cheirogaleidae (primates) based on mitochondrial DNA sequences.";  
RL Mol. Phylogenet. Evol. 19:45-56(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22281620; PubMed=12393004;  
RA Pastorini J., Forstner M.R., Martin R.D.;  
RT "Phylogenetic relationships among Lemuridae (Primates): evidence from mtDNA.";  
RL J. Hum. Evol. 43:463-478(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).  
DR EMBL; AF224641; AAK70615.1; -.  
DR EMBL; AF224642; AAK70619.1; -.

DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1 1  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
Query Match 42.0%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
QY 3 YWLTWG 9  
DB 5 YW---WG 8  
RESULT 12  
Q94NB0  
ID Q94NB0 PRELIMINARY; PRT; 9 AA.  
AC Q94NB0  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Microcebus rufus (Brown mouse lemur).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;  
OC Microcebus.  
OX NCBI\_TaxID=122232;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21184272; PubMed=11286490;  
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
RT "Molecular phylogeny of the lemur family Cheirogaleidae (primates) based on mitochondrial DNA sequences.";  
RL Mol. Phylogenet. Evol. 19:45-56(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22631663; PubMed=12719521;  
RA Pastorini J., Thalmann U., Martin R.D.;  
RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).  
DR EMBL; AF224636; AAK70595.1; -.  
DR EMBL; AF224637; AAK70599.1; -.  
DR EMBL; AF224638; AAK70603.1; -.  
DR EMBL; AF224639; AAK70607.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
FT NON TER 1 1  
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
Query Match 42.0%; Score 23.5; DB 2; Length 9;  
Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
QY 3 YWLTWG 9  
DB 5 YW---WG 8  
RESULT 13  
Q94NB1  
ID Q94NB1 PRELIMINARY; PRT; 9 AA.  
AC Q94NB1  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cytochrome oxidase subunit III (Fragment).  
GN Name=COIII;  
OS Microcebus ravelobensis.  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
OC Microcebus.
OX NCBI_TaxID=122231;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184272; PubMed=11286490;
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates)
RL based on mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 19:45-56(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22631663; PubMed=12719521;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
RL lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
DR EMBL; AF224630; AAK70571.1; -.
DR EMBL; AF224631; AAK70575.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;

Query Match 42.0%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 YWLTWIG 9
DB 5 YW---WG 8

RESULT 14
O94NB2 PRELIMINARY; PRT; 9 AA.
AC Q94NB2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit III (Fragment).
GN Name=COLII;
OS Microcebus murinus (Lesser mouse lemur).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;
OC Microcebus.
OX NCBI_TaxID=30608;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21184272; PubMed=11286490;
RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;
RT "Molecular phylogeny of the lemur family cheirogaleidae (primates)
RL based on mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 19:45-56(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22631663; PubMed=12719521;
RA Pastorini J., Thalmann U., Martin R.D.;
RT "A molecular approach to comparative phylogeography of extant Malagasy
RL lemurs.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).
DR EMBL; AF224624; AAK70547.1; -.
DR EMBL; AF224625; AAK70551.1; -.
DR EMBL; AF224626; AAK70555.1; -.
DR EMBL; AF224627; AAK70559.1; -.
DR EMBL; AF224628; AAK70563.1; -.
DR EMBL; AF224629; AAK70567.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;

Query Match 42.0%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 YWLTWIG 9
DB 5 YW---WG 8

RESULT 15
O94XE6 PRELIMINARY; PRT; 9 AA.
AC Q94XE6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit III (Fragment).
GN Name=cox3;
OS Tectocoris diophthalmus (cotton harlequin bug).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Panheteroptera; Pentatomomorpha; Pentatomoidea; Pentatomidae;
OC Tectocoris.
OX NCBI_TaxID=159956;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396409; PubMed=11504862;
RA Shao R., Campbell N.J., Schmidt E.R., Barker S.C.;
RT "Increased rate of gene rearrangement in the mitochondrial genomes of
RL three orders of hemipteroid insects.";
RL Mol. Biol. Evol. 18:1828-1832(2001).
DR EMBL; AF335990; AAK5283.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1206 MW; A2C563636B5041A6 CRC64;

Query Match 42.0%; Score 23.5; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 3 YWLTWIG 9
DB 5 YW---WG 8

Search completed: December 29, 2004, 21:41:52
Job time : 101 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:55:07 ; Search time 69.6226 Seconds  
(without alignments)  
51.525 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23sep04: \*  
1: Genesecp1980s: \*  
2: Genesecp1990s: \*  
3: Genesecp2000s: \*  
4: Genesecp2001s: \*  
5: Genesecp2002s: \*  
6: Genesecp2003as: \*  
7: Genesecp2003bs: \*  
8: Genesecp2004s: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	96.4	10	5	ABP53931
2	54	96.4	10	5	ABP53932
3	43	76.8	13	6	AAO26093 FC region
4	43	76.8	13	8	ADJ50760 Human ser
5	43	76.8	474	6	ABU30004 Protein e
6	43	76.8	492	7	ADC97318
7	42	75.0	120	4	AAE62747
8	42	75.0	1140	4	AAE09365 Human ATP
9	42	75.0	1498	4	AAE09362 Mouse ATP
10	42	75.0	1503	2	AAV43544 A human M
11	42	75.0	1503	4	AAE09361 Human ATP
12	42	75.0	1503	4	AAE09370 Human ATP
13	42	75.0	1503	4	AAE09367 Human ATP
14	42	75.0	1503	4	AAE09368 Human ATP
15	42	75.0	1503	4	AAE09369 Human ATP
16	42	75.0	1503	4	AAE09364 Human ATP
17	42	75.0	1503	4	AAE09371 Human ATP
18	42	75.0	1503	4	AAE09363 Human ATP
19	42	75.0	1503	5	ABP52113 Homo sapi
20	41	73.2	14	6	AAO26134 FC region
21	41	73.2	14	8	ADJ50801 Human ser
22	41	73.2	34	4	ABB38460 Peptide #
23	41	73.2	34	4	AAM31901 Peptide #
24	41	73.2	34	4	AAM71604 Human bon
25	41	73.2	34	4	AAM59071 Human bra

26	41	73.2	34	4	ABG53286	Abg53286 Human liv
27	41	73.2	34	5	ABG41416	Abg41416 Human pep
28	41	73.2	222	2	AAAY00213	Aay00213 Enterococ
29	41	73.2	222	5	ABP43432	Abp43432 E faecali
30	41	73.2	222	6	ABU88460	Abu88460 E faecal
31	41	73.2	222	6	ABU13711	Abu13711 Enterococ
32	41	73.2	229	7	ADH85745	Adh85745 Enterococ
33	41	73.2	266	2	AAAY00212	Aay00212 Enterococ
34	41	73.2	266	5	ABP43431	Abp43431 E faecali
35	41	73.2	266	6	ABU88459	Abu88459 E faecal
36	41	73.2	266	6	ABU13710	Abu13710 Enterococ
37	41	73.2	567	8	ADN46152	Adn46152 Thermococ
38	40	71.4	116	2	AAAI5437	Aai15437 Heavy cha
39	40	71.4	116	6	ABO27261	AbO27261 ICAM-1 bi
40	40	71.4	116	6	ABO27269	AbO27269 ICAM-1 bi
41	40	71.4	116	6	ABO27263	AbO27263 ICAM-1 bi
42	40	71.4	116	6	ABO27259	AbO27259 ICAM-1 bi
43	40	71.4	116	6	ABO27255	AbO27255 ICAM-1 bi
44	40	71.4	116	6	ABO27277	AbO27277 Humanised
45	40	71.4	116	6	ABO27273	AbO27273 Murine 1A

ALIGNMENTS

RESULT 1  
ABP53931  
ID ABP53931 standard; peptide; 10 AA.  
AC ABP53931;  
DT 09-JAN-2003 (first entry)  
DE VEGFR-3 binding peptide SEQ ID NO:34.

KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytosolic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnary; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX Homo sapiens.  
OS Synthetic.

XX Key Location/Qualifiers  
FT Misc-difference 1 /note= "any amino acid"  
FT Misc-difference 10 /note= "any amino acid"  
WO200257299-A2.  
25-JUL-2002.

16-JAN-2002; 2002WO-IB0000099.  
17-JAN-2001; 2001US-0262476P.  
(LUDW-) LUDWIG INST CANCER RES.  
(LICN) LICENTIA LTD.

Alitalo K, Koivunen E, Kubo H;  
WPI; 2002-691521/74.

New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
such as cancer and diseases of neovascularization.

Claim 12; Page 80; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and

CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
 CC antidiabetic and vulnery activities, and can be used in gene therapy.  
 CC Compositions and methods from the present invention are useful for  
 CC diagnosing, evaluating and treating disorders mediated by the activity of  
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
 CC represents a specifically claimed VEGFR-3 binding peptide from the  
 CC present invention  
 XX Sequence 10 AA;  
 SQ

Query Match 96.4%; Score 54; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.091;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
 Db |||||

RESULT 3  
 ABP53932  
 ID ABP53932 standard; peptide; 10 AA.  
 XX  
 AC  
 XX  
 DT 09-JAN-2003 (first entry)  
 DE VEGFR-3 binding peptide SEQ ID NO:35.  
 XX  
 KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
 KW cyostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
 KW vulnery; cell surface receptor; cancer; neovascularisation;  
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
 KW diabetes; PDGF; platelet derived growth factor.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN W0200257299-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 16-JAN-2002; 2002WO-IB000099.  
 XX  
 PR 17-JAN-2001; 2001US-0262476P.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 PA (LICN) LICENTIA LTD.  
 XX  
 PI Aitalo K, Koivunen E, Kubo H;  
 XX  
 DR WPI; 2002-691521/74.  
 XX  
 PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
 PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
 PT such as cancer and diseases of neovascularization.  
 XX  
 PS Claim 13; Page 80; 149pp; English.  
 XX  
 CC The present invention describes an isolated peptide (I) that binds to and  
 CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
 CC antidiabetic and vulnery activities, and can be used in gene therapy.  
 CC Compositions and methods from the present invention are useful for  
 CC diagnosing, evaluating and treating disorders mediated by the activity of  
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
 CC represents a specifically claimed VEGFR-3 binding peptide from the  
 CC present invention  
 XX Sequence 10 AA;  
 SQ

Query Match 96.4%; Score 54; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.091;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
 Db |||||

RESULT 3  
 AAO26093  
 ID AAO26093 standard; peptide; 13 AA.  
 XX  
 AC AAO26093;  
 XX  
 DT 03-APR-2003 (first entry)  
 DE Fc region binding peptide SEQ ID NO 73.  
 XX  
 KW Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk;  
 KW antibody response; half-life; stability; circulatory system.  
 XX  
 OS Unidentified.  
 XX  
 PN W0200286070-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 18-APR-2002; 2002WO-US012492.  
 XX  
 PR 18-APR-2001; 2001US-0284534P.  
 XX  
 PA (DYAX-) DYAX CORP.  
 XX  
 PI Rondon IJ, Wu Q, Ley AC, Stochl M, Ransohoff TC, Potter MD;  
 XX  
 DR WPI; 2003-201220/19.  
 XX  
 PT New polypeptides, useful as binding molecules for detecting, isolating or  
 PT purifying immunoglobulin Fc-region polypeptides present in a solution, or  
 PT for regulating or preventing an antibody response.  
 XX  
 PS Claim 3; Page 76; 152pp; English.  
 XX  
 CC The invention relates to novel isolated polypeptides comprising a  
 CC sequence that binds an immunoglobulin Fc region. The polypeptides are  
 CC useful as binding molecules for detecting, isolating or purifying  
 CC immunoglobulin Fc-region polypeptides present in a solution, e.g. whole  
 CC blood, plasma or transgenic milk. The Fc-region binding polypeptides are  
 CC also useful for regulating or preventing an antibody response, or for  
 CC increasing the half-life and over all stability of a therapeutic or  
 CC diagnostic compound that is administered to or enters the circulatory  
 CC system of an individual. This sequence represents an Fc region binding  
 CC peptide of the invention  
 XX  
 SQ Sequence 13 AA;  
 Query Match 76.8%; Score 43; DB 6; Length 13;  
 Best Local Similarity 62.5%; Pred. No. 5.2;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
 ||| :||

```

'Db      1 GYWCNVWG 8

RESULT 4
ADJ50760
ID  ADJ50760 standard; peptide; 13 AA.
XX
XX  AC  ADJ50760;
XX
XX  DT  06-MAY-2004 (first entry)
XX
XX  DE  Human serum albumin binding peptide, Seq ID No 297.
XX
XX  KW  human serum albumin; HSA; serum; blood; tumour; human.
XX
XX  OS  Homo sapiens.
XX
XX  PN  WO2003106493-A1.
XX
XX  PD  24-DEC-2003.
XX
XX  PF  16-JUN-2003; 2003WO-US018896.
XX
XX  PR  14-JUN-2002; 2002US-0388642P.
XX
XX  PA  (DYAX-) DYAX CORP.
XX
XX  PI  Sato AK, Dawson BM;
XX
XX  WPI; 2004-082161/08.
XX
XX  Evaluating sample comprising soluble serum protein by forming complex
XX  comprising serum protein and physically associated compounds using
XX  peptide ligand that specifically binds with proteins, which is separated
XX  and evaluated.
XX
XX  Disclosure; SEQ ID NO 297; 191pp; English.
XX
XX  The invention relates to a method of evaluating sample by providing a
XX  soluble serum protein (1), one or more compounds physically associated
XX  with (1), and a (1)-binding agent that comprises a peptide that
XX  specifically binds to (1), allowing the (1)-binding agent to bind to (1)
XX  to form a complex including one or more compounds physically associated
XX  with (1), separating the complex from one or more components of the
XX  sample, and evaluating one or more of the physically associated
XX  compounds. The sample comprises blood or serum, or is obtained from a
XX  biopsy. The sample may also be obtained from a tumour or a region within
XX  5 mm of a tumour. The method is useful for detecting modulators that
XX  modulate interaction of serum protein-binding compound and serum protein
XX  and for identifying binding ligands for serum protein. The present
XX  sequence represents a serum albumin-binding peptide identified using the
XX  method of the invention.
XX
XX  Sequence 13 AA;

Query Match      76.8%; Score 43; DB 8; Length 13;
Best Local Similarity 62.5%; Pred. No. 5.2;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GYWLTIWG 9
      ||| :||
      1 GYWCNVWG 8

Db

RESULT 5
ABU30004
ID  ABU30004 standard; protein; 474 AA.
XX
XX  AC  ABU30004;
XX
XX  DT  19-JUN-2003 (first entry)
XX
XX  DE  Protein encoded by Prokaryotic essential gene #15531.
XX

XX  Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX  Enterococcus faecium.
XX
XX  WO200277183-A2.
XX
XX  03-OCT-2002.
XX
XX  21-MAR-2002; 2002WO-US009107.
XX
XX  21-MAR-2001; 2001US-00815242.
XX
XX  06-SEP-2001; 2001US-00948993.
XX
XX  25-OCT-2001; 2001US-0342923P.
XX
XX  08-FEB-2002; 2002US-00072851.
XX
XX  06-MAR-2002; 2002US-0362699P.
XX
XX  (ELIT-) ELITRA PHARM INC.
XX
XX  Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KU, Zykkind JW;
XX  Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX  WPI; 2003-029926/02.
XX
XX  N-PSDB; ACA33874.
XX
XX  New antisense nucleic acids, useful for identifying proteins or screening
XX  for homologous nucleic acids required for cellular proliferation to
XX  isolate candidate molecules for rational drug discovery programs.
XX
XX  Claim 25; SEQ ID NO 57928; 1766pp; English.
XX
XX  The invention relates to an isolated nucleic acid comprising any one of
XX  the 6213 antisense sequences given in the specification where expression
XX  of the nucleic acid inhibits proliferation of a cell. Also included are:
XX  (1) a vector comprising a promoter operably linked to the nucleic acid
XX  encoding a polypeptide whose expression is inhibited by the antisense
XX  nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX  polypeptide or its fragment whose expression is inhibited by the
XX  antisense nucleic acid; (4) an antibody capable of specifically binding
XX  the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX  proliferation or the activity of a gene in an operon required for
XX  proliferation; (7) identifying a compound that influences the activity of
XX  the gene product or that has an activity against a biological pathway
XX  required for proliferation, or that inhibits cellular proliferation; (8)
XX  identifying a gene required for cellular proliferation or the biological
XX  pathway in which a proliferation-required gene or its gene product lies
XX  or a gene on which the test compound that inhibits proliferation of an
XX  organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX  compound's activity; (11) a culture comprising strains in which the gene
XX  product is overexpressed or underexpressed; (12) determining the extent
XX  to which each of the strains is present in a culture or collection of
XX  strains; or (13) identifying the target of a compound that inhibits the
XX  proliferation of an organism. The antisense nucleic acids are useful for
XX  identifying proteins or screening for homologous nucleic acids required
XX  for cellular proliferation to isolate candidate molecules for rational
XX  drug discovery programs, or for screening homologous nucleic acids
XX  required for proliferation in cells other than S. aureus, S. typhimurium,
XX  K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
XX  the target prokaryotic essential genes. Note: The sequence data for this
XX  patent did not form part of the printed specification, but was obtained
XX  in electronic format directly from WIPO at
XX  ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 474 AA;

Query Match      76.8%; Score 43; DB 6; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
      |||||
      94 GYWLTCW 100

Db

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```

RESULT 6
ADC97318
ID ADC97318 standard; protein; 492 AA.
XX AC
XX ADC97318;
XX AC
XX 01-JAN-2004 (first entry)
XX DE
XX E. faecium protein sequence SEQ ID 6945.
XX XX
XX Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
XX KW abdominal-pelvic infection.
XX KW
XX Enterococcus faecium.
XX OS
XX US6583275-B1.
XX PN
XX 24-JUN-2003.
XX PD
XX 30-JUN-1998; 98US-00107532.
XX PF
XX 02-JUL-1997; 97US-0051571P.
XX PR
XX 14-MAY-1998; 98US-0085598P.
XX PR
XX (GENO-) GENOME THERAPEUTICS CORP.
XX PA
XX Doucette-Stamm LA, Bush D;
XX PI
XX WPI; 2003-799836/75.
XX DR
XX N-PSDB; ADC93664.
XX DR
XX
XX New isolated nucleic acid derived from Enterococcus faecium encoding an
XX PT Enterococcus faecium polypeptide useful for detection, prevention and
XX PT treatment of a pathological condition resulting from a bacterial
XX PT infection.
XX PT
XX Example 1; SEQ ID NO 6945; 243pp; English.
XX PS
XX The invention relates to an isolated nucleic acid derived from
XX CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
XX CC one of 10 fully defined sequences given in the (or comprising 40
XX CC sequential nucleotides chosen from any of the nucleic acids; its
XX CC complement or sequences hybridising to it). Also included are a
XX CC recombinant vector comprising the nucleic acid operably linked to
XX CC transcription regulatory element, a cell comprising the vector and a
XX CC single-stranded probe comprising the nucleic acid. The nucleic acids are
XX CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
XX CC The nucleic acids are useful for diagnosing pathological conditions
XX CC resulting from E. faecium bacterial infection (e.g. urinary tract
XX CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
XX CC infection) and for screening drugs such as agonists and antagonists. The
XX CC nucleic acid is useful for recombinant production of Candida albicans -
XX CC derived peptides or antisense polypeptides. Pharmaceutical compositions
XX CC and vaccines containing the nucleic acid are useful for preventing or
XX CC treating Enterococcus faecium infections. The present sequence represents
XX CC one if the disclosed E. faecium proteins.
XX CC
XX Sequence 492 AA;
XX
Query Match 76.8%; Score 43; DB 7; Length 492;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8
Db 112 GYWLTCW 118
|||||
|||||

RESULT 7
AAB62747
ID AAB62747 standard; protein; 120 AA.
XX

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```

AC AAB62747;
XX
XX 03-APR-2001 (first entry)
XX DE
XX Human HIV-1 monoclonal antibody SEQ ID NO: 46.
XX KW Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
XX KW envelope glycoprotein; gp120; diagnosis.
XX OS
XX Homo sapiens.
XX XX
XX WO200100678-A1.
XX PN
XX 04-JAN-2001.
XX PD
XX 23-JUN-2000; 2000WO-US017327.
XX PF
XX 30-JUN-1999; 99US-0141701P.
XX PR
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA
XX Watkins BA, Reitz MS;
XX PI
XX WPI; 2001-112438/12.
XX DR
XX N-PSDB; AAF29048.
XX DR
XX
XX Novel human monoclonal antibody immunoreactive with human
XX PT immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1
XX PT in biological sample and providing passive immunotherapy to HIV-1
XX PT infected mammal.
XX PT
XX Claim 1; Page 51-52; 81pp; English.
XX PS
XX The present invention provides the protein and coding sequences for the
XX CC variable regions of human monoclonal antibodies which are immunoreactive
XX CC with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120.
XX CC These can be used in diagnosis and therapy of HIV-1 infection
XX CC
XX Sequence 120 AA;
XX
Query Match 75.0%; Score 42; DB 4; Length 120;
Best Local Similarity 62.5%; Pred. No. 65;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTIW 9
Db 104 GYWVSYW 111
||||: ||
||||: ||

RESULT 8
AAE09365
ID AAE09365 standard; protein; 1140 AA.
XX
XX AAE09365;
XX AC
XX 19-NOV-2001 (first entry)
XX DT
XX Human ATP-binding cassette transporter ABCG6, MRP6 truncated mutant.
XX DE
XX Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
XX KW Multidrug Resistance-associated protein 6; macular degeneration; ABCG6;
XX KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
XX KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;
XX KW mutant; mutein.
XX KW
XX Homo sapiens.
XX OS
XX Synthetic.
XX OS
XX WO200162977-A2.
XX PN
XX 30-AUG-2001.
XX PD
XX 23-FEB-2001; 2001WO-US005741.
XX PF

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FT      /note= "encoded by ACT"
FT Misc-difference 1274
FT      /note= "encoded by TGC"
FT Misc-difference 1287
FT      /note= "encoded by TTC"
FT Misc-difference 1455
FT      /note= "encoded by CCC"
XX
XX WO9949735-A1.
XX
XX 07-OCT-1999.
XX
XX 26-MAR-1999; 99WO-US006644.
XX
XX 27-MAR-1998; 98US-0079759P.
XX 03-AUG-1998; 98US-0095153P.
XX (FOX-) FOX CHASE CANCER CENT.
XX
XX Kruh G, Lee K, Belinsky M, Bain L;
XX
XX WPI; 1999-610812/52.
XX N-PSDB; AAZ30081.
XX
XX New transporter gene useful for screening for anti-cancer drugs.
XX
XX Claim 39; Page 144-147; 153pp; English.
XX
XX The present sequence represents a human MPR-related ABC transporter
CC (MOAT) protein, designated MOAT-B. The protein comprises a multi-domain
CC structure including a tandem repeat of nucleotide binding folds appended
CC C-terminal to a hydrophobic domain, having Walker A and B ATP binding
CC sites and several potential membrane spanning domains. The MOAT nucleic
CC acids are useful for screening a test compound for inhibition of MOAT
CC mediated transport, indicated by restoration of anticancer drug
CC sensitivity, which in turn causes a reduction of transporter mediated
CC cellular efflux of anticancer agents. MOAT DNA or RNA may be used as
CC probes to detect the presence or expression of genes encoding MOAT
CC proteins. Anti-MOAT antibodies are useful for detecting and quantitating
CC MOAT proteins
XX
XX Sequence 1503 AA;
XX
XX Query Match 75.0%; Score 42; DB 2; Length 1503;
XX Best Local Similarity 71.4%; Pred. No. 7.7e+02;
XX Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 GYWLTIW 8
XX ||||:|
XX 965 GYWLTLW 971
XX
XX RESULT 11
XX AAE09361
XX ID AAE09361 standard; protein; 1503 AA.
XX
XX AC AAE09361;
XX
XX DT 19-NOV-2001 (first entry)
XX
XX DE Human ATP-binding cassette transporter ABCC6 (MRP6) protein.
XX
XX KW Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;
XX Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;
XX ATP-binding cassette transporter; arterial insufficiency; chromosome 16;
XX Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT 656..679
XX FT /note= "Nucleotide binding fold-1 (NFB-1) region"
XX FT 747..768

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FT      /note= "Nucleotide binding fold-1 (NFB-1) region"
FT 775..784
FT      /note= "Nucleotide binding fold-1 (NFB-1) region"
FT 1292..1307
FT      /note= "Nucleotide binding fold-2 (NFB-2) region"
FT 1321..1327
FT      /note= "Nucleotide binding fold-2 (NFB-2) region"
FT 1403..1433
FT      /note= "Nucleotide binding fold-2 (NFB-2) region"
XX
XX WO200162977-A2.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-US005741.
XX
XX 23-FEB-2000; 2000US-0184269P.
XX
XX (PXEI-) PXE INT INC.
XX (UYHA-) UNIV HAWAII.
XX
XX Boyd CD, Caiszar K, Lesaux O, Urban Z, Terry S;
XX
XX WPI; 2001-536645/59.
XX N-PSDB; AAD16230, AAD16231.
XX
XX Screening presence of Pseudoxanthoma elasticum mutation useful for
XX identifying homozygotes, compound heterozygotes or carriers involves
XX determining presence of mutation in MRP6 (ABCC6) nucleic acid.
XX
XX Example 2; Fig 3; 163pp; English.
XX
XX The invention relates to methods and compositions for diagnosing and
XX treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological
XX dysfunctions. The invention is useful for screening for the presence of a
XX PXE mutation. Mutations associated with PXE maps to the ATP-binding
XX cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-
XX 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa
XX protein located in the plasma membrane containing 17 membrane-spanning
XX helices grouped into three transmembrane domains. PXE is inherited as an
XX autosomal recessive phenotype or appears as a sporadic phenotype. PXE is
XX a heritable disorder characterised by mineralisation of elastic fibers in
XX skin, arteries and the retina, that result in dermal lesions with
XX associated laxity and loss of elasticity, arterial insufficiency,
XX cardiovascular disease and retinal haemorrhages leading to macular
XX degeneration. The method is useful for screening a population of
XX individuals in order to identify individuals with one or more PXE
XX associated MRP6 alleles who are then provided with appropriate genetic
XX counselling in view of the PXE status. The methods are useful for
XX identifying homozygotes, compound heterozygotes or carriers and thus are
XX useful in the area of genetic testing, carrier detection and prenatal
XX diagnosis. The present sequence is human ATP-binding cassette (ABC)
XX transporter, ABCC6 (MRP6) protein belonging to sub-family "C". Since
XX ABCC6 protein is involved in drug-resistance it is also called Multidrug
XX Resistance associated protein 6 (MRP6)
XX
XX Sequence 1503 AA;
XX
XX Query Match 75.0%; Score 42; DB 4; Length 1503;
XX Best Local Similarity 71.4%; Pred. No. 7.7e+02;
XX Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 GYWLTIW 8
XX ||||:|
XX 965 GYWLTLW 971
XX
XX Db
XX
XX RESULT 12
XX AAE09370
XX ID AAE09370 standard; protein; 1503 AA.
XX
XX AC AAE09370;
XX

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DT 19-NOV-2001 (first entry)

DE Human ATP-binding cassette transporter ABCC6 (MRP6) R1314W mutant.

XX Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;

XX Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;

KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;

KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;

XX mutant; mutuin.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1314

FT /note= "Wild type Arg substituted with Trp"

XX WO200162977-A2.

PN 30-AUG-2001.

XX 23-FEB-2001; 2001WO-US005741.

XX 23-FEB-2000; 2000US-0184269P.

XX (PXEI-) PXE INT INC.

PA (UYHA-) UNIV HAWAII.

XX Boyd CD, Csizsar K, Lesaux O, Urban Z, Terry S;

XX WPI; 2001-536645/59.

DR N-PSDB; AAD16263.

XX Screening presence of Pseudoxanthoma elasticum mutation useful for

PT identifying homozygotes, compound heterozygotes or carriers involves

PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.

XX Claim 13; Page; 163pp; English.

XX The invention relates to methods and compositions for diagnosing and

CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological

CC dysfunctions. The invention is useful for screening for the presence of a

CC PXE mutation. Mutations associated with PXE maps to the ATP-binding

CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-

CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa

CC protein located in the plasma membrane containing 17 membrane- spanning

CC helices grouped into three transmembrane domains. PXE is inherited as an

CC autosomal recessive phenotype or appears as a sporadic phenotype. PXE is

CC a heritable disorder characterised by mineralisation of elastic fibers in

CC skin, arteries and the retina, that result in dermal lesions with

CC associated laxity and loss of elasticity, arterial insufficiency,

CC cardiovascular disease and retinal haemorrhages leading to macular

CC degeneration. The method is useful for screening a population of

CC individuals in order to identify individuals with one or more PXE

CC associated MRP6 alleles who are then provided with appropriate genetic

CC counselling in view of the PXE status. The methods are useful for

CC identifying homozygotes, compound heterozygotes or carriers and thus are

CC useful in the area of genetic testing, carrier detection and prenatal

CC diagnosis. The present sequence is human ATP-binding cassette (ABC)

CC transporter, ABCC6 (MRP6) R1314W mutant protein. Note: The present

CC sequence is not shown in the specification but is derived from human ATP-

CC binding cassette transporter ABCC6 (MRP6) protein [SEQ ID NO: 3] shown in

CC figure 3 of the specification (AAE09361)

XX Sequence 1503 AA;

XX

Query Match 75.0%; Score 42; DB 4; Length 1503;

Best Local Similarity 71.4%; Pred. No. 7.7e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8

DB 965 GYWLTLW 971

RESULT 13

AAE09367

ID AAE09367 standard; protein; 1503 AA.

XX AAE09367;

AC AAE09367;

XX 19-NOV-2001 (first entry)

DT Human ATP-binding cassette transporter ABCC6 (MRP6) V1298F mutant.

DE Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;

XX Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;

KW ATP-binding cassette transporter; arterial insufficiency; chromosome 16;

KW Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;

XX mutant; mutuin.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1298

FT /note= "Wild type Val substituted with Phe"

XX WO200162977-A2.

PN 30-AUG-2001.

XX 23-FEB-2001; 2001WO-US005741.

XX 23-FEB-2000; 2000US-0184269P.

XX (PXEI-) PXE INT INC.

PA (UYHA-) UNIV HAWAII.

XX Boyd CD, Csizsar K, Lesaux O, Urban Z, Terry S;

XX WPI; 2001-536645/59.

DR N-PSDB; AAD16260.

XX Screening presence of Pseudoxanthoma elasticum mutation useful for

PT identifying homozygotes, compound heterozygotes or carriers involves

PT determining presence of mutation in MRP6 (ABCC6) nucleic acid.

XX Claim 13; Page; 163pp; English.

XX The invention relates to methods and compositions for diagnosing and

CC treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological

CC dysfunctions. The invention is useful for screening for the presence of a

CC PXE mutation. Mutations associated with PXE maps to the ATP-binding

CC cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-

CC 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa

CC protein located in the plasma membrane containing 17 membrane- spanning

CC helices grouped into three transmembrane domains. PXE is inherited as an

CC autosomal recessive phenotype or appears as a sporadic phenotype. PXE is

CC a heritable disorder characterised by mineralisation of elastic fibers in

CC skin, arteries and the retina, that result in dermal lesions with

CC associated laxity and loss of elasticity, arterial insufficiency,

CC cardiovascular disease and retinal haemorrhages leading to macular

CC degeneration. The method is useful for screening a population of

CC individuals in order to identify individuals with one or more PXE

CC associated MRP6 alleles who are then provided with appropriate genetic

CC counselling in view of the PXE status. The methods are useful for

CC identifying homozygotes, compound heterozygotes or carriers and thus are

CC useful in the area of genetic testing, carrier detection and prenatal

CC diagnosis. The present sequence is human ATP-binding cassette (ABC)

CC transporter, ABCC6 (MRP6) V1298F mutant protein. Note: The present

CC sequence is not shown in the specification but is derived from human ATP-

CC binding cassette transporter ABCC6 (MRP6) protein [SEQ ID NO: 3] shown in

CC figure 3 of the specification (AAE09361)

XX Sequence 1503 AA;

XX

Query Match 75.0%; Score 42; DB 4; Length 1503;  
Best Local Similarity 71.4%; Pred. No. 7.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
| | | | : |  
DB 965 GYWLTLW 971

RESULT 14  
AAE09368  
ID AAE09368 standard; protein; 1503 AA.  
XX AC AAE09368;  
XX 19-NOV-2001 (first entry)  
XX Human ATP-binding cassette transporter ABCC6 (MRP6) G1302R mutant.  
XX Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;  
XX Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;  
XX ATP-binding cassette transporter; arterial insufficiency; chromosome 16;  
XX Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;  
XX mutant; mutuin.  
XX Homo sapiens.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH Misc-difference 1302  
FT /note= "Wild type Gly substituted with Arg"  
XX WO200162977-A2.  
XX 30-AUG-2001.  
XX 23-FEB-2001; 2001WO-US005741.  
XX 23-FEB-2000; 2000US-0184269P.  
XX (PXEI-) PXE INT INC.  
XX (UYHA-) UNIV HAWAII.  
XX Boyd CD, Csizsar K, Lesaux O, Urban Z, Terry S;  
XX WPI; 2001-536645/59.  
XX N-PSDB; AAD16261.  
XX Screening presence of Pseudoxanthoma elasticum mutation useful for  
XX identifying homozygotes, compound heterozygotes or carriers involves  
XX determining presence of mutation in MRP6 (ABCC6) nucleic acid.  
XX Claim 13; Page; 163pp; English.  
XX The invention relates to methods and compositions for diagnosing and  
XX treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological  
XX dysfunctions. The invention is useful for screening for the presence of a  
XX PXE mutation. Mutations associated with PXE maps to the ATP-binding  
XX cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-  
XX 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa  
XX protein located in the plasma membrane containing 17 membrane-spanning  
XX helices grouped into three transmembrane domains. PXE is inherited as an  
XX autosomal recessive phenotype or appears as a sporadic phenotype. PXE is  
XX a heritable disorder characterised by mineralisation of elastic fibers in  
XX skin, arteries and the retina, that result in dermal lesions with  
XX associated laxity and loss of elasticity, arterial insufficiency,  
XX cardiovascular disease and retinal haemorrhages leading to macular  
XX degeneration. The method is useful for screening a population of  
XX individuals in order to identify individuals with one or more PXE  
XX associated MRP6 alleles who are then provided with appropriate genetic  
XX counselling in view of the PXE status. The methods are useful for  
XX identifying homozygotes, compound heterozygotes or carriers and thus are

CC useful in the area of genetic testing, carrier detection and prenatal  
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)  
CC transporter, ABCC6 (MRP6) G1302R mutant protein. Note: The present  
CC sequence is not shown in the specification but is derived from human ATP-  
CC binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: 3] shown in  
CC figure 3 of the specification (AAE09361)  
XX  
SQ Sequence 1503 AA;  
Query Match 75.0%; Score 42; DB 4; Length 1503;  
Best Local Similarity 71.4%; Pred. No. 7.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
| | | | : |  
DB 965 GYWLTLW 971

RESULT 15  
AAE09369  
ID AAE09369 standard; protein; 1503 AA.  
XX AC AAE09369;  
XX 19-NOV-2001 (first entry)  
XX Human ATP-binding cassette transporter ABCC6 (MRP6) A1303P mutant.  
XX Human; prenatal diagnosis; dermal lesion; cardiovascular disease; MRP6;  
XX Multidrug Resistance-associated protein 6; macular degeneration; ABCC6;  
XX ATP-binding cassette transporter; arterial insufficiency; chromosome 16;  
XX Pseudoxanthoma elasticum; PXE; heritable disorder; retinal haemorrhage;  
XX mutant; mutuin.  
XX Homo sapiens.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH Misc-difference 1303  
FT /note= "Wild type Ala substituted with Pro"  
XX WO200162977-A2.  
XX 30-AUG-2001.  
XX 23-FEB-2001; 2001WO-US005741.  
XX 23-FEB-2000; 2000US-0184269P.  
XX (PXEI-) PXE INT INC.  
XX (UYHA-) UNIV HAWAII.  
XX Boyd CD, Csizsar K, Lesaux O, Urban Z, Terry S;  
XX WPI; 2001-536645/59.  
XX N-PSDB; AAD16262.  
XX Screening presence of Pseudoxanthoma elasticum mutation useful for  
XX identifying homozygotes, compound heterozygotes or carriers involves  
XX determining presence of mutation in MRP6 (ABCC6) nucleic acid.  
XX Claim 13; Page; 163pp; English.  
XX The invention relates to methods and compositions for diagnosing and  
XX treating Pseudoxanthoma elasticum (PXE) and PXE associated physiological  
XX dysfunctions. The invention is useful for screening for the presence of a  
XX PXE mutation. Mutations associated with PXE maps to the ATP-binding  
XX cassette transporter ABCC6 (MRP6-Multidrug Resistance associated protein-  
XX 6) gene locus on chromosome 16. ABCC6 (MRP6) gene encodes a 165 kDa  
XX protein located in the plasma membrane containing 17 membrane-spanning  
XX helices grouped into three transmembrane domains. PXE is inherited as an  
XX autosomal recessive phenotype or appears as a sporadic phenotype. PXE is  
XX a heritable disorder characterised by mineralisation of elastic fibers in  
XX skin, arteries and the retina, that result in dermal lesions with  
XX associated laxity and loss of elasticity, arterial insufficiency,  
XX cardiovascular disease and retinal haemorrhages leading to macular  
XX degeneration. The method is useful for screening a population of  
XX individuals in order to identify individuals with one or more PXE  
XX associated MRP6 alleles who are then provided with appropriate genetic  
XX counselling in view of the PXE status. The methods are useful for  
XX identifying homozygotes, compound heterozygotes or carriers and thus are

CC skin, arteries and the retina, that result in dermal lesions with  
CC associated laxity and loss of elasticity, arterial insufficiency,  
CC cardiovascular disease and retinal haemorrhages leading to macular  
CC degeneration. The method is useful for screening a population of  
CC individuals in order to identify individuals with one or more PXE  
CC associated MRP6 alleles who are then provided with appropriate genetic  
CC counselling in view of the PXE status. The methods are useful for  
CC identifying homozygotes, compound heterozygotes or carriers and thus are  
CC useful in the area of genetic testing, carrier detection and prenatal  
CC diagnosis. The present sequence is human ATP-binding cassette (ABC)  
CC transporter, ABCC6 (MRP6) A1303P mutant protein. Note: The present  
CC sequence is not shown in the specification but is derived from human ATP-  
CC binding cassette transporter ABCC6 (MRP6) protein [SED ID NO: 3] shown in  
CC figure 3 of the specification (AAE09361)  
XX  
SQ Sequence 1503 AA;

Query Match 75.0%; Score 42; DB 4; Length 1503;  
Best Local Similarity 71.4%; Pred. NO. 7.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
DB 965 GYWLISLW 971  
||||:|

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Job time : 72.6226 secs

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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:59:07 ; Search time 23.0189 Seconds  
(without alignments)  
28.810 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/1aa/5B-COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A-COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6C-COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/6D-COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	76.8	492	US-09-107-532A-6945	Sequence 6945, Ap
2	42	75.0	1498	US-09-792-616-9	Sequence 9, Appli
3	42	75.0	1503	US-09-792-616-3	Sequence 3, Appli
4	41	73.2	222	US-09-071-035-408	Sequence 408, App
5	41	73.2	229	US-09-134-000C-3630	Sequence 3630, Ap
6	41	73.2	266	US-09-071-035-406	Sequence 406, App
7	40	71.4	668	US-09-248-796A-19350	Sequence 19350, A
8	39	69.6	478	US-09-107-532A-6868	Sequence 6868, Ap
9	38	67.9	328	US-09-540-236-2629	Sequence 2629, Ap
10	37	66.1	24	US-09-270-767-41173	Sequence 41173, A
11	37	66.1	132	US-09-270-767-56389	Sequence 56389, A
12	37	66.1	24	US-09-248-796A-22785	Sequence 22785, A
13	37	66.1	278	US-09-145-828A-11	Sequence 11, Appl
14	37	66.1	278	US-09-903-456-18	Sequence 18, Appl
15	37	66.1	499	US-09-252-991A-23328	Sequence 23328, A
16	37	66.1	591	US-09-561-077C-18	Sequence 18, Appl
17	37	66.1	591	US-09-221-014-18	Sequence 18, Appl
18	37	66.1	865	US-09-252-991A-19339	Sequence 19339, A
19	36.5	65.2	612	US-09-252-991A-19134	Sequence 19134, A
20	36	64.3	119	US-08-518-157B-5	Sequence 5, Appli
21	36	64.3	119	US-09-253-794-5	Sequence 5, Appli
22	36	64.3	172	US-09-107-532A-6560	Sequence 6560, Ap
23	36	64.3	219	US-09-247-373B-52	Sequence 52, Appl
24	36	64.3	242	US-08-512-955-4	Sequence 4, Appli
25	36	64.3	247	US-09-252-991A-26736	Sequence 26736, A
26	36	64.3	268	US-08-861-512-3	Sequence 3, Appli
27	36	64.3	280	US-08-414-685-2	Sequence 2, Appli

28	36	64.3	367	4	US-09-248-796A-15188	Sequence 15188, A
29	36	64.3	1528	1	US-08-463-092B-6	Sequence 6, Appli
30	36	64.3	1528	2	US-08-463-109A-6	Sequence 6, Appli
31	36	64.3	1528	3	US-08-460-907B-6	Sequence 6, Appli
32	36	64.3	1528	3	US-08-463-179A-6	Sequence 6, Appli
33	36	64.3	1528	3	US-08-461-384B-6	Sequence 6, Appli
34	36	64.3	1531	1	US-08-141-893-2	Sequence 2, Appli
35	36	64.3	1531	1	US-08-463-092B-2	Sequence 2, Appli
36	36	64.3	1531	1	US-08-463-092B-4	Sequence 2, Appli
37	36	64.3	1531	2	US-08-462-109A-2	Sequence 2, Appli
38	36	64.3	1531	2	US-08-462-109A-4	Sequence 2, Appli
39	36	64.3	1531	2	US-08-460-907B-2	Sequence 2, Appli
40	36	64.3	1531	2	US-08-460-907B-4	Sequence 2, Appli
41	36	64.3	1531	3	US-08-463-179A-2	Sequence 2, Appli
42	36	64.3	1531	3	US-08-463-179A-4	Sequence 2, Appli
43	36	64.3	1531	3	US-08-461-384B-2	Sequence 2, Appli
44	36	64.3	1531	3	US-08-461-384B-4	Sequence 2, Appli
45	36	64.3	1531	3	US-08-407-207A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-107-532A-6945  
; Sequence 6945, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arintello, Pamela Deneka  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 6945:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 492 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEetical: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...492  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6945:  
; US-09-107-532A-6945

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Query Match      76.8%; Score 43; DB 4; Length 492;
Best Local Similarity 85.7%; Pred. No. 66;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8
Db 112 GYWLTCW 118

RESULT 2
US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; FILE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9

Query Match      75.0%; Score 42; DB 4; Length 1498;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8
Db 960 GYWLTLW 966

RESULT 3
US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; FILE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-616-3

Query Match      75.0%; Score 42; DB 4; Length 1503;
Best Local Similarity 71.4%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8
Db 965 GYWLTLW 971

RESULT 4
US-09-071-035-408
; Sequence 408, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
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; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 408:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-408
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Query Match      73.2%; Score 41; DB 4; Length 222;
Best Local Similarity 62.5%; Pred. No. 59;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Qy 2 GYWLTIW 9
Db 179 GTWITLW 186
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RESULT 5
US-09-134-000C-3630
; Sequence 3630, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3630
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3630
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Query Match      73.2%; Score 41; DB 4; Length 229;
Best Local Similarity 62.5%; Pred. No. 61;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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Qy 2 GYWLTIW 9
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Db      203 GTWITLWG 210
| | | | |
; LENGTH: 668
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19350

Query Match      71.4%; Score 40; DB 4; Length 668;
Best Local Similarity 83.3%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 YWLTW 8
Db      372 YWLTW 377
| | | | |

RESULT 6
US-09-071-035-406
; Sequence 406, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 406:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-071-035-406

Query Match      73.2%; Score 41; DB 4; Length 266;
Best Local Similarity 62.5%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 GYWLTIWG 9
Db      203 GTWITLWG 210
| | | | |

RESULT 7
US-09-248-796A-19350
; Sequence 19350, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19350

Query Match      69.6%; Score 39; DB 4; Length 478;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
Db      98 GYWLSAW 104
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RESULT 9
US-09-540-236-2629
; Sequence 2629, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540.236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2629
; LENGTH: 328
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2629

Query Match      67.9%; Score 38; DB 4; Length 328;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GYWLTIW 8
Db      116 GWLTLW 122

RESULT 10
US-09-270-767-41173
; Sequence 41173, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41173
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-41173

Query Match      66.1%; Score 37; DB 4; Length 24;
Best Local Similarity 57.1%; Pred. No. 26;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      3 YWLTIWG 9
Db      16 HWLSLWG 22

RESULT 11
US-09-270-767-56389
; Sequence 56389, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 56389
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-56389

Query Match      66.1%; Score 37; DB 4; Length 24;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      3 YWLTIWG 9
Db      16 HWLSLWG 22

RESULT 12
US-09-248-796A-22785
; Sequence 22785, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074.725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096.409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 22785
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (6),(77),(85)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-22785

Query Match      66.1%; Score 37; DB 4; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GYWLTI 7
Db      123 GYWLTI 128

RESULT 13
US-09-145-828A-11
; Sequence 11, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.01
; CURRENT APPLICATION NUMBER: US/09/145.828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11

Query Match      66.1%; Score 37; DB 4; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GYWLTIW 8
```

Job time : 24.0189 secs

Db 108 GYWIFLW 114

## RESULT 14

US-09-903-456-18  
; Sequence 18, Application US/09903456  
; Patent No. 6677145  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Leonard, Amanda Eun-Yeong  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Pereira, Suzette L.  
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF  
; FILE REFERENCE: 6407.US.P3  
; CURRENT APPLICATION NUMBER: US/09/903,456  
; CURRENT FILING DATE: 2001-07-11  
; PRIOR APPLICATION NUMBER: US 09/624,670  
; PRIOR FILING DATE: 2000-07-24  
; PRIOR APPLICATION NUMBER: US 09/379,095  
; PRIOR FILING DATE: 1999-08-23  
; PRIOR APPLICATION NUMBER: US 09/145,828  
; PRIOR FILING DATE: 1998-09-02  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18  
; LENGTH: 278  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-09-903-456-18

Query Match 66.1%; Score 37; DB 4; Length 278;  
Best Local Similarity 57.1%; Pred. No. 2.8e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8

Db 108 GYWIFLW 114

## RESULT 15

US-09-252-991A-23328  
; Sequence 23328, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23328  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23328

Query Match 66.1%; Score 37; DB 4; Length 499;  
Best Local Similarity 57.1%; Pred. No. 5e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8

Db 111 GYWISAW 117

Search completed: December 30, 2004, 13:19:19

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 13:08:04 ; Search time 74.5283 Seconds  
(without alignments)  
48.267 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 KGYWLTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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18: /cgn2\_6/prodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	96.4	10	13	US-10-046-922-34
2	54	96.4	10	13	US-10-046-922-34
3	43	76.8	13	14	US-10-125-869A-73
4	43	76.8	13	15	US-10-462-262-297
5	43	76.8	474	15	US-10-282-122A-57928
6	43	76.8	671	16	US-10-437-963-190740
7	42	75.0	1498	10	US-09-792-616-9
8	42	75.0	1498	16	US-10-764-328-9
9	42	75.0	1503	10	US-09-792-616-3
10	42	75.0	1503	16	US-10-764-328-3
11	41	73.2	14	14	US-10-125-869A-114
12	41	73.2	14	15	US-10-462-262-338
13	41	73.2	34	9	US-09-864-761-43458

14	73.2	82	15	US-10-424-599-240891	Sequence 240891,
15	73.2	222	9	US-09-071-035-408	Sequence 408, App
16	73.2	222	14	US-10-206-576-408	Sequence 408, App
17	73.2	266	9	US-09-071-035-406	Sequence 406, App
18	73.2	266	14	US-10-206-576-406	Sequence 406, App
19	71.4	101	15	US-10-424-599-194869	Sequence 194869
20	71.4	116	10	US-09-910-483-1	Sequence 1, Appli
21	71.4	116	10	US-09-910-483-5	Sequence 5, Appli
22	71.4	116	10	US-09-910-483-9	Sequence 9, Appli
23	71.4	116	10	US-09-910-483-13	Sequence 13, Appli
24	71.4	116	10	US-09-910-483-17	Sequence 17, Appli
25	71.4	116	10	US-09-910-483-21	Sequence 21, Appli
26	71.4	116	10	US-09-910-483-25	Sequence 25, Appli
27	71.4	116	10	US-09-910-483-29	Sequence 29, Appli
28	71.4	116	10	US-09-910-483-33	Sequence 33, Appli
29	71.4	116	10	US-09-910-483-37	Sequence 37, Appli
30	71.4	116	10	US-09-910-483-41	Sequence 41, Appli
31	71.4	116	10	US-09-910-483-43	Sequence 43, Appli
32	71.4	138	14	US-10-160-232-86	Sequence 86, Appli
33	71.4	138	14	US-10-160-232-90	Sequence 90, Appli
34	71.4	373	14	US-10-369-493-8834	Sequence 8834, Ap
35	69.6	13	14	US-10-125-869A-75	Sequence 75, Appli
36	69.6	13	15	US-10-462-262-299	Sequence 299, App
37	69.6	57	15	US-10-424-599-226815	Sequence 226815,
38	69.6	86	17	US-10-425-115-188067	Sequence 188067,
39	69.6	91	14	US-10-156-761-13764	Sequence 13764, A
40	69.6	162	9	US-09-738-626-5178	Sequence 5178, Ap
41	69.6	452	14	US-10-091-007-88	Sequence 88, Appli
42	69.6	474	15	US-10-282-122A-52805	Sequence 52805, A
43	69.6	475	15	US-10-282-122A-57680	Sequence 57680, A
44	69.6	794	9	US-09-738-626-4579	Sequence 4579, Ap
45	68.8	101	17	US-10-425-115-260407	Sequence 260407,

ALIGNMENTS

RESULT 1  
US-10-046-922-34  
; Sequence 34, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGF-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 34  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Isolated peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (10)..(10)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-34

Query Match 96.4% ; Score 54; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.22; Indels 0; Gaps 0;  
Matches 8; Conservative 0; Mismatches 0;  
QY 2 GYWLTING 9  
DB 2 GYWLTING 9

RESULT 2  
US-10-046-922-35  
; Sequence 35, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: isolated peptide  
US-10-046-922-35

Query Match 96.4%; Score 54; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.22; Length 10;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYMLTWG 9  
|||||  
Db 2 GYMLTWG 9

RESULT 3  
US-10-125-869A-73  
; Sequence 73, Application US/10125869A  
; Publication No. US20030195671A1  
; GENERAL INFORMATION:  
; APPLICANT: Rondon, Isaac Jesus  
; APPLICANT: Wu, Qi-Long  
; APPLICANT: Ley, Arthur C.  
; APPLICANT: Stochl, Mark  
; APPLICANT: Ransohoff, Thomas C.  
; APPLICANT: Potter, M. Daniel (deceased)  
; TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION  
; FILE REFERENCE: 3421.1006-001  
; CURRENT APPLICATION NUMBER: US/10/125,869A  
; CURRENT FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: 60/284,534  
; PRIOR FILING DATE: 2001-04-18  
; NUMBER OF SEQ ID NOS: 200  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 73  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fc region binding polypeptide  
US-10-125-869A-73

Query Match 76.8%; Score 43; DB 14; Length 13;  
Best Local Similarity 62.5%; Pred. No. 10;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GYMLTWG 9  
|||||  
Db 1 GYWCNVWG 8

RESULT 4  
US-10-462-262-297  
; Sequence 297, Application US/10462262  
; Publication No. US20040009534A1  
; GENERAL INFORMATION:  
; APPLICANT: Sato, Aaron K.  
; APPLICANT: Dawson, Bruce M.

; TITLE OF INVENTION: PROTEIN ANALYSIS  
; FILE REFERENCE: 10280-052001  
; CURRENT APPLICATION NUMBER: US/10/462,262  
; CURRENT FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: US 60/388,642  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 430  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 297  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: immunoglobulin binding polypeptide  
US-10-462-262-297

Query Match 76.8%; Score 43; DB 15; Length 13;  
Best Local Similarity 62.5%; Pred. No. 10;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GYMLTWG 9  
|||||  
Db 1 GYWCNVWG 8

RESULT 5  
US-10-282-122A-57928  
; Sequence 57928, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Onisen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 57928  
; LENGTH: 474  
; TYPE: PRT  
; ORGANISM: Enterococcus faecium

US-10-282-122A-57928

Query Match 76.8%; Score 43; DB 15; Length 474;  
Best Local Similarity 85.7%; Pred. No. 2.4e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
      |||||  
Db 94 GYWLTCW 100

## RESULT 6

US-10-437-963-190740  
; Sequence 9, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 190740  
; LENGTH: 671  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_87125C.1.pgp  
US-10-437-963-190740

Query Match 76.8%; Score 43; DB 16; Length 671;  
Best Local Similarity 85.7%; Pred. No. 3.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YWLTIWG 9  
      |||  
Db 329 YWTTIWG 335

## RESULT 7

US-09-792-616-9  
; Sequence 9, Application US/09792616  
; Publication No. US20030165828A1  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; TITLE OF INVENTION: Pseudoxanthoma Elasticum  
; FILE REFERENCE: PXE-001  
; CURRENT APPLICATION NUMBER: US/09/792,616  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 1498  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-792-616-9

Query Match 75.0%; Score 42; DB 10; Length 1498;  
Best Local Similarity 71.4%; Pred. No. 9.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
      |||||

Db 960 GYWLSLW 966

## RESULT 8

US-10-764-328-9  
; Sequence 9, Application US/10764328  
; Publication No. US20040166521A1  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; TITLE OF INVENTION: Pseudoxanthoma Elasticum  
; FILE REFERENCE: PXE-001PC  
; CURRENT APPLICATION NUMBER: US/10/764,328  
; CURRENT FILING DATE: 2004-01-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 1498  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-764-328-9

Query Match 75.0%; Score 42; DB 16; Length 1498;  
Best Local Similarity 71.4%; Pred. No. 9.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
      |||||  
Db 960 GYWLSLW 966

## RESULT 9

US-09-792-616-3  
; Sequence 3, Application US/09792616  
; Publication No. US20030165828A1  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; TITLE OF INVENTION: Pseudoxanthoma Elasticum  
; FILE REFERENCE: PXE-001  
; CURRENT APPLICATION NUMBER: US/09/792,616  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 1503  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-792-616-3

Query Match 75.0%; Score 42; DB 10; Length 1503;  
Best Local Similarity 71.4%; Pred. No. 9.3e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
      |||||  
Db 965 GYWLSLW 971

## RESULT 10

US-10-764-328-3  
; Sequence 3, Application US/10764328  
; Publication No. US20040166521A1  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; APPLICANT: University of Hawaii  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; TITLE OF INVENTION: Pseudoxanthoma Elasticum  
; FILE REFERENCE: PXE-001PC  
; CURRENT APPLICATION NUMBER: US/10/764,328  
; CURRENT FILING DATE: 2004-01-23

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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-328-3

Query Match      75.0%; Score 42; DB 16; Length 1503;
Best Local Similarity 71.4%; Pred. No. 9.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GYWLTIW 8
Db      965 GYWLTLW 971

RESULT 11
US-10-125-869A-114
; Sequence 114, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Lev, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ransohoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
; TITLE OF INVENTION: POLYPEPTIDES
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-114

Query Match      73.2%; Score 41; DB 14; Length 14;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GYWLTIW 9
Db      1 GFWCTFWG 8

RESULT 12
US-10-462-262-338
; Sequence 338, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 338
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: MAP TO AC000403.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-764-328-3

Query Match      73.2%; Score 41; DB 15; Length 14;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 GYWLTIW 9
Db      1 GFWCTFWG 8

RESULT 13
US-09-864-761-43458
; Sequence 43458, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43458
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC000403.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
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; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4  
US-09-864-761-43458

Query Match 73.2%; Score 41; DB 9; Length 34;  
Best Local Similarity 62.5%; Pred. No. 46;  
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIW 9  
Db 25 GYWIIVFG 32

## RESULT 14

US-10-424-599-240891  
; Sequence 240891, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 240891  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(82)  
; OTHER INFORMATION: unsure at all Xaa locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_59551C.1.pap  
US-10-424-599-240891

Query Match 73.2%; Score 41; DB 15; Length 82;  
Best Local Similarity 71.4%; Pred. No. 16+02;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8  
Db 76 GYWLNLW 82

## RESULT 15

US-09-071-035-408  
; Sequence 408, Application US/09071035  
; Publication No. US20020045737A1  
; GENERAL INFORMATION:  
; APPLICANT: Gil H. Choi  
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
; NUMBER OF SEQUENCES: 496  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,035

; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: A. Anders Brookes  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB369P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 408:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 222 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-071-035-408

Query Match 73.2%; Score 41; DB 9; Length 222;  
Best Local Similarity 62.5%; Pred. No. 2.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTIW 9  
Db 179 GTWITLWG 186

Search completed: December 30, 2004, 13:50:00  
Job time : 75.5283 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:58:17 ; Search time 11.5094 Seconds  
(without alignments)  
83.598 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	75.0	441	2 C95307	probable transport
2	42	75.0	1502	2 T42216	multidrug resistanc
3	41	73.2	391	2 PC4117	replication protei
4	41	73.2	419	2 E90446	permease (importe
5	40	71.4	142	2 C34903	Ig heavy chain pre
6	40	71.4	425	2 B71038	probable Na+/H+-ex
7	40	71.4	508	2 C95282	probable ABC trans
8	39	69.6	376	2 AF1978	hypothetical prote
9	39	69.6	475	2 T46745	arginine/ornithine
10	39	69.6	490	2 C86879	arginine/ornithine
11	38	67.9	118	2 T35739	probable integral
12	38	67.9	426	2 C75176	na+/h+ antiporter
13	38	67.9	477	2 G90251	ABC transporter (im
14	38	67.9	583	2 T50103	probable oxidoredu
15	38	67.9	829	2 S58888	Ins P4-binding pro
16	38	67.9	829	2 S71847	Ins P4-binding pro
17	37.5	67.0	1063	2 A33830	cation efflux syst
18	37.5	67.0	1063	2 JC4700	cadmium, zinc, cob
19	37	66.1	123	1 AVMS14	Ig heavy chain V r
20	37	66.1	167	2 AF0881	probable exported
21	37	66.1	172	2 AI2232	hypothetical prote
22	37	66.1	187	1 S13868	ubiquinol-cytochro
23	37	66.1	197	2 AF2356	hypothetical prote
24	37	66.1	218	2 S76385	hypothetical prote
25	37	66.1	286	2 E88690	protein F41H10.7 [
26	37	66.1	292	2 S49164	lyser-type protein
27	37	66.1	360	2 S74751	CDP-glucose 4,6-de
28	37	66.1	380	2 S12839	Ig heavy chain pre
29	37	66.1	416	2 AF1127	rod shape-determin

30 37 66.1 472 2 E83497 probable amino aci  
31 37 66.1 482 2 JH0110 arginine/ornithine  
32 37 66.1 497 2 G86878 arginine/ornithine  
33 36.5 65.2 607 2 F82966 probable transcarb  
34 36 64.3 164 2 F89990 hypothetical prote  
35 36 64.3 171 2 E83140 phosphatidylglycer  
36 36 64.3 239 2 H85756 partial probable m  
37 36 64.3 241 2 G82391 hypothetical prote  
38 36 64.3 247 2 G81013 1-acyl-sn-glycerol  
39 36 64.3 247 2 A81957 1-acylglycerol-3-p  
40 36 64.3 250 2 A69843 hypothetical prote  
41 36 64.3 280 2 S81111 GP12 protein - yea  
42 36 64.3 292 2 A83779 hypothetical prote  
43 36 64.3 351 2 D84541 hypothetical prote  
44 36 64.3 385 2 S43540 YSD83 protein - ye  
45 36 64.3 387 2 B90862 probable membrane

ALIGNMENTS

RESULT 1

C95307  
probable transport protein Sma0684 [imported] - Sinorhizobium meliloti (strain 1021) mag  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: C95307  
R:Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows  
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti  
A:Reference number: A95262; MUID:21396509; PMID:11481432  
A:Accession: C95307  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-441 <UNP>  
A:Cross-references: UNIPROT:Q92ZT6; GB:AE006469; PIDN:AAK65021.1; PID:g14523451; GSPDB:G  
A:Experimental source: strain 1021, megaplasmid pSymA  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pella, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kias, E.; Komp, C.; Lelaure,  
habault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: Sma0684  
A:Genome: plasmid  
C:Superfamily: L-lysine transport protein

Query Match 75.0%; Score 42; DB 2; Length 441;  
Best Local Similarity 71.4%; Pred. No. 32;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
|||:|  
DB 92 GYWSIW 98

RESULT 2

T42216  
multidrug resistance-associated protein homolog MLP-1 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: T42216  
R:Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.  
Mol. Pharmacol. 53, 1068-1075, 1998  
A:Title: Hepatic expression of multidrug resistance-associated protein-like proteins mai  
A:Reference number: Z22081; MUID:98279126; PMID:9614210  
A:Accession: T42216  
A:Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA  
A;Residues: 1-1502 <HIR>  
A;Cross-references: UNIPROT:O88269; EMBL:AB010466; NID:g3242457; PIDN:BAA28954.1; PID:g3242457  
A;Experimental source: strain Sprague-Dawley; liver  
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 75.0%; Score 42; DB 2; Length 1502;  
Best Local Similarity 71.4%; Pred. No. 1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8  
| | | | |  
Db 964 GYWLTLW 970

RESULT 3  
PC4117  
replication protein homolog - Pyrococcus sp. (fragment)  
N;Alternate names: hypothetical 391 protein  
C;Species: Pyrococcus sp.  
C;Date: 07-Feb-1996 #sequence\_revision 19-Apr-1996 #text\_change 17-May-1996  
C;Accession: PC4117  
R;Rashid, N.; Morikawa, M.; Imanaka, T.  
Gene 166, 139-143, 1995  
A;Title: An abnormally acidic TATA-binding protein from a hyperthermophilic archaeon.  
A;Reference number: JC4514; MUID:96105215; PMID:8529878  
A;Accession: PC4117  
A;Molecule type: DNA  
A;Residues: 1-391 <RAS>  
A;Cross-references: DDBJ:DS0018

Query Match 73.2%; Score 41; DB 2; Length 391;  
Best Local Similarity 85.7%; Pred. No. 41;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YWLTIWG 9  
| | | | |  
Db 155 YWLTEWG 161

RESULT 4  
E90446  
permease [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C;Accession: E90446  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: E90446  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-419 <KUR>  
A;Cross-references: UNIPROT:Q97VB7; GB:AE006641; NID:g13816037; PIDN:AAK42828.1; GSPDB:G  
C;Genetics:  
A;Gene: SS02718

Query Match 73.2%; Score 41; DB 2; Length 419;  
Best Local Similarity 62.5%; Pred. No. 43;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9  
| | | | |  
Db 365 GFWE TLWG 372

RESULT 5  
C34903  
Ig heavy chain precursor V region (5-27) - mouse  
C;Species: Mus musculus (house mouse)

A;Molecule type: mRNA  
A;Residues: 1-1502 <HIR>  
A;Cross-references: UNIPROT:O88269; EMBL:AB010466; NID:g3242457; PIDN:BAA28954.1; PID:g3242457  
A;Experimental source: strain Sprague-Dawley; liver  
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 75.0%; Score 42; DB 2; Length 1502;  
Best Local Similarity 71.4%; Pred. No. 1e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8  
| | | | |  
Db 964 GYWLTLW 970

C;Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 16-Aug-1996  
C;Accession: C34903  
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
J. Biol. Chem. 265, 133-136, 1990  
A;Title: Active site structure and antigen binding properties of idiotypically cross-reacting antibodies  
A;Reference number: A34903; MUID:90094387; PMID:2104617  
A;Accession: C34903  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-142 <BED>  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;34-119/Domain: immunoglobulin homology <IMW>

Query Match 71.4%; Score 40; DB 2; Length 142;  
Best Local Similarity 62.5%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9  
| | | | |  
Db 126 GYWFATWG 133

RESULT 6  
B71038  
probable Na+/H+-exchanging protein - Pyrococcus horikoshii  
C;Species: Pyrococcus horikoshii  
C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 12-Jul-2004  
C;Accession: B71038  
R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine,  
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,  
DNA Res. 5, 55-76, 1998  
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon  
A;Reference number: A71000; MUID:98344137; PMID:9679194  
A;Accession: B71038  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-425 <KAW>  
A;Cross-references: UNIPROT:O59255; GB:AP000006; NID:g3236133; PIDN:BAA30706.1; PID:g3236133  
A;Experimental source: strain OT3  
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank  
C;Genetics:  
A;Gene: PH1594

Query Match 71.4%; Score 40; DB 2; Length 425;  
Best Local Similarity 75.0%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9  
| | | | |  
Db 319 GAWLTATWG 326

RESULT 7  
C95282  
probable ABC transporter, periplasmic solute-binding protein, family 5 Sma0302 [imported]  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: C95282  
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bower,  
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti  
A;Reference number: A95262; MUID:21396509; PMID:11481432  
A;Accession: C95282  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-508 <KUR>  
A;Cross-references: UNIPROT:Q930N2; GB:AE006469; PIDN:AAK64821.1; PID:g14523232; GSPDB:G  
A;Experimental source: strain 1021, megaplasmid pSymA  
R;Gallbert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001  
A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: Sma0302  
A:Genome: plasmid

Query Match 71.4%; Score 40; DB 2; Length 508;  
Best Local Similarity 85.7%; Pred. No. 74; Mismatches 1; Indels 0; Gaps 0;  
Matches 6; Conservative 0

QY 2 GYWLTIW 8  
|||||  
DB 393 GYWDTIW 399

RESULT 8  
AF1978  
hypothetical protein alr1377 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AF1978  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iritiguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120  
A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AF1978  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-376 <KUR>  
A:Cross-references: UNIPROT:Q8YX40; GB:BA000019; PIDN:BA873334.1; PID:G17130724; GSPDB:G17130724  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: alr1377

Query Match 69.6%; Score 39; DB 2; Length 376;  
Best Local Similarity 75.0%; Pred. No. 79; Mismatches 2; Indels 0; Gaps 0;  
Matches 6; Conservative 0

QY 2 GYWLTIW 9  
|||||  
DB 124 GEWLRWG 131

RESULT 9  
T46745  
arginine/ornithine antiporter [imported] - Lactobacillus sakei  
C:Species: Lactobacillus sakei  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: T46745  
R:Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, J. Bacteriol. 180, 4154-4159, 1998  
A:Title: Structural and functional analysis of the gene cluster encoding the enzymes of arginine catabolism  
A:Reference number: Z23141; MUID:98361304; PMID:9696763  
A:Accession: T46745  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-475 <ZUN>  
A:Cross-references: UNIPROT:O53092; EMBL:AJ001330; NID:G2764610; PIDN:CAA04686.1; PID:G2764610  
C:Genetics:  
A:Gene: arcD  
C:Function:  
A:Description: necessary for arginine transport; involved in ornithine-arginine exchange  
A:Pathway: arginine catabolism  
C:Superfamily: L-lysine transport protein

Query Match 69.6%; Score 39; DB 2; Length 475;  
Best Local Similarity 71.4%; Pred. No. 99;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GYWLTIW 8  
|||||  
DB 94 GYWLSAW 100

RESULT 10  
C86879  
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: C86879  
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: C86879  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-490 <STO>  
A:Cross-references: UNIPROT:Q9CB15; GB:AE005176; PID:G12725084; PIDN:AAK06133.1; GSPDB:G12725084  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: arcD  
C:Superfamily: L-lysine transport protein

Query Match 69.6%; Score 39; DB 2; Length 490;  
Best Local Similarity 71.4%; Pred. No. 1e+02; Mismatches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GYWLTIW 8  
|||||  
DB 93 GYWLSAW 99

RESULT 11  
T35739  
probable integral membrane protein - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
C:Accession: T35739  
R:Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.F. submitted to the EMBL Data Library, August 1999  
A:Reference number: Z21588  
A:Accession: T35739  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-118 <SAU>  
A:Cross-references: UNIPROT:Q9S2K9; EMBL:AL109732; PIDN:CAB52050.1; GSPDB:GN00070; SCORDB:GN00070  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCORDB:SC7H2.08  
C:Superfamily: Streptomyces coelicolor probable integral membrane protein SC7H2.08

Query Match 67.9%; Score 38; DB 2; Length 118;  
Best Local Similarity 57.1%; Pred. No. 38; Mismatches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 3 YWLTIMG 9  
:|||||  
DB 51 FWLSLWG 57

RESULT 12  
C75176  
na+/h+ antiporter (napa-2) PAB0390 - Pyrococcus abyssi (strain Orsay)  
C:Species: Pyrococcus abyssi  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004  
C:Accession: C75176  
R:anonymous, Genoscope  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure

A;Reference number: A75001  
 A;Accession: C75176  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-426 <RAW>  
 A;Cross-references: UNIPROT:Q9V160; GB:AJ248284; GB:AL096836; NID:G5457730; PIDN:CAB4949  
 A;Experimental source: strain Orsay  
 C;Genetics:  
 A;Gene: napA-2; PAB0390  
 C;Superfamily: Aquifex aeolicus Na<sup>+</sup>/H<sup>+</sup>-exchanging protein napA1

Query Match 67.9%; Score 38; DB 2; Length 426;  
 Best Local Similarity 62.5%; Pred. No. 1.3e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9

Db 320 GAWITAWG 327

# RESULT 13

ABCTransporter [imported] - Sulfolobus solfataricus  
 C;Species: Sulfolobus solfataricus  
 C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
 C;Accession: G90251  
 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-  
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.  
 arrett, R.A.; Ragan, M.A.; Sensesen, C.W.; Van der Oost, J.  
 submitted to GenBank, April 2001  
 A;Description: Sulfolobus solfataricus complete genome.  
 A;Reference number: A99139  
 A;Accession: G90251  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-477 <KUR>  
 A;Cross-references: UNIPROT:Q97ZC3; GB:AE006641; NID:G13814184; PIDN:AAK41270.1; GSPDB:G  
 C;Genetics:  
 A;Gene: SSO0999

Query Match 67.9%; Score 38; DB 2; Length 477;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 WLTIWG 9

Db 415 WITWVG 420

# RESULT 14

T50103  
 Probable oxidoreductase [imported] - fission yeast (Schizosaccharomyces pombe)  
 C;Species: Schizosaccharomyces pombe  
 C;Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
 C;Accession: T50103  
 R;Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
 submitted to the EMBL Data Library, January 2000  
 A;Reference number: Z25038  
 A;Accession: T50103  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-583 <SEE>  
 A;Cross-references: UNIPROT:Q9US28; EMBL:AL136499; PIDN:CAB66164.1; GSPDB:GN000066; SPDB:  
 A;Experimental source: strain 972h(-); cosmid ci1783  
 C;Genetics:  
 A;Gene: SPDB:SPAC1783.01  
 A;Map position: 1

Query Match 67.9%; Score 38; DB 2; Length 583;  
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9

Db 244 GRWPTIWG 251

# RESULT 15

S58888  
 Ins P4-binding protein - human  
 C;Species: Homo sapiens (man)  
 C;Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 04-Apr-2004  
 C;Accession: S58888  
 R;Cullen, P.J.; Hsuan, J.J.; Truong, O.; Letcher, A.J.; Jackson, T.R.; Dawson, A.P.; Irv  
 Nature 376, 527-530, 1995  
 A;Title: Identification of a specific Ins(1,3,4,5)P(4)-binding protein as a member of the  
 A;Reference number: S58888; MUID:95364929; PMID:7637787  
 A;Accession: S58888  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-829 <CUL>  
 A;Cross-references: EMBL:X89399  
 F;328-539/Domain: ras-specific GAP catalytic domain homology <GAP>  
 F;571-670/Domain: pleckstrin repeat homology <PLK>

Query Match 67.9%; Score 38; DB 2; Length 829;  
 Best Local Similarity 62.5%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9

Db 689 GHWLCCWG 696

Search completed: December 30, 2004, 13:17:12  
 Job time : 13.6761 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:57:52 ; Search time 92.2641 Seconds  
(without alignments)  
62.362 Million cell updates/sec

Title: US-10-046-922-34  
Perfect score: 56  
Sequence: 1 XGYWLTWGX 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	76.8	221	2 Q74JK6	Q74JK6 lactobacill
2	43	76.8	221	2 AAS08923	AAS08923 lactobacil
3	43	76.8	733	2 Q8H2N7	Q8H2N7 oryza sativ
4	42	75.0	284	2 G6MC01	G6MC01 parachlamyd
5	42	75.0	284	2 CAF23898	CAF23898 parachlam
6	42	75.0	441	2 Q922T6	Q922T6 rhizobium m
7	42	75.0	1308	2 Q876H2	Q876H2 dictyosteli
8	42	75.0	1498	1 MRP6_MOUSE	MRP6_MOUSE rattus norv
9	42	75.0	1502	1 MRP6_RAT	MRP6_RAT rattus norv
10	42	75.0	1503	1 MRP6_HUMAN	MRP6_HUMAN homo sapien
11	41	73.2	366	2 Q822B5	Q822B5 enterococcu
12	41	73.2	376	2 Q6CBE4	Q6CBE4 yarrowia li
13	41	73.2	413	2 Q9HKA9	Q9HKA9 thermoplasma
14	41	73.2	419	2 Q97VB7	Q97VB7 sulfolobus
15	41	73.2	736	2 Q8DMV4	Q8DMV4 synechococc
16	41	73.2	1052	2 Q7VZ84	Q7VZ84 plasmodium
17	41	73.2	1652	2 Q74DR3	Q74DR3 geobacter s
18	41	73.2	1652	2 AAR34628	AAR34628 geobacter
19	40	71.4	167	1 OB_MACMU	OB_MACMU macaca mula
20	40	71.4	331	2 Q775C7	Q775C7 bordetella
21	40	71.4	331	2 AAR97683	AAR97683 bordetell
22	40	71.4	401	2 Q9KHQ6	Q9KHQ6 bacteroides
23	40	71.4	425	2 Q59255	Q59255 pyrococcus
24	40	71.4	508	2 Q930N2	Q930N2 rhizobium m
25	40	71.4	1970	2 Q88H71	Q88H71 pseudomonas
26	39	69.6	91	2 Q82A22	Q82A22 streptomyce
27	39	69.6	117	2 Q7S013	Q7S013 neurospora
28	39	69.6	144	2 Q6M566	Q6M566 corynebacte
29	39	69.6	144	2 CAF21531	CAF21531 corynebac
30	39	69.6	162	2 Q8NQ86	Q8NQ86 corynebacte
31	39	69.6	253	2 Q32816	Q32816 lactococcus

32	39	69.6	257	2 Q9ARZ0	Q9ARZ0 oryza sativ
33	39	69.6	312	2 Q6C129	Q6C129 yarrowia li
34	39	69.6	376	2 Q8YX40	Q8YX40 anabaena sp
35	39	69.6	432	2 Q8ZUS8	Q8ZUS8 pyrobaculum
36	39	69.6	443	2 Q7NSJ2	Q7NSJ2 chromobacte
37	39	69.6	459	2 Q9KGV3	Q9KGV3 lactococcus
38	39	69.6	469	2 Q6TK71	Q6TK71 streptococc
39	39	69.6	469	2 AAR30325	AAR30325 streptoco
40	39	69.6	471	2 Q6HP27	Q6HP27 bacillus th
41	39	69.6	471	2 Q73E85	Q73E85 bacillus th
42	39	69.6	471	2 Q81IH9	Q81IH9 bacillus ce
43	39	69.6	471	2 AAS39409	AAS39409 bacillus
44	39	69.6	475	1 ARCD_LACSK	ARCD_LACSK lactobacill
45	39	69.6	475	2 Q8DWP9	Q8DWP9 streptococo

ALIGNMENTS

RESULT 1  
Q74JK6 PRELIMINARY; PRT; 221 AA.  
AC Q74JK6;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Hemolysin-like protein.  
GN OrderedLocusNames=LJ1101;  
OS Lactobacillus johnsonii.  
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
OC Lactobacillus.  
OX NCBI\_TaxID=33959;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NCC 533;  
RX PubMed=14966310;  
RA Pittmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,  
RA Pittet A.-C., Zwaalen M.-C., Rouvet M., Altermann E., Barrangou R.,  
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;  
RT "The genome sequence of the probiotic intestinal bacterium  
RT Lactobacillus johnsonii NCC 533."  
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).  
DR EMBL; AE017203; AAS08923.1; -;  
DR InterPro; IPR004254; HlyVIII related.  
DR InterPro; IPR005744; HlyIII-  
DR Pfam; PF03006; HlyVIII; 1.  
DR TIGRPFAMs; TIGR01065; hlyVIII; 1.  
KW Complete proteome.  
SQ SEQUENCE 221 AA; 24721 MW; 1D8C78FF9810E152 CRC64;

Query Match 76.8%; Score 43; DB 2; Length 221;  
Best Local Similarity 62.5%; Pred. No. 70;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GYWLITWG 9  
|:|:| :|:  
Db 172 GFLLVWG 179

RESULT 2  
AAS08923 PRELIMINARY; PRT; 221 AA.  
AC AAS08923;  
DT 02-MAR-2004 (Tremblrel. 27, Created)  
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)  
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)  
DE Hemolysin-like protein.  
GN LJ1101.  
OS Lactobacillus johnsonii.  
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
OC Lactobacillus.  
OX NCBI\_TaxID=33959;  
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=NCC 533;
RX PubMed=14966310;
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klaenhamer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
RT Lactobacillus johnsonii NCC 533.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517 (2004).
DR EMBL; AE017203; AAS08923.1; -.
SQ SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;

Query Match 76.8%; Score 43; DB 2; Length 221;
Best Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTING 9
Db 172 GFWLLVWG 179

RESULT 3
Q8H2N7 PRELIMINARY; PRT; 733 AA.
AC Q8H2N7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein O01138_B05.118.
GN Name=OJ1138_B05.118;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005486; BAC16197.1; -.
DR Gramene; Q8H2N7; -.
DR InterPro; IPR007658; DUF594.
DR Pfam; PF04578; DUF594; 1.
KW Hypothetical protein.
SQ SEQUENCE 733 AA; 82939 MW; E95884DAD1DC2AC9 CRC64;

Query Match 76.8%; Score 43; DB 2; Length 733;
Best Local Similarity 85.7%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 YWLTING 9
Db 328 YWTTING 334

RESULT 4
Q6MC01 PRELIMINARY; PRT; 284 AA.
AC Q6MC01;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN ORFNames=pc1174;
OS Parachlamydia sp. (strain UWE25) (subsp. Acanthamoeba sp.).
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=null;
RC Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.J., Drooge M., Frishman D.,
RA Rattei T., Mewes H.-W., Wagner M.;

```

```

RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RT the evolutionary history of chlamydiae.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX908798; CAF23898.1; -.
KW Hypothetical protein.
SQ SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;

Query Match 75.0%; Score 42; DB 2; Length 284;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YWLTING 9
Db 273 YWLSLWG 279

RESULT 5
CAF23898 PRELIMINARY; PRT; 284 AA.
AC CAF23898;
DT 14-APR-2004 (TrEMBLrel. 27, Created)
DT 14-APR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN PC1174.
OS Parachlamydia sp. UWE25.
OC Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Parachlamydia.
OX NCBI_TaxID=264201;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=UWE25;
RC Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.J., Drooge M., Frishman D.,
RA Rattei T., Mewes H., Wagner M.;
RT "Genome sequence of an amoeba symbiont and its use for reconstructing
RT the evolutionary history of chlamydiae.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=UWE25;
RA Horn M., Collingro A., Schmitz-Esser S., Beier C.L., Purkhold U.,
RA Fartmann B., Brandt P., Nyakatura G.J., Drooge M., Frishman D.,
RA Rattei T., Mewes H., Wagner M.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX908798; CAF23898.1; -.
KW Hypothetical protein.
SQ SEQUENCE 284 AA; 33607 MW; 569E29F0D7F6AECA CRC64;

Query Match 75.0%; Score 42; DB 2; Length 284;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YWLTING 9
Db 273 YWLSLWG 279

RESULT 6
Q92ZT6 PRELIMINARY; PRT; 441 AA.
AC Q92ZT6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable transport protein.
GN OrderedLocNames=RA0363; ORFNames=SMA0684;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymA.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.

```





DR ProDom; PD000006; ABC\_transporter; 1.  
 DR SMART; SM00382; AAA; 2.  
 DR TIGRFAM; TIGR00957; MRP\_assoc\_pro; 1.  
 DR PROSITE; PS00929; ABC\_TMIF; 2.  
 DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 2.  
 DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 2.  
 KW ATP-binding; Glycoprotein; Repeat; Transmembrane; Transport.  
 FT DOMAIN 5 37  
 FT TRANSMEM 38 58  
 FT DOMAIN 59 78  
 FT TRANSMEM 79 99  
 FT DOMAIN 100 104  
 FT TRANSMEM 105 125  
 FT DOMAIN 126 137  
 FT TRANSMEM 138 155  
 FT DOMAIN 156 173  
 FT TRANSMEM 174 194  
 FT DOMAIN 195 300  
 FT TRANSMEM 301 321  
 FT DOMAIN 322 347  
 FT TRANSMEM 348 368  
 FT DOMAIN 369 424  
 FT TRANSMEM 425 445  
 FT DOMAIN 446 468  
 FT TRANSMEM 449 469  
 FT DOMAIN 470 531  
 FT TRANSMEM 532 552  
 FT DOMAIN 553 574  
 FT TRANSMEM 575 595  
 FT DOMAIN 596 938  
 FT TRANSMEM 939 959  
 FT DOMAIN 960 996  
 FT TRANSMEM 997 1017  
 FT DOMAIN 1018 1060  
 FT TRANSMEM 1061 1081  
 FT DOMAIN 1082 1082  
 FT TRANSMEM 1083 1103  
 FT DOMAIN 1104 1174  
 FT TRANSMEM 1175 1195  
 FT DOMAIN 1196 1197  
 FT TRANSMEM 1198 1218  
 FT DOMAIN 1219 1502  
 FT TRANSMEM 1220 1502  
 FT DOMAIN 1503 1502  
 FT TRANSMEM 1503 1502  
 FT NP\_BIND 661 668  
 FT NP\_BIND 1298 1305  
 FT CARBOHYD 21 21  
 SQ SEQUENCE 1502 AA; 164995 MW; 539901B674A74A28 CRC64;

Query Match 75.0%; Score 42; DB 1; Length 1502;  
 Best Local Similarity 71.4%; Pred. No. 66+02;  
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLITW 8  
 |||:::  
 Db 964 GYWLSLW 970

## RESULT 10

MRP6\_HUMAN STANDARD; PRT; 1503 AA.  
 AC O95255; P78420; Q9UM27;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Multidrug resistance-associated protein 6 (ATP-binding cassette, sub-family C, member 6) (Anthracycline resistance-associated protein)  
 DE (Multi-specific organic anion transporter-E) (MOAT-E).  
 GN Name=ABCC6; Synonyms=MRP6, ARA;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99107222; PubMed=9892204;  
 RA Kool M., van der Linden M.P., de Haas M., Baas F., Borst P.;  
 RT "Expression of human MRP6, a homologue of the multidrug resistance  
 RT protein gene MRP1, in tissues and cancer cells.";  
 RL Cancer Res. 59:175-182(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99425270; PubMed=10493829;  
 RA Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,  
 RA Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,  
 RA Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,  
 RA Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;  
 RT "Genome duplications and other features in 12 Mb of DNA sequence from  
 RT human chromosome 16p and 16q.";  
 RL Genomics 60:295-308(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99352020; PubMed=10424734;  
 RA Belinsky M.G., Kruh G.D.;  
 RT "MOAT-E (ARA) is a full-length MRP/CMOAT subfamily transporter  
 RT expressed in kidney and liver.";  
 RL Br. J. Cancer 80:1342-1349(1999).  
 RN [4]  
 RP FUNCTION, AND CHARACTERIZATION OF VARIANTS PXE PHE-1298; ARG-1302 AND  
 RP SER-1321.  
 RX MEDLINE=21988190; PubMed=11880368; DOI=10.1074/jbc.M110918200;  
 RA Ilias A., Urban Z., Seidl T.L., Le Saux O., Boyd C.D.,  
 RA Sarkadi B., Varadi A.;  
 RT "Loss of ATP-dependent transport activity in pseudoxanthoma elasticum-  
 RT associated mutants of human ABCC6 (MRP6).";  
 RL J. Biol. Chem. 277:16860-16867(2002).  
 RN [5]  
 RP REVIEW, AND VARIANT PXE PRO-455.  
 RX MEDLINE=21321623; PubMed=11427982; DOI=10.1016/S1471-4914(00)01869-4;  
 RA Uitto J., Pulkkinen L., Ringpfeil F.;  
 RT "Molecular genetics of pseudoxanthoma elasticum: a metabolic disorder  
 RT at the environment-genome interface?";  
 RL Trends Mol. Med. 7:13-17(2001).  
 RN [6]  
 RP VARIANT GLN-1268.  
 RX MEDLINE=20374463; PubMed=10913334; DOI=10.1006/bbrc.2000.3101;  
 RA Germain D.P., Perdu J., Remones V., Jeunemaitre X.;  
 RT "Homozygosity for the R1268Q mutation in MRP6, the pseudoxanthoma  
 RT elasticum gene, is not disease-causing.";  
 RL Biochem. Biophys. Res. Commun. 274:297-301(2000).  
 RN [7]  
 RP VARIANT ARG-64.  
 RX MEDLINE=20514578; PubMed=11058917;  
 RA DOI=10.1002/1098-1004(200011)16:5<449::AID-HUMU24>3.0.CO;2-O;  
 RA Germain D.P., Perdu J., Remones V., Manzoni K., Jeunemaitre X.;  
 RT "Identification of two polymorphisms (C189G>C; C190T>C) in exon 2 of  
 RT the human MRP6 gene (ABCC6) by screening of pseudoxanthoma elasticum  
 RT patients: possible sequence correction?";  
 RL Hum. Mutat. 16:449-449(2000).  
 RN [8]  
 RP VARIANT PXE CVS-1339, AND VARIANT GLN-632.  
 RX MEDLINE=20408303; PubMed=10954200;  
 RA Strub B., Cai L., Zaech S., Ji W., Chung J., Lumsden A., Stumm M.,  
 RA Huber M., Schaefer L., Kim C.-A., Goldsmith L.A., Viljoen D.,  
 RA Figuera L.E., Fuchs W., Munier F., Ramesar R., Hohl D., Richards R.,  
 RA Neldner K.H., Lindpaintner K.;  
 RT "Mutations of the gene encoding the transmembrane transporter protein  
 RT ABC-C6 cause pseudoxanthoma elasticum.";  
 RL J. Mol. Med. 78:282-286(2000).  
 RN [9]  
 RP VARIANTS PXE PRO-1114; GLN-1138 AND TRP-1314, AND VARIANT ALA-614.  
 RX MEDLINE=20296630; PubMed=10835642; DOI=10.1038/76102;  
 RA Le Saux O., Urban Z., Tschuch C., Csizsar K., Bacchelli B.,  
 RA Quagliaro D., Pasquali-Ronchetti I., Pope F.M., Richards A., Terry S.,  
 RA Bercovich L., de Paeppe A., Boyd C.D.;  
 RT "Mutations in a gene encoding an ABC transporter cause pseudoxanthoma

RT elasticum.";

RL Nat. Genet. 25:223-227(2000).

RN [10]

RP VARIANT PXE TRP-1138, AND VARIANT GLN-1268.

RA MEDLINE=20283940; PubMed=10811882; DOI=10.1073/pnas.100041297;

RX Ringfeil F., Lebowitz M.G., Christiano A.M., Uitto J.;

RT "Pseudoxanthoma elasticum; mutations in the MRP6 gene encoding a

RT transmembrane ATP-binding cassette (ABC) transporter.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:6001-6006(2000).

RN [11]

RP VARIANTS PXE LYS-411; GLN-518; SER-568; PRO-673; GLN-765; PRO-1114;

RP TRP-1121; PRO-1138; ASP-1203; PHE-1298; ILE-1301; ARG-1302;

RP PRO-1303; GLN-1314; TRP-1314; SER-1321; CYS-1339; HIS-1347; ASN-1361;

RP LYS-1424, AND VARIANTS ASP-61; ARG-207; GLY-265; GLU-281; VAL-319;

RP LYS-497; ALA-614; GLN-632; HIS-953; CYS-1241 AND GLN-1268.

RX MEDLINE=21426347; PubMed=11536079;

RA Leaux O., Beck K., Sachinger C., Silvestri C., Treiber C.,

RA Goering H.H., Johnson E.W., De Paape A., Pope F.M.,

RA Pasquali-Ronchetti I., Bercovich L., Terry S., Boyd C.D.;

RT "A spectrum of ABC6 mutations is responsible for pseudoxanthoma

RT elasticum.";

RL Am. J. Hum. Genet. 69:749-764(2001).

RN [12]

RP VARIANTS PXE 60-ARG--TYR-62 DEL; ARG-364 AND ARG-1354, AND VARIANT

RP GLY-265.

RX MEDLINE=21558431; PubMed=11702217; DOI=10.1007/s004390100582;

RA Pulkkinen L., Nakano A., Ringfeil F., Uitto J.;

RT "Identification of ABC6 pseudogenes on human chromosome 16p:

RT implications for mutation detection in pseudoxanthoma elasticum.";

RL Hum. Genet. 109:356-365(2001).

RN [13]

RP VARIANTS ALA-614; GLN-632 AND GLN-1268.

RX MEDLINE=21632106; PubMed=11776382;

RA Wang J., Near S., Young K., Connolly P.W., Hegele R.A.;

RT "ABC6 gene polymorphism associated with variation in plasma

RT lipoproteins.";

RL J. Hum. Genet. 46:699-705(2001).

CC -1- FUNCTION: May participate directly in the active transport of

CC drugs into subcellular organelles or influence drug distribution

CC indirectly. Transports glutathione conjugates as leukotriene-4

CC (LTC4) and N-ethylmaleimide S-glutathione (NEM-GS).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

CC -1- TISSUE SPECIFICITY: Expressed in kidney and liver. Very low

CC expression in other tissues.

CC -1- DISEASE: Defects in ABC6 are a cause of autosomal dominant

CC pseudoxanthoma elasticum (AD-PXE) [MIM:177850]. PXE is a disorder

CC characterized by calcification of elastic fibers in skin, arteries

CC and retina that results in dermal lesions with associated laxity

CC and loss of elasticity, arterial insufficiency and retinal

CC hemorrhages leading to macular degeneration.

CC -1- DISEASE: Defects in ABC6 are a cause of autosomal recessive

CC pseudoxanthoma elasticum (AR-PXE) [MIM:264800].

CC -1- SIMILARITY: Belongs to the ABC transporter family. MRP subfamily.

CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous

CC gene model prediction.

CC -1- DATABASE: NAME=Mutations of the ABC6 gene;

CC NOTE=Retina International's Scientific Newsletter;

CC WWW="http://www.retina-international.com/sci-news/abcc6mut.htm".

CC -----

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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

CC -----

CC EMBL: AF076622; AAC79696.1; -

CC EMBL: U91318; AAC15785.1; ALT\_SEQ.

CC EMBL: AF168791; AAD51233.1; -

CC HSSP: P08716; IMT0.

CC Genew; HGNC:57; ABC6.

CC MIM; 603234; -

DR MIM; 177850; -

DR MIM; 264800; -

DR GO; GO:0005624; C:membrane fraction; TAS.

DR GO; GO:0005886; C:plasma membrane; TAS.

DR GO; GO:0005524; F:ATP binding; TAS.

DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; TAS.

DR GO; GO:0005215; F:transporter activity; TAS.

DR GO; GO:0042493; P:response to drug; TAS.

DR GO; GO:0006810; P:transport; TAS.

DR InterPro; IPR001593; AAA\_ATPase.

DR InterPro; IPR001140; ABC\_TM\_transp.

DR InterPro; IPR003439; ABC transporter.

DR InterPro; IPR005292; MRP assoc.

DR Pfam; PF00664; ABC membrane; 2.

DR Pfam; PF00005; ABC\_tran; 2.

DR ProDom; PD000006; ABC\_transporter; 1.

DR SMART; SM00382; AAA; 2.

DR TIGRFAMs; TIGR00957; MRP\_assoc\_pro; 1.

DR PROSITE; PS00929; ABC\_TMIF; 2.

DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; 2.

DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 2.

DR ATP-binding; Disease mutation; Glycoprotein; Polymorphism; Repeat;

KW Transmembrane; Transport; Vision.

KW DOMAIN 1 31 Extracellular (By similarity).

FT TRANSMEM 32 52 1 (By similarity).

FT DOMAIN 53 72 Cytoplasmic (By similarity).

FT TRANSMEM 73 93 2 (By similarity).

FT DOMAIN 94 98 Extracellular (By similarity).

FT TRANSMEM 99 119 3 (By similarity).

FT DOMAIN 120 131 Cytoplasmic (By similarity).

FT TRANSMEM 132 149 4 (By similarity).

FT DOMAIN 150 167 Extracellular (By similarity).

FT TRANSMEM 168 188 5 (By similarity).

FT DOMAIN 189 302 Cytoplasmic (By similarity).

FT TRANSMEM 303 323 Extracellular (By similarity).

FT DOMAIN 324 349 6 (By similarity).

FT TRANSMEM 350 370 7 (By similarity).

FT DOMAIN 371 426 Cytoplasmic (By similarity).

FT TRANSMEM 427 447 8 (By similarity).

FT DOMAIN 448 450 Extracellular (By similarity).

FT TRANSMEM 451 471 9 (By similarity).

Query Match 75.0%; Score 42; DB 1; Length 1503;

Best Local Similarity 71.4%; Pred. No. 6e+02;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8

Db 965 GYWLTLW 971

|||||::|

PRELIMINARY; PRT; 266 AA.

Q82Z85 AC Q82Z85; (T-EMBLrel. 24, Created)

DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Hypothetical protein.

GN OrderedLocusNames=EF3185;

OS Enterococcus faecalis (Streptococcus faecalis).

OX Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.

OC NCBI\_TaxID=1351;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=V583 / ATCC 700802;

RX MEDLINE=22550857; PubMed=12663927; DOI=10.1126/science.1080613;

RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,

RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,

RA Tettelin H., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,

RA Dougherty J.C., DeBoy R.T., Durkin S.A., Kolonay J.F., Madupu R.,

RA Nelson W.C., Vamathevan J.J., Tran B., Upton J., Hansen T., Shetty J.,

RA Khouri H.M., Utterback T.R., Radune D., Ketchum K.A., Dougherty B.A.,

RA Fraser C.M.;  
 RT "Role of mobile DNA in the evolution of vancomycin-resistant  
 RT Enterococcus faecalis";  
 RL Science 299:2071-2074(2003).  
 DR EMBL; AE016957; AA082859.1; --  
 DR TIGR; EF3185; --  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 266 AA; 28291 MW; CD6E72C4DF55A36 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 266;  
 Best Local Similarity 62.5%; Pred. No. 1.7e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTLWG 9  
 Db 203 GTWTLWG 210

## RESULT 12

Q6CBE4 PRELIMINARY; PRT; 376 AA.

AC Q6CBE4  
 DT 01-OCT-2004 (TRENBLrel. 28, Created)  
 DT 01-OCT-2004 (TRENBLrel. 28, Last sequence update)  
 DE Similar to sp|P38071 Saccharomyces cerevisiae YBR026c.  
 GN ORFNames=VALI0C19624g;  
 OS Yarrowia lipolytica (Candida lipolytica).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 CC Saccharomycetales; Dipodascaceae; Yarrowia.  
 OX NCBI\_TaxID=4952;  
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CLIB99;

RG GENOLEVURES;

RA DuJon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,  
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
 RA Boiarane A., Boyer J., Catolico L., Confaniolieri F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dunazet H., Groppi A.,  
 RA Hannequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Niclaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,  
 RA Pellens S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
 RA Swennene D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
 RA Wincker P., Souciet J.L.;  
 RT "Genome evolution in yeasts";  
 RL Nature 430:35-44(2004).  
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CLIB99;

RA Genoscope;

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; CR382129; CAG82338.1; --

SQ SEQUENCE 376 AA; 41206 MW; E085FF7C3379DCB CRC64;

Query Match 73.2%; Score 41; DB 2; Length 376;  
 Best Local Similarity 85.7%; Pred. No. 2.3e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTLWG 8

Db 301 GYWLTLWG 307

## RESULT 13

Q9HKA9 PRELIMINARY; PRT; 413 AA.

ID Q9HKA9

AC Q9HKA9;

DT 01-MAR-2001 (TRENBLrel. 16, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update).  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Transport protein related protein.  
 GN OrderedLocusNames=Ta0692;  
 OS Thermoplasma acidophilum.  
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;  
 CC Thermoplasmataceae; Thermoplasma.  
 OX NCBI\_TaxID=2303;  
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DSM 1728;

RE MEDLINE=20479972; PubMed=11029001;

RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,

RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;

RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma

RT acidophilum";

RL Nature 407:508-513(2000).

DR EMBL; AL445085; CAC11830.1; --

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR007114; MFS.

DR PROSITE; PS50850; MFS; 1.

KW Complete proteome.

SQ SEQUENCE 413 AA; 45192 MW; 307093BC358063D4 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 413;  
 Best Local Similarity 62.5%; Pred. No. 2.5e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTLWG 9

Db 354 GFWETLWG 361

## RESULT 14

Q97VB7

ID Q97VB7

AC Q97VB7

DT 01-OCT-2001 (TRENBLrel. 18, Created)

DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE Permease.

GN OrderedLocusNames=SSO2718;

OS Sulfolobus solfataricus.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

CC Sulfolobus.

OX NCBI\_TaxID=2287;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 35092 / DSM 1617 / P2;

RE MEDLINE=21332296; PubMed=11427726;

RA She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,

RA Aweez M.J., Chan-Weher C.C.-Y., Clausen I.G., Curtis B.A.,

RA De Moors A., Erasus G., Fletcher C., Gordon P.M.K.,

RA Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,

RA Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,

RA Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,

RA Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;

RT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2";

RL Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).

DR EMBL; AE006865; AAK42828.1; --

DR PIR; E90446; E90446.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR007114; MFS.

DR Pfam; PF00083; Sugar tr; 1.

DR PROSITE; PS50850; MFS; 1.

KW Complete proteome.

SQ SEQUENCE 419 AA; 46499 MW; 6DB6AB6B5C6DA267 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 419;  
Best Local Similarity 62.5%; Pred. No. 2.6e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 2 GYWLTIW 9  
|:| |:  
Db 365 GFWETLWG 372

## RESULT 15

Q8DMV4  
ID Q8DMV4 PRELIMINARY; PRT; 736 AA.  
AC Q8DMV4;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cellulose synthase.  
DE OrderedLocustNames=t110007;  
OS Synechococcus elongatus (Thermosynechococcus elongatus).  
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
OX NCBI\_TaxID=32046;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BP-1;  
RX MEDLINE=22225144; PubMed=12240834;  
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Kato H., Sasamoto S.,  
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,  
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,  
RA Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the thermophilic cyanobacterium  
RT Thermosynechococcus elongatus BP-1.";  
RL DNA Res. 9:123-130(2002).  
DR EMBL: AP005369; BAC07560.1; -;  
DR InterPro; IPR001173; Glyco\_trans 2.  
DR Pfam; PF00535; Glycos\_transf\_2; 1.  
KW Complete proteome.  
SQ SEQUENCE 736 AA; 85049 MW; D31C506166FD9624 CRC64;

Query Match 73.2%; Score 41; DB 2; Length 736;  
Best Local Similarity 85.7%; Pred. No. 4.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8  
|:| |:  
Db 557 GYWLHIW 563

Search completed: December 30, 2004, 13:16:08  
Job time : 96.2641 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 21:19:46 ; Search time 94 Seconds  
(without alignments)  
38.163 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGYWLTIWG 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 444336

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	10	5	ABP53932
2	54	75.0	10	5	ABP53931
3	50	69.4	10	5	ABP53968
4	39.5	54.9	9	5	ABJ04472
5	35.5	49.3	9	5	ABJ04461
6	35	48.6	9	5	ABJ04460
7	33.5	46.5	7	5	ABJ04531
8	33	45.8	7	5	ABP53964
9	33	45.8	8	2	AAV03715
10	33	45.8	8	3	AAV76817
11	33	45.8	8	5	ABP53965
12	33	45.8	8	7	ADG94005
13	33	45.8	8	8	ADL98014
14	33	45.8	10	5	ABBA46346
15	33	45.8	10	5	ABBA46607
16	32	44.4	7	3	AAV76794
17	32	44.4	7	5	ABP53418
18	32	44.4	9	4	ABP22609
19	32	44.4	9	4	ABP20314
20	32	44.4	9	5	AAU90543
21	32	44.4	9	5	AAU90464
22	32	44.4	9	5	AAU90542
23	32	44.4	9	5	AAU90541
24	32	44.4	10	2	AAW43886
25	32	44.4	10	3	AAV66209

26	32	44.4	10	3	AAV66213
27	32	44.4	10	4	ABP20316
28	32	44.4	10	4	ABP20318
29	32	44.4	10	4	ABP22613
30	32	44.4	10	4	ABP14381
31	32	44.4	10	4	ABP22611
32	32	44.4	10	5	AAU88395
33	32	44.4	10	5	AAU90462
34	32	44.4	10	5	AAU90463
35	32	44.4	10	5	AAU90535
36	32	44.4	10	8	AD564384
37	32	44.4	10	8	ADH58622
38	31	43.1	8	2	AAW97529
39	31	43.1	9	5	ABP53933
40	31	43.1	9	5	ABJ04488
41	31	43.1	9	8	ADN64476
42	31	43.1	10	4	AAG95260
43	30.5	42.4	10	2	AAW14709
44	30	41.7	8	2	AAW12859
45	30	41.7	8	3	AAV91924

ALIGNMENTS

RESULT 1  
ABP53932  
ID ABP53932 standard; peptide; 10 AA.  
XX  
AC ABP53932;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:35.  
XX

KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnary; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
PN WO200257299-A2.  
XX  
PD 25-JUL-2002.

XX 16-JAN-2002; 2002WO-IB0000099.  
XX 17-JAN-2001; 2001US-0262476P.  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX (LICN) LICENTIA LTD.  
XX Alitalo K, Koivunen E, Kubo H;  
XX WPI; 2002-691521/74.  
XX  
XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.  
XX  
XX Claim 13; Page 80; 149pp; English.

XX The present invention describes an isolated peptide (I) that binds to and  
XX inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulnary activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
 CC represents a specifically claimed VEGFR-3 binding peptide from the  
 CC present invention  
 XX  
 SQ Sequence 10 AA;

Query Match 100.0%; Score 72; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0025;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10  
 |||||  
 Db 1 CGYWLTIWGC 10

RESULT 2  
 ABP53931  
 ID ABP53931 standard; peptide; 10 AA.  
 XX AC  
 AC ABP53931;  
 XX  
 DT 09-JAN-2003 (first entry)  
 XX  
 DE VEGFR-3 binding peptide SEQ ID NO:34.  
 XX  
 KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
 KW cytosolic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
 KW vulnary; cell surface receptor; cancer; neovascularisation;  
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
 KW diabetes; PDGF; platelet derived growth factor.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

Key Location/Qualifiers  
 FT Misc-difference 1 /note= "any amino acid"  
 FT Misc-difference 10 /note= "any amino acid"  
 FT  
 FT  
 FT  
 XX WO200257299-A2.  
 XX  
 XX 25-JUL-2002.  
 XX  
 XX 16-JAN-2002; 2002WO-IB000099.  
 XX  
 XX 17-JAN-2001; 2001US-0262476P.  
 XX  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX (LICN) LICENTIA LTD.  
 XX  
 XX Alitalo K, Koivunen E, Kubo H;  
 XX  
 XX WPI; 2002-691521/74.  
 XX  
 XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
 XX diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
 XX PT such as cancer and diseases of neovascularization.  
 XX  
 XX Claim 12; Page 80; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and  
 inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
 have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
 antidiabetic and vulnary activities, and can be used in gene therapy.  
 Compositions and methods from the present invention are useful for  
 diagnosing, evaluating and treating disorders mediated by the activity of  
 the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
 CC represents a specifically claimed VEGFR-3 binding peptide from the  
 CC present invention  
 XX  
 SQ Sequence 10 AA;

Query Match 75.0%; Score 54; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.67;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
 |||||  
 Db 2 GYWLTIWG 9

RESULT 3  
 ABP53968  
 ID ABP53968 standard; peptide; 10 AA.  
 XX AC  
 AC ABP53968;  
 XX  
 DT 09-JAN-2003 (first entry)  
 XX  
 DE VEGFR-3 binding peptide SEQ ID NO:73.  
 XX  
 KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
 KW cytosolic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
 KW vulnary; cell surface receptor; cancer; neovascularisation;  
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
 KW diabetes; PDGF; platelet derived growth factor.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

Key Location/Qualifiers  
 FT Misc-difference 5.7 /note= "X is any amino acid"  
 FT Misc-difference 9 /note= "X is any amino acid"  
 FT  
 FT  
 FT  
 XX WO200257299-A2.  
 XX  
 XX 25-JUL-2002.  
 XX  
 XX 16-JAN-2002; 2002WO-IB000099.  
 XX  
 XX 17-JAN-2001; 2001US-0262476P.  
 XX  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX (LICN) LICENTIA LTD.  
 XX  
 XX Alitalo K, Koivunen E, Kubo H;  
 XX  
 XX WPI; 2002-691521/74.  
 XX  
 XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
 XX diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
 XX PT such as cancer and diseases of neovascularization.  
 XX  
 XX Disclosure; Page 147; 149pp; English.

The present invention describes an isolated peptide (I) that binds to and  
 inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
 have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
 antidiabetic and vulnary activities, and can be used in gene therapy.  
 Compositions and methods from the present invention are useful for  
 diagnosing, evaluating and treating disorders mediated by the activity of  
 the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
 CC represents a VEGFR-3 binding peptide, which is given in the  
 XX exemplification of the present invention

SQ Sequence 10 AA;  
 Query Match 69.4%; Score 50; DB 5; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 2.3;  
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10  
 |||||  
 Db 1 CGYWXWXC 10

RESULT 4  
 ABJ04472  
 ID ABJ04472 standard; peptide; 9 AA.  
 AC ABJ04472;  
 XX  
 XX  
 XX 24-OCT-2002 (first entry)  
 DT  
 DE Stem cell (mesenchymal) targeting peptide 61.  
 DE  
 XX  
 XX BRASIL; targeting peptide; bacterial infection;  
 KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;  
 KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;  
 KW viral infection; cardiovascular disease; degenerative disease.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200220822-A2.  
 PN  
 XX 14-MAR-2002.  
 PD  
 XX 07-SEP-2001; 2001WO-US028124.  
 PF  
 XX 08-SEP-2000; 2000US-0231266P.  
 PR  
 PR 17-JAN-2001; 2001US-00765101.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Arap W, Pasqualini R;  
 PI  
 XX WPI; 2002-404697/43.  
 DR  
 XX  
 XX Identification of targeting peptides that can be used to treat diseases  
 PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis  
 PT of Selective Ligands) method comprises a single differential  
 PT centrifugation step.  
 XX  
 XX Example 5; Page 76; 167pp; English.  
 PS  
 XX The invention comprises a method (BRASIL - Biopanning and Rapid Analysis  
 CC of Selective Interactive Ligands) to obtain a targeting peptide. The  
 CC BRASIL method of the invention involves: exposing a target to a phage  
 CC display library in a first phase; exposing the first phase to a second  
 CC phase; and separating the phage bound to the target from unbound phage.  
 CC The BRASIL method of the invention allows cell phages to be separated  
 CC from the remaining unbound phage in a single differential centrifugation  
 CC step. When compared to conventional cell panning methods, the BRASIL  
 CC method shows a significant increase in recovery of specific phage and a  
 CC substantial decrease in background. The BRASIL method is useful for  
 CC identifying targeting peptides. The targeting peptides identified by the  
 CC method of the invention are useful for treating disease states, such as:  
 CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune  
 CC disease; bacterial infection; viral infection; cardiovascular disease and  
 CC degenerative disease. The present amino acid sequence represents a

CC targeting peptide of the invention  
 XX Sequence 9 AA;  
 SQ

Query Match 54.9%; Score 39.5; DB 5; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 1.7e+06;  
 Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWLTIWGC 10  
 |||||  
 Db 1 CG-WFSWGC 9

RESULT 5  
 ABJ04461  
 ID ABJ04461 standard; peptide; 9 AA.  
 XX  
 XX AC ABJ04461;  
 AC  
 XX 24-OCT-2002 (first entry)  
 DT  
 DE Stem cell (mesenchymal) targeting peptide 50.  
 DE  
 XX  
 XX BRASIL; targeting peptide; bacterial infection;  
 KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;  
 KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;  
 KW viral infection; cardiovascular disease; degenerative disease.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200220822-A2.  
 PN  
 XX 14-MAR-2002.  
 PD  
 XX 07-SEP-2001; 2001WO-US028124.  
 PF  
 XX 08-SEP-2000; 2000US-0231266P.  
 PR  
 PR 17-JAN-2001; 2001US-00765101.  
 XX  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA  
 XX Arap W, Pasqualini R;  
 PI  
 XX WPI; 2002-404697/43.  
 DR  
 XX  
 XX Identification of targeting peptides that can be used to treat diseases  
 PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis  
 PT of Selective Ligands) method comprises a single differential  
 PT centrifugation step.  
 XX  
 XX Example 5; Page 76; 167pp; English.  
 PS  
 XX The invention comprises a method (BRASIL - Biopanning and Rapid Analysis  
 CC of Selective Interactive Ligands) to obtain a targeting peptide. The  
 CC BRASIL method of the invention involves: exposing a target to a phage  
 CC display library in a first phase; exposing the first phase to a second  
 CC phase; and separating the phage bound to the target from unbound phage.  
 CC The BRASIL method of the invention allows cell phages to be separated  
 CC from the remaining unbound phage in a single differential centrifugation  
 CC step. When compared to conventional cell panning methods, the BRASIL  
 CC method shows a significant increase in recovery of specific phage and a  
 CC substantial decrease in background. The BRASIL method is useful for  
 CC identifying targeting peptides. The targeting peptides identified by the  
 CC method of the invention are useful for treating disease states, such as:  
 CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune  
 CC disease; bacterial infection; viral infection; cardiovascular disease and  
 CC degenerative disease. The present amino acid sequence represents a  
 CC targeting peptide of the invention

SQ Sequence 9 AA;  
 Query Match 49.3%; Score 35.5; DB 5; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
QY 1 CGYWLTIWGC 10  
| : | : | : |  
Db 1 CGWW-GLWPC 9

RESULT 6  
ABJ04460  
ID ABJ04460 standard; peptide; 9 AA.

XX AC ABJ04460;  
XX  
DT 24-OCT-2002 (first entry)  
XX  
DE Stem cell (mesenchymal) targeting peptide 49.  
XX  
XX BRASIL; targeting peptide; bacterial infection;  
KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;  
KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;  
KW viral infection; cardiovascular disease; degenerative disease.  
XX

OS Unidentified.  
XX  
XX WO200220822-A2.  
XX  
XX 14-MAR-2002.

XX 07-SEP-2001; 2001WO-US028124.  
XX  
XX 08-SEP-2000; 2000US-0231266P.  
XX  
XX 17-JAN-2001; 2001US-00765101.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Arap W, Pasqualini R;

XX WPI; 2002-404697/43.

XX  
XX  
PT Identification of targeting peptides that can be used to treat diseases  
PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis  
PT of Selective Ligands) method comprises a single differential  
PT centrifugation step.

XX Example 5; Page 76; 167pp; English.

XX The invention comprises a method (BRASIL - Biopanning and Rapid Analysis  
XX of Selective Interactive Ligands) to obtain a targeting peptide. The  
XX BRASIL method of the invention involves: exposing a target to a phage  
XX display library in a first phase; exposing the first phase to a second  
XX phase; and separating the phage bound to the target from unbound phage.  
XX The BRASIL method of the invention allows cell phages to be separated  
XX from the remaining unbound phage in a single differential centrifugation  
XX step. When compared to conventional cell panning methods, the BRASIL  
XX method shows a significant increase in recovery of specific phage and a  
XX substantial decrease in background. The BRASIL method is useful for  
XX identifying targeting peptides. The targeting peptides identified by the  
XX method of the invention are useful for treating disease states, such as:  
XX diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune  
XX disease; bacterial infection; viral infection; cardiovascular disease and  
XX degenerative disease. The present amino acid sequence represents a  
XX targeting peptide of the invention

XX Sequence 9 AA;

Query Match 48.6%; Score 35; DB 5; Length 9;  
Best Local Similarity 50.0%; Pred. NO. 1.7e+06;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGYWLTIW 8  
| : | : | : |  
Db 1 CDWWTAW 8

RESULT 7  
ABJ04531  
ID ABJ04531 standard; peptide; 7 AA.

XX AC ABJ04531;

XX 24-OCT-2002 (first entry)

XX Molt-4 leukaemia cell line targeting peptide 16.

XX BRASIL; targeting peptide; bacterial infection;  
KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;  
KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;  
KW viral infection; cardiovascular disease; degenerative disease.

XX Unidentified.

XX WO200220822-A2.

XX 14-MAR-2002.

XX 07-SEP-2001; 2001WO-US028124.

XX 08-SEP-2000; 2000US-0231266P.

XX 17-JAN-2001; 2001US-00765101.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Arap W, Pasqualini R;

XX WPI; 2002-404697/43.

XX  
XX  
PT Identification of targeting peptides that can be used to treat diseases  
PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis  
PT of Selective Ligands) method comprises a single differential  
PT centrifugation step.

XX Claim 79; Page 100; 167pp; English.

XX The invention comprises a method (BRASIL - Biopanning and Rapid Analysis  
XX of Selective Interactive Ligands) to obtain a targeting peptide. The  
XX BRASIL method of the invention involves: exposing a target to a phage  
XX display library in a first phase; exposing the first phase to a second  
XX phase; and separating the phage bound to the target from unbound phage.  
XX The BRASIL method of the invention allows cell phages to be separated  
XX from the remaining unbound phage in a single differential centrifugation  
XX step. When compared to conventional cell panning methods, the BRASIL  
XX method shows a significant increase in recovery of specific phage and a  
XX substantial decrease in background. The BRASIL method is useful for  
XX identifying targeting peptides. The targeting peptides identified by the  
XX method of the invention are useful for treating disease states, such as:  
XX diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune  
XX disease; bacterial infection; viral infection; cardiovascular disease and  
XX degenerative disease. The present amino acid sequence represents a  
XX targeting peptide of the invention

XX Sequence 7 AA;

Query Match 46.5%; Score 33.5; DB 5; Length 7;  
Best Local Similarity 50.0%; Pred. NO. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 1 CGYWLTIWGC 10  
| : | : | : |  
Db 1 CSVM---WGC 7

RESULT 8  
ABP53964  
ID ABP53964 standard; peptide; 7 AA.

XX AC ABP53964;

XX 09-JAN-2003 (first entry)  
 XX VEGFR-3 binding peptide SEQ ID NO:67.  
 XX  
 XX Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
 KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
 KW vulnary; cell surface receptor; cancer; neovascularisation;  
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
 KW diabetes; PDGF; platelet derived growth factor.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 4..6 /note= "X is any amino acid"  
 FT  
 XX WO200257299-A2.  
 XX  
 XX 25-JUL-2002.  
 XX  
 XX 16-JAN-2002; 2002WO-IB000099.  
 XX  
 XX 17-JAN-2001; 2001US-0262476P.  
 XX  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA (LICN) LICENTIA LTD.  
 XX  
 XX Alltalo K, Koivunen E, Kubo H;  
 PI WPI; 2002-691521/74.  
 DR  
 XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
 PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
 PT such as cancer and diseases of neovascularization.  
 XX  
 XX Claim 21; Page 81; 149pp; English.  
 PS  
 XX The present invention describes an isolated peptide (I) that binds to and  
 CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
 CC antidiabetic and vulnary activities, and can be used in gene therapy.  
 CC Compositions and methods from the present invention are useful for  
 CC diagnosing, evaluating and treating disorders mediated by the activity of  
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
 CC represents a specifically claimed VEGFR-3 binding peptide from the  
 CC present invention  
 XX  
 SQ Sequence 7 AA;  
 XX  
 XX Query Match 45.8%; Score 33; DB 5; Length 7;  
 XX Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
 XX Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 GYWLTIW 8  
 DB |||||  
 1 GYWXW 7

## RESULT 9

AA03715  
 ID AA03715 standard; peptide; 8 AA.

XX  
 AC AA03715;

XX 08-JUN-1999 (first entry)  
 DT

XX Fluorine-18 (F-18) labeled peptide 2.  
 XX  
 XX 18F radionuclide; targeting vector; positron emission tomography; F-18;  
 KW radiolabeling; thiol; fluorine-18.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Misc-difference 1 /note= "N-terminal acetylation; optionally has a free or  
 FT protected thiol group"  
 FT  
 FT Misc-difference 2 /note= "D-form residue"  
 FT  
 FT Misc-difference 3 /note= "D-form residue"  
 FT  
 FT Misc-difference 5 /note= "D-form residue"  
 FT  
 FT Misc-difference 7 /note= "D-form residue; optionally has a free or  
 FT protected thiol group"  
 FT  
 FT Misc-difference 8 /note= "D-form residue"  
 FT  
 XX WO9911590-A1.  
 PN  
 XX 11-MAR-1999.  
 XX  
 XX 03-SEP-1998; 98WO-US018268.  
 PF  
 XX 03-SEP-1997; 97US-0057485P.  
 PR  
 XX (IMMU-) IMMUNOMEDICS INC.  
 PA  
 XX Griffiths GL;  
 PI  
 XX WPI; 1999-228967/19.  
 DR  
 XX Radiolabeling thiol-containing peptides with fluorine-18.  
 XX  
 XX Claim 14; Page 15; 22pp; English.  
 PS  
 XX The invention relates to a method for incorporating 18F radionuclide into  
 CC peptide-containing targeting vectors for use in clinical positron  
 CC emission tomography. Radiolabeling thiol-containing peptides with  
 CC fluorine-18 (F-18) comprises reacting a peptide comprising a free thiol  
 CC group with a labeling reagent of formula: 18F-(CH<sub>2</sub>)<sub>m</sub>-CR1R2-(CH<sub>2</sub>)<sub>n</sub>-X, or a  
 CC fluorinated alkene in which at least one of the two double bonded carbon  
 CC atoms bears at least one leaving group comprising 1, Br, Cl, azide,  
 CC tosylate, mesylate, nosylate or triflate. n, m = 0-2; X = I,  
 CC Br, Cl, azide, tosylate, mesylate, nosylate, triflate, maleimide  
 CC (optionally substituted by 1-2 alkyl) or 3-sulfomaleimide; R1, R2 = I,  
 CC Br, Cl, azide, tosylate, mesylate, nosylate, triflate, H, CONH<sub>2</sub>, COOH,  
 CC OH, sulfonic acid, tertiary amine, quaternary ammonium, alkyl (optionally  
 CC substituted by CONH<sub>2</sub>, COOH, OH, sulfonic acid, tertiary amine or  
 CC quaternary ammonium), COOR', CONR'2 or COR'; and R' = 1-6C alkyl or  
 CC phenyl. The method is used for Radiolabeling peptide-containing targeting  
 CC vectors such as proteins, antibodies, antibody fragments and receptor-  
 CC targeted peptides for use in routine clinical positron emission  
 CC tomography. The method is simple and efficient. The method uses the  
 CC unique property of the free thiol groups which are rapidly alkylated at  
 CC neutral pH and moderate temperature. Sequences AA03714-716 represent  
 CC examples of F-18 labeled peptides used in the method of detecting a  
 CC tissue  
 XX  
 XX Sequence 8 AA;  
 XX  
 XX Query Match 45.8%; Score 33; DB 2; Length 8;  
 XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGYW 4  
 |||||

Db 5 CGYW 8

RESULT 10  
AAV76817

XX ID AAY76817 standard; peptide; 8 AA.

XX AC AAY76817;

XX DT 28-APR-2000 (first entry)

XX XX

DE XX Immunogenic peptide for bi-specific antibody recognition.

XX XX

KW Immunogenic peptide; bi-specific antibody; diagnosis; immune response;

KW diseased tissue identification; therapy.

XX OS Synthetic.

XX XX

FH Key Location/Qualifiers

FT Misc-difference 1 /note= "acetylated; modified with free amino acid group, protected amino acid group, chelating agent or a metal-chelate complex"

FT FT

FT Misc-difference 2 /note= "D-form residue"

FT FT

FT Misc-difference 3 /note= "D-form residue"

FT FT

FT Misc-difference 5 /note= "D-form residue; modified with free amino acid group, protected amino acid group, chelating agent or a metal-chelate complex"

FT FT

FT Misc-difference 7 /note= "D-form residue"

FT FT

FT Misc-difference 8 /note= "D-form residue"

FT FT

XX WO966951-A2.

XX PN

XX XX

XX PD 29-DEC-1999.

XX XX

XX PF 22-JUN-1999; 99WO-US013879.

XX PR 22-JUN-1998; 98US-0090142P.

XX PR 14-OCT-1998; 98US-0104156P.

XX XX

PA (IMMU-) IMMUNOMEDICS INC.

XX XX

PI Hansen HU, Griffiths GL, Leung S, McBride WJ, Qu Z;

XX XX

XX WPI; 2000-160561/14.

XX DR

XX XX Bi-specific antibodies that bind specific target tissue and targeted conjugates.

XX PT

XX XX

XX PS Claim 22; Page 61; 76pp; English.

XX CC

CC This sequence represents an immunogenic peptide for a bi-specific antibody. The invention relates to a method of treating or identifying diseased tissues in a patient comprising administering a bi-specific antibody (or fragment) having at least 1 arm (A) that specifically binds a targeted tissue and at least 1 arm (B) that specifically binds a targetable conjugate. The methods and bi-specific antibodies and fusion proteins are useful for pre-targeting methods of diagnosis and therapy. It is advantageous to raise bi-specific antibodies against a targetable conjugate that is capable of carrying at least 1 diagnostic or therapeutic agent. The characteristics of the chelator, metal chelate complex, therapeutic agent or diagnostic agent can be varied to accommodate differing applications without raising new bi-specific antibodies for each new application. The targetable conjugate is selected to elicit sufficient immune responses and also for rapid in vivo clearance when used within the bi-specific antibody targeting method

XX SQ Sequence 8 AA;

Query Match 45.8%; Score 33; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGYW 4  
Db 5 CGYW 8

RESULT 11  
ABP53965

ID ABP53965 standard; peptide; 8 AA.

XX AC ABP53965;

XX DT 09-JAN-2003 (first entry)

XX XX

DE XX VEGFR-3 binding peptide SEQ ID NO:68.

XX XX

KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3; angiogenesis; lymphangiogenesis; vascular endothelial growth factor; cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic; vulnary; cell surface receptor; cancer; neovascularisation; KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma; diabetes; PDGF; platelet derived growth factor.

XX XX

OS Homo sapiens.

OS Synthetic.

XX XX

FH Key Location/Qualifiers

FT Misc-difference 4 .6

FT FT

FT Misc-difference 8 /note= "X is any amino acid"

FT FT

FT Misc-difference 8 /note= "any amino acid"

XX XX

XX PN WO200257299-A2.

XX XX

XX PD 25-JUL-2002.

XX XX

XX PF 16-JAN-2002; 2002WO-IB000099.

XX XX

XX PR 17-JAN-2001; 2001US-0262476P.

XX PR

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PA (LICN) LICENTIA LTD.

XX XX

PI Alitalo K, Koivunen E, Kubo H;

XX XX

XX WPI; 2002-691521/74.

XX XX

XX PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity, such as cancer and diseases of neovascularization.

XX PT

XX XX

XX PS Claim 22; Page 81; 149pp; English.

XX CC

CC The present invention describes an isolated peptide (I) that binds to and inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I) have cytostatic, hepatotropic, antiinflammatory, hypotensive, antidiabetic and vulnary activities, and can be used in gene therapy. Compositions and methods from the present invention are useful for diagnosing, evaluating and treating disorders mediated by the activity of the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, oesophagus, bone, marrow or blood, and diseases of neovascularisation, e.g. liver diseases, hypertension, post-trauma, chronic hepatitis, haemangiomas and diabetes. The present sequence represents a specifically claimed VEGFR-3 binding peptide from the present invention

XX XX

XX SQ Sequence 8 AA;

Query Match 45.8%; Score 33; DB 5; Length 8;  
Best Local Similarity 57.1%; Pred. NO. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
| | | |  
Db 1 GYWXKXW 7

RESULT 12  
ADG94005  
ID ADG94005 standard; peptide; 8 AA.  
XX AC ADG94005;  
XX DT 11-MAR-2004 (first entry)  
XX DE Immunogenic peptide.  
XX KW Immunogenic peptide; multi-specific antibody; polymer conjugate; tumour;  
XX KW cytostatic; photodynamic therapy.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Modified-site 1  
FT Misc-difference 2 /note= "Optionally methylated or Acetylated"  
FT Misc-difference 3 /note= "D-form residue"  
FT Misc-difference 5 /note= "D-form residue"  
FT Misc-difference 7 /note= "D-form residue"  
FT Misc-difference 8 /note= "D-form residue"  
XX US2003026764-A1.  
XX PD 06-FEB-2003.  
XX PF 31-JUL-2002; 2002US-00209592.  
XX PR 31-JUL-2001; 2001US-0308605P.  
XX PA (IMMU-) IMMUNOMEDICS INC.  
XX PI Griffiths GL;  
XX DR WPI; 2003-801085/75.  
XX Targeting an agent towards a target site in a tissue, by administering in  
PT a tissue, a multi-specific antibody or its fragment and a polymer  
PT conjugate that binds to the capture arm of the multi-specific antibody.  
XX Disclosure; Page 14; 19pp; English.

XX The invention relates to targeting an agent towards a target site in a  
CC tissue, comprising administering to the tissue, a multi-specific antibody  
CC or its fragment, comprising a targeting arm that binds to an antigen of  
CC the target site and a capture arm that binds to a polymer conjugate, and  
CC administering a polymer conjugate that binds to the capture arm, the  
CC conjugate has a polymer conjugated to the agent such as therapeutic  
CC agent, a peptide, an enzyme and a labelled ligand. Also included is a kit  
CC useful for targeting a target site within a tissue in a subject or tissue  
CC sample comprising the above mentioned multi-specific antibody or its  
CC fragment and a polymer conjugate. The method is used for targeting an  
CC agent towards a target site in a tissue (e.g. a tumour). The method is  
CC also useful for therapeutic or diagnostic purposes and further in  
CC photodynamic therapy. The present sequence is an immunogenic peptide used

CC in the method of the invention.  
XX SQ Sequence 8 AA;  
Query Match 45.8%; Score 33; DB 7; Length 8;  
Best Local Similarity 100.0%; Pred. NO. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGYW 4  
| | | |  
Db 5 CGYW 8

RESULT 13  
ADL98014  
ID ADL98014 standard; peptide; 8 AA.  
XX AC ADL98014;  
XX DT 20-MAY-2004 (first entry)  
XX DE Peptide haptens #2.  
XX KW photodynamic diagnosis; cancer; tumour; cardiovascular lesion;  
XX KW inflammatory disease; neurodegenerative disease; metabolic disease;  
XX KW infectious disease; B-cell malignancy; Alzheimer's disease; amyloidosis;  
XX KW autoimmune disease; bacterial infection; fungal infection;  
XX KW parasitic infection; viral infection;  
XX KW carcinoembryonic antigen-expressing tumour.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Modified-site 1  
FT Misc-difference 2 /note= "Optionally Cyeteinyl; if Cys the residue is  
FT Misc-difference 3 /note= "D form residue" methylated; N-terminal acetylated."  
FT Misc-difference 5 /note= "D form residue"  
FT Modified-site 5  
FT Misc-difference 7 /note= "Optionally Cysteiny; if Cys the residue is  
FT Misc-difference 8 /note= "D form residue" methylated; N-terminal acetylated."  
XX US2004043030-A1.  
XX PD 04-MAR-2004.  
XX PF 09-JUN-2003; 2003US-00456580.  
XX PR 31-JUL-2001; 2001US-0308605P.  
XX PR 31-JUL-2002; 2002US-00209592.  
XX PA (IMMU-) IMMUNOMEDICS INC.  
XX PI Griffiths GL, Goldenberg DM, Hansen HJ;  
XX DR WPI; 2004-313738/29.  
XX Treating cancer and metabolic diseases by administering a multi-specific  
PT antibody having a targeting arm that binds to an antigen and a capture  
PT arm that binds to a polymer conjugate comprising a therapeutic agent.  
XX Disclosure; Page 16; 24pp; English.  
XX The invention relates to a method of diagnosing or treating a disease or  
CC disorder. The method involves administering to a tissue a multi-specific  
CC antibody (I) or antibody fragment, comprising a targeting arm that binds  
CC to an antigen on the target site, and a capture arm that binds to a

polymer conjugate, and administering to the tissue a polymer conjugate that binds to the capture arm, the polymer conjugate comprising a polymer conjugated to a diagnostic or therapeutic agent. Also included is a method for photodynamic diagnosis or treatment of a disease or disorder; or intravascular or endoscopic method for diagnosing or treating a disease or disorder. The method is useful for diagnosing or treating a disease or disorder chosen from cancer (oesophageal, gastric, colonic, rectal, pancreatic, lung, breast, ovarian, urinary bladder, endometrial, cervical, testicular, renal, adrenal and liver cancer, solid tumour, B-cell malignancy or T-cell malignancy); cardiovascular lesion; an inflammatory disease; neurodegenerative disease; metabolic disease; and an infectious disease. The B-cell malignancy is chosen from indolent forms of B-cell lymphomas, aggressive forms of B-cell lymphomas, chronic lymphatic leukaemias, acute lymphatic leukaemias, and multiple myeloma. The solid tumour is chosen melanoma, carcinoma (preferably renal carcinoma, lung carcinoma, intestinal carcinoma, and stomach carcinoma), glioma and sarcoma. The cardiovascular lesion is chosen from infarct, clot, embolus, atherosclerotic plaque and ischaemia. The neurodegenerative disease is Alzheimer's disease. The metabolic disease is amyloidosis, where the antibody binds amyloid. The disease or disorder is displaced or ectopic normal tissue chosen from endometrium, thymus, spleen and parathyroid. The method can be used for normal tissue ablation, where the tissue is chosen from bone marrow and spleen. The disease or disorder is an autoimmune disease such as myasthenia gravis, lupus nephritis, lupus erythematosus, and rheumatoid arthritis. Class III autoimmune diseases such as immune-mediated thrombocytopenias, such as acute idiopathic thrombocytopenic purpura and chronic idiopathic thrombocytopenic purpura, dermatomyositis, Sjogren's syndrome, multiple sclerosis, Sydenham's chorea, myasthenia gravis, systemic lupus erythematosus, lupus nephritis, rheumatic fever, polyglanular syndromes, bullous pemphigoid, diabetes mellitus, Henoch-Schonlein purpura, post-streptococcal nephritis, erythema nodosum, Takayasu's arteritis, Addison's disease, rheumatoid arthritis, sarcoidosis, ulcerative colitis, erythema multiforme, IgA nephropathy, polyarteritis nodosa, ankylosing spondylitis, Goodpasture's syndrome, thromboangiitis obliterans, primary biliary cirrhosis, Hashimoto's thyroiditis, thyrotoxicosis, scleroderma, chronic active hepatitis, polymyositis/dermatomyositis, polychondritis, pemphigus vulgaris, Wegener's granulomatosis, membranous nephropathy, amyotrophic lateral sclerosis, tabes dorsalis, giant cell arteritis/polymyalgia, pernicious anaemia, rapidly progressive glomerulonephritis, or fibrosing alveolitis. The infectious disease is chosen from bacterial, fungal, parasitic and viral lesion. The infectious disease is caused by a fungus chosen from Microsporium, Trichophyton, Epidermophyton, Sporothrix schenckii, Cryptococcus neoformans, Coccidioides immitis, Histoplasma capsulatum, Blastomyces dermatitidis, from HIV, herpes virus, cytomegalovirus, rabies virus, influenza virus, hepatitis B virus, Sendai virus, feline leukemia virus, Reo virus, polio virus, human serum parvo-like virus, simian virus 40, respiratory syncytial virus, mouse mammary tumour virus, Varicella-Zoster virus, Dengue virus, rubella virus, measles virus, adenovirus, human T-cell leukemia viruses, Epstein-Barr virus, murine leukemia virus, mumps virus, vesicular stomatitis virus, Sindbis virus, lymphocytic choriomeningitis virus, wart virus and blue tongue virus. The infectious disease is caused by a bacterium chosen from Bacillus anthracis, Streptococcus agalactiae, Legionella pneumophila, Streptococcus pyogenes, Escherichia coli, Neisseria gonorrhoeae, Neisseria meningitidis, Pneumococcus, Haemophilus influenzae B, Treponema pallidum, Lyme disease spirochetes, Pseudomonas aeruginosa, Mycobacterium leprae, Brucella abortus, Mycobacterium tuberculosis, and Tetanus toxin. The infectious disease is caused by a protozoa chosen from Plasmodium falciparum, Plasmodium vivax, Toxoplasma gondii, Trypanosoma rangeli, Trypanosoma cruzi, Trypanosoma rhodesiense, Trypanosoma brucei, Schistosoma mansoni, Schistosoma japonicum, Babesia bovis, Elmeria tenella, Onchocerca volvulus, Leishmania tropica, Trichinella spiralis, Onchocerca volvulus, Theileria parva, Taenia hydatigena, Taenia ovis, Taenia saginata, Echinococcus granulosus, and Mesocostoides corti. The infectious disease is caused by a mycoplasma chosen from Mycoplasma arthritis, M. hyorhinis, M. orale, M. arginini, Acholeplasma laidlawii, M. salivarium and M. pneumoniae. The cancer is preferably chosen from carcinoembryonic antigen (CEA)-expressing tumour or a CD20-expressing malignancy. The present sequence represents a peptide used in the method of the invention.

## SQ Sequence 8 AA;

Query Match 45.8%; Score 33; DB 8; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGYW 4  
 Db 5 CGIW 8

## RESULT 14

ABB46346  
 ID ABB46346 standard; peptide; 10 AA.

XX ABB46346;

DT 30-JAN-2002 (first entry)

XX Desmoglein-2 CAR sequence cyclic peptide SEQ ID NO 1090.

XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
 KW cytoskeletal; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
 KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.  
 XX Synthetic.

XX WO200172956-A2.

PD 04-OCT-2001.

PF 27-MAR-2001; 2001WO-IB001400.

XX 27-MAR-2000; 2000US-00535852.

PR (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Symonds JM, Gour BJ;

XX WPI; 2002-025778/03.

XX Modulating agents for inhibiting or enhancing desmosomal cadherin  
 mediated cell adhesion, useful for facilitating wound healing and/or  
 PT reducing scar tissue, treating cancer and inducing apoptosis.

XX Claim 18; Page 101; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing  
 desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
 comprising a desmosomal cadherin cell adhesion recognition CAR sequence  
 (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
 sequence, a substance such as an antibody or antigen-binding fragment  
 that specifically binds a desmosomal cadherin CAR sequence and/or a  
 polynucleotide encoding a polypeptide that comprises a desmosomal  
 cadherin CAR sequence or analogue. The modulating agents have  
 immunosuppressive, cytostatic and antiapoptotic activity and are used to  
 facilitate wound healing and/or reduce scar tissue, for enhancing  
 adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
 CC treating an autoimmune blistering disorder and to treat cancer (e.g.  
 CC carcinoma, leukaemia or melanoma) and induce apoptosis

## SQ Sequence 10 AA;

Query Match 45.8%; Score 33; DB 5; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 4.6e+02;  
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10  
 Db 1 CGYALDARGC 10

## RESULT 15

ABB46607  
ID ABB46607 standard; peptide; 10 AA.  
XX  
AC ABB46607;  
XX  
DT 30-JAN-2002 (first entry)  
XX  
DE Desmocollin-1 CAR cyclic peptide 9.  
XX  
KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
KW cytototoxic; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.  
XX  
OS Synthetic.  
XX  
PN WO200172956-A2.  
XX  
PD 04-OCT-2001.  
XX  
PF 27-MAR-2001; 2001WO-IB001400.  
XX  
PR 27-MAR-2000; 2000US-00535852.  
XX  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuk OW, Symonds JM, Gour BJ;  
XX  
DR WPI; 2002-025778/03.  
XX  
XX  
PT Modulating agents for inhibiting or enhancing desmosomal cadherin  
PT mediated cell adhesion, useful for facilitating wound healing and/or  
PT reducing scar tissue, treating cancer and inducing apoptosis.  
XX  
PS Claim 23; Page 109; 127pp; English.  
XX  
CC The invention relates to modulating agents for inhibiting or enhancing  
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence  
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
CC sequence, a substance such as an antibody or antigen-binding fragment  
CC that specifically binds a desmosomal cadherin CAR sequence and/or a  
CC polynucleotide encoding a polypeptide that comprises a desmosomal  
CC cadherin CAR sequence or analogue. The modulating agents have  
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to  
CC facilitate wound healing and/or reduce scar tissue, for enhancing  
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
CC treating an autoimmune blistering disorder and to treat cancer (e.g.  
CC carcinoma, leukaemia or melanoma) and induce apoptosis  
XX  
SQ Sequence 10 AA;

Query Match 45.8%; Score 33; DB 5; Length 10;  
Best Local Similarity 60.0%; Pred.No. 4.6e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYVLTWGC 10  
||| |  
Db 1 CGVATTADGC 10

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OM protein - protein search, using sw model

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Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62  
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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 110780

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	45.8	10	4	US-09-535-852-1090
2	33	45.8	10	4	US-09-535-852-1352
3	30	41.7	8	2	US-08-520-535-12
4	30	41.7	8	2	US-09-079-432-12
5	30	41.7	9	2	US-08-986-234-92
6	30	41.7	9	4	US-09-311-784A-374
7	30	41.7	9	4	US-09-790-497A-1
8	30	41.7	10	3	US-09-108-709-22
9	30	41.7	10	4	US-09-790-497A-110
10	29	40.3	5	1	US-07-946-237-4
11	29	40.3	5	2	US-08-530-566-10
12	29	40.3	5	3	US-09-195-726-10
13	29	40.3	5	3	US-09-067-755-10
14	29	40.3	5	4	US-08-239-765C-4
15	29	40.3	7	4	US-09-069-827A-94
16	29	40.3	9	4	US-09-311-784A-348
17	29	40.3	10	2	US-08-735-253-8
18	29	40.3	10	2	US-08-481-968A-21
19	29	40.3	10	3	US-08-154-712B-21
20	29	40.3	10	4	US-09-947-925A-21
21	29	40.3	8	3	US-09-315-304B-1649
22	28	38.9	10	1	US-08-250-789A-119
23	28	38.9	10	4	US-09-462-917A-73
24	28	38.9	10	4	US-09-125-641-3
25	28	38.9	10	4	US-09-790-497A-5
26	28	38.9	10	4	US-09-790-497A-24
27	28	38.9	10	4	US-09-790-497A-24

28	27.5	38.2	6	1	US-08-191-571-12	Sequence 12, Appl
29	27.5	38.2	6	5	PCT-US95-00296-12	Sequence 12, Appl
30	27	37.5	8	3	US-08-925-002-12	Sequence 12, Appl
31	27	37.5	8	3	US-08-586-670A-17	Sequence 17, Appl
32	27	37.5	8	3	US-09-082-279B-1495	Sequence 1495, Ap
33	27	37.5	8	4	US-09-834-784-1495	Sequence 1495, Ap
34	27	37.5	8	4	US-09-910-552-12	Sequence 12, Appl
35	27	37.5	8	4	US-09-350-641C-1650	Sequence 1650, Ap
36	27	37.5	10	3	US-09-315-304B-1587	Sequence 1587, Ap
37	27	37.5	10	4	US-09-350-325-47	Sequence 47, Appl
38	27	37.5	10	4	US-09-535-852-1357	Sequence 1357, Ap
39	27	37.5	10	4	US-09-350-641C-1587	Sequence 1587, Ap
40	27	37.5	10	4	US-09-239-043D-2474	Sequence 2474, Ap
41	27	37.5	10	4	US-09-620-091-28	Sequence 28, Appl
42	27	37.5	10	4	US-09-620-091-42	Sequence 42, Appl
43	27	37.5	10	4	US-09-620-091-47	Sequence 47, Appl
44	26.5	36.8	10	3	US-09-186-958-12	Sequence 12, Appl
45	26.5	36.8	10	3	US-09-669-271A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-09-535-852-1090  
; Sequence 1090, Application US/09535852  
; Patent No. 6638911  
; GENERAL INFORMATION:  
; APPLICANT: Symonds, James W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND ETHODS FOR MODULATING  
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C6  
; CURRENT APPLICATION NUMBER: US/09/535,852  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1090  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence  
US-09-535-852-1090

Query Match 45.8%; Score 33; DB 4; Length 10;  
Best Local Similarity 60.0%; Pred. No. 81;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10  
|||  
Db 1 CGYALDARGC 10

RESULT 2  
US-09-535-852-1352  
; Sequence 1352, Application US/09535852  
; Patent No. 6638911  
; GENERAL INFORMATION:  
; APPLICANT: Symonds, James W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND ETHODS FOR MODULATING  
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C6  
; CURRENT APPLICATION NUMBER: US/09/535,852  
; CURRENT FILING DATE: 2001-05-21  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1352  
; LENGTH: 10

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclicized modulating agent comprising
; OTHER INFORMATION: desmocollin-1 cell adhesion recognition sequence
US-09-535-852-1352

Query Match          45.8%; Score 33; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10
    |||||
Db 1 CGYATTADGC 10

RESULT 3
US-08-520-535-12
; Sequence 12, Application US/08520535
; Patent No. 5817750
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,535
; FILING DATE: 28-AUG-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; US-08-520-535-12

Query Match          41.7%; Score 30; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGYWL 5
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Db 1 CDYWL 5

RESULT 4
US-09-079-432-12
; Sequence 12, Application US/09079432
; Patent No. 5955572
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,432
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/520,535
; FILING DATE: 28-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; US-09-079-432-12

Query Match          41.7%; Score 30; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGYWL 5
    ||||
Db 1 CDYWL 5

RESULT 5
US-08-986-234-92
; Sequence 92, Application US/08986234
; Patent No. 5981706
; GENERAL INFORMATION:
; APPLICANT: Wallen, et al.
; TITLE OF INVENTION: Methods for Synthesizing Heat Shock Protein Complexes
; FILE REFERENCE: UNME-0008-1
; CURRENT APPLICATION NUMBER: US/08/986,234
; CURRENT FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
; US-08-986-234-92

Query Match          41.7%; Score 30; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IWGC 10
    |||||
Db 2 IWGC 5

RESULT 6
US-09-311-784A-374
; Sequence 374, Application US/09311784A
; Patent No. 6534482
```

; GENERAL INFORMATION:  
; APPLICANT: Fikes, John D.  
; APPLICANT: Hermanson, Gary G.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Ishioka, Glenn Y.  
; APPLICANT: Livingston, Brian  
; APPLICANT: Chesnut, Robert W.  
; APPLICANT: Epimmune Inc.  
; TITLE OF INVENTION: Expression Vectors for Stimulating an  
; TITLE OF INVENTION: Immune Response and Methods of Using the Same  
; FILE REFERENCE: 39963-20022.01  
; CURRENT APPLICATION NUMBER: US/09/311,784A  
; CURRENT FILING DATE: 1999-05-13  
; PRIOR FILING DATE: 1998-05-15  
; NUMBER OF SEQ ID NOS: 463  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 374  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV1 ENV 69 (peptide 25.0113)  
US-09-311-784A-374

Query Match 41.7%; Score 30; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10  
DB 1 IWGC 4

RESULT 7  
US-09-790-497A-1  
; Sequence 1, Application US/09790497A  
; Patent No. 6649735  
; GENERAL INFORMATION:  
; APPLICANT: De Leys, Robert  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING  
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN  
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF  
; TITLE OF INVENTION: BOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS  
; TITLE OF INVENTION: CONTAINING THEM  
; FILE REFERENCE: 2752-16  
; CURRENT APPLICATION NUMBER: US/09/790,497A  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR FILING DATE: 1996-09-30  
; PRIOR FILING DATE: 1993-11-22  
; PRIOR FILING DATE: 1993-03-08  
; PRIOR FILING DATE: 1992-03-06  
; NUMBER OF SEQ ID NOS: 600  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-09-790-497A-1

Query Match 41.7%; Score 30; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10  
DB 1 IWGC 4

Db 1 IWGC 4

RESULT 8  
US-09-108-709-22  
; Sequence 22, Application US/09108709  
; Patent No. 6008044  
; GENERAL INFORMATION:  
; APPLICANT: Cotropia, Joseph P.  
; TITLE OF INVENTION: Human Monoclonal Antibodies Directed Against the Transmembrane Gl  
; TITLE OF INVENTION: (gp41) of Human Immunodeficiency Virus-1 (HIV-1) and Prognosis Tes  
; TITLE OF INVENTION: Detecting the Presence and Concentration of Antibodies Inhibiting  
; TITLE OF INVENTION: Fusion-associated Epitope (GCSGLIC) in gp-41  
; FILE REFERENCE: 10586/00406  
; CURRENT APPLICATION NUMBER: US/09/108,709  
; CURRENT FILING DATE: 1998-07-01  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 22  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (1)..(10)  
; OTHER INFORMATION: amino acids 600-609 according to the Gnan  
; OTHER INFORMATION: numbering system  
US-09-108-709-22

Query Match 41.7%; Score 30; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10  
DB 1 IWGC 4

RESULT 9  
US-09-790-497A-110  
; Sequence 110, Application US/09790497A  
; Patent No. 6649735  
; GENERAL INFORMATION:  
; APPLICANT: De Leys, Robert  
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING  
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN  
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF  
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT  
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS  
; TITLE OF INVENTION: CONTAINING THEM  
; FILE REFERENCE: 2752-16  
; CURRENT APPLICATION NUMBER: US/09/790,497A  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR FILING DATE: 1996-09-30  
; PRIOR FILING DATE: 1993-11-22  
; PRIOR FILING DATE: 1993-03-08  
; PRIOR FILING DATE: 1992-03-06  
; NUMBER OF SEQ ID NOS: 600  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 110  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-09-790-497A-110

Query Match 41.7%; Score 30; DB 4; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 IWGC 10  
Db 1 IWGC 4

RESULT 10  
US-07-946-237-4  
; Sequence 4, Application US/07946237  
; Patent No. 5348874  
; GENERAL INFORMATION:  
; APPLICANT: Savakis, Charalambos  
; APPLICANT: Franz, Gerald H.  
; APPLICANT: Loukeris, Athanasios  
; TITLE OF INVENTION: Eukaryotic Transposable Element  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 19920914  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: David E. Brook  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: BTT92-01  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: AMINO ACID  
; MOLECULE TYPE: peptide  
US-07-946-237-4

Query Match 40.3%; Score 29; DB 1; Length 5;  
Best Local Similarity 75.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0;

Qy 7 IWGC 10  
Db 2 VMGC 5

RESULT 11  
US-08-530-566-10  
; Sequence 10, Application US/08530566  
; Patent No. 5840865  
; GENERAL INFORMATION:  
; APPLICANT: Savakis, Charalambos  
; APPLICANT: Franz, Gerald H.  
; APPLICANT: Loukeris, Athanasios  
; TITLE OF INVENTION: Eukaryotic Transposable Element  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 20-SEP-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION NUMBER: US 08/239,765  
; FILING DATE: 09-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/946,237  
; FILING DATE: 14-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brook, David E.  
; REGISTRATION NUMBER: 22,592  
; REFERENCE/DOCKET NUMBER: BTT92-01ZA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540

INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-530-566-10

Query Match 40.3%; Score 29; DB 2; Length 5;  
Best Local Similarity 75.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0;

Qy 7 IWGC 10  
Db 2 VMGC 5

RESULT 12  
US-09-195-726-10  
; Sequence 10, Application US/09195726  
; Patent No. 6159717  
; GENERAL INFORMATION:  
; APPLICANT: Savakis, Charalambos  
; APPLICANT: Franz, Gerald H.  
; APPLICANT: Loukeris, Athanasios  
; TITLE OF INVENTION: Eukaryotic Transposable Element  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02421

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/195,726  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/530,566  
; FILING DATE: 20-SEP-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/239,765  
; FILING DATE: 09-MAY-1994  
; PRIOR APPLICATION DATA:

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/ APPLICATION NUMBER: US 07/946,237
/ FILING DATE: 14-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Carroll, Alice O.
/ REGISTRATION NUMBER: 33,542
/ REFERENCE/DOCKET NUMBER: IMB92-012A2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (781) 861-6240
/ TELEFAX: (781) 861-9540
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-09-195-726-10

Query Match 40.3%; Score 29; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
Db 2 VMGC 5

RESULT 13
US-09-067-755-10
/ Sequence 10, Application US/09067755
/ Patent No. 6225121
/ GENERAL INFORMATION:
/ APPLICANT: Savakis, Charalambos
/ APPLICANT: Franz, Gerald H.
/ APPLICANT: Loukeris, Athanasios
/ APPLICANT: Klinakis, Apostolos G.
/ TITLE OF INVENTION: Eukaryotic Transposable Element
/ NUMBER OF SEQUENCES: 12
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
/ CITY: Lexington
/ STATE: Massachusetts
/ COUNTRY: USA
/ ZIP: 02421
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/067,755
/ FILING DATE: 27-APR-1998
/ CLASSIFICATION: 800
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/530,566
/ FILING DATE: 20-SEP-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/239,765
/ FILING DATE: 09-MAY-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/946,237
/ FILING DATE: 14-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Carroll, Alice O.
/ REGISTRATION NUMBER: 33,542
/ REFERENCE/DOCKET NUMBER: IMB92-012A2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (781) 861-6240
/ TELEFAX: (781) 861-9540
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
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/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-09-067-755-10

Query Match 40.3%; Score 29; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
Db 2 VMGC 5

RESULT 14
US-08-239-765C-4
/ Sequence 4, Application US/08239765C
/ Patent No. 6469228
/ GENERAL INFORMATION:
/ APPLICANT: Savakis, Charalambos
/ APPLICANT: Franz, Gerald H.
/ APPLICANT: Loukeris, Athanasios
/ TITLE OF INVENTION: Eukaryotic Transposable Element
/ FILE REFERENCE: 18747/1130
/ CURRENT APPLICATION NUMBER: US/08/239,765C
/ CURRENT FILING DATE: 1994-05-09
/ PRIOR APPLICATION NUMBER: 07/946,237
/ PRIOR FILING DATE: 1992-09-14
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patent in version 3.1
/ SEQ ID NO 4
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Conserved amino acid sequence of the TC-1 family of transposable
/ OTHER INFORMATION: elements
US-08-239-765C-4

Query Match 40.3%; Score 29; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10
Db 2 VMGC 5

RESULT 15
US-09-069-827A-94
/ Sequence 94, Application US/09069827A
/ Patent No. 6617114
/ GENERAL INFORMATION:
/ APPLICANT: FOWLKES, Dana M
/ KAY, Brian K
/ FRELINGER, Jeffrey A
/ HYDE-DERUYSCHE, Robin P
/ TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING
/ COMPLEMENTARY COMBINATORIAL LIBRARIES
/ NUMBER OF SEQUENCES: 178
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NETMARK, P.L.L.C.
/ STREET: 624 Ninth Street N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20001
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,827A
; FILING DATE: 30-APR-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/050,359
; FILING DATE: 31-MAR-1998
; APPLICATION NUMBER: PCT/US97/19638
; FILING DATE: 31-OCT-1997
; APPLICATION NUMBER: US 08/740,671
; FILING DATE: 31-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: FOWLKES=4C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 94:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-069-827A-94

Query Match      40.3%; Score 29; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      3 YWLTING 9
Db      1 YWMPDWG 7

Search completed: December 29, 2004, 21:36:45
Job time : 24.6667 secs
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Result No.	Query			ID	Description	
	Score	Match	Length			
1	72	100.0	10	13	US-10-046-922-35	Sequence 35, Appl
2	54	75.0	10	13	US-10-046-922-34	Sequence 34, Appl
3	50	69.4	10	13	US-10-046-922-73	Sequence 73, Appl
4	33	45.8	7	13	US-10-046-922-67	Sequence 67, Appl
5	33	45.8	8	13	US-10-046-922-68	Sequence 68, Appl
6	33	45.8	10	17	US-10-654-578-1090	Sequence 1090, Ap
7	33	45.8	10	17	US-10-654-578-1352	Sequence 1352, Ap
8	32	44.4	10	8	US-08-821-739A-90	Sequence 90, Appl
9	32	44.4	10	14	US-10-133-210-39	Sequence 39, Appl
10	32	44.4	10	14	US-10-133-210-69	Sequence 69, Appl
11	31	43.1	9	13	US-10-046-922-36	Sequence 36, Appl
12	31	43.1	12	8	US-09-572-404B-1454	Sequence 1454, Ap
13	30	41.7	9	8	US-08-821-739A-78	Sequence 78, Appl

; APPLICANT: Kubo, Hajime  
 ; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
 ; FILE REFERENCE: 28967/37084A  
 ; CURRENT APPLICATION NUMBER: US/10/046,922  
 ; CURRENT FILING DATE: 2002-01-15  
 ; NUMBER OF SEQ ID NOS: 80  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 34  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: isolated peptide  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (1)..(1)  
 ; OTHER INFORMATION: X is any amino acid  
 ; NAME/KEY: SITE  
 ; LOCATION: (10)..(10)  
 ; OTHER INFORMATION: X is any amino acid  
 ; US-10-046-922-34

Query Match 75.0%; Score 54; DB 13; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.72;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9  
 Db 2 GYWLTIWG 9

RESULT 3  
 US-10-046-922-73  
 ; Sequence 73, Application US/10046922  
 ; Publication No. US20020164667A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alitalo, Kari  
 ; APPLICANT: Koivunen, Erkki  
 ; APPLICANT: Kubo, Hajime  
 ; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
 ; FILE REFERENCE: 28967/37084A  
 ; CURRENT APPLICATION NUMBER: US/10/046,922  
 ; CURRENT FILING DATE: 2002-01-15  
 ; NUMBER OF SEQ ID NOS: 80  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 73  
 ; LENGTH: 10  
 ; TYPE: PRT  
 ; ORGANISM: peptide library  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (5)..(7)  
 ; OTHER INFORMATION: X is any amino acid  
 ; NAME/KEY: SITE  
 ; LOCATION: (9)..(9)  
 ; OTHER INFORMATION: X is any amino acid  
 ; US-10-046-922-73

Query Match 69.4%; Score 50; DB 13; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 2.5;  
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10  
 Db 1 CGYWXXXWC 10

RESULT 4  
 US-10-046-922-67  
 ; Sequence 67, Application US/10046922  
 ; Publication No. US20020164667A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alitalo, Kari  
 ; APPLICANT: Koivunen, Erkki  
 ; APPLICANT: Kubo, Hajime

; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
 ; FILE REFERENCE: 28967/37084A  
 ; CURRENT APPLICATION NUMBER: US/10/046,922  
 ; CURRENT FILING DATE: 2002-01-15  
 ; NUMBER OF SEQ ID NOS: 80  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 67  
 ; LENGTH: 7  
 ; TYPE: PRT  
 ; ORGANISM: peptide  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (4)..(6)  
 ; OTHER INFORMATION: X at position 4-6 is any amino acid  
 ; US-10-046-922-67

Query Match 45.8%; Score 33; DB 13; Length 7;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8  
 Db 1 GYWXXXW 7

RESULT 5  
 US-10-046-922-68  
 ; Sequence 68, Application US/10046922  
 ; Publication No. US20020164667A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alitalo, Kari  
 ; APPLICANT: Koivunen, Erkki  
 ; APPLICANT: Kubo, Hajime  
 ; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
 ; FILE REFERENCE: 28967/37084A  
 ; CURRENT APPLICATION NUMBER: US/10/046,922  
 ; CURRENT FILING DATE: 2002-01-15  
 ; NUMBER OF SEQ ID NOS: 80  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 68  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: peptide  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (4)..(6)  
 ; OTHER INFORMATION: X is any amino acid  
 ; NAME/KEY: SITE  
 ; LOCATION: (8)..(8)  
 ; OTHER INFORMATION: X is any amino acid  
 ; US-10-046-922-68

Query Match 45.8%; Score 33; DB 13; Length 8;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+06;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GYWLTIW 8  
 Db 1 GYWXXXW 7

RESULT 6  
 US-10-654-578-1090  
 ; Sequence 1090, Application US/10654578  
 ; Publication No. US20040229811A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blachuk, Orest W.  
 ; APPLICANT: Symonds, James Matthew  
 ; APPLICANT: Gour, Barbara J.  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
 ; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
 ; FILE REFERENCE: 100086.407C10  
 ; CURRENT APPLICATION NUMBER: US/10/654,578

; CURRENT FILING DATE: 2003-09-03  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1090  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmoglein-2 cell adhesion recognition sequence  
US-10-654-578-1090

Query Match 45.8%; Score 33; DB 17; Length 10;  
Best Local Similarity 60.0%; Pred. No. 5e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10  
||| |||  
Db 1 CGYALDARGC 10

RESULT 7  
US-10-654-578-1352  
; Sequence 1352, Application US/10654578  
; Publication No. US20040229811A1  
; GENERAL INFORMATION:  
; APPLICANT: Blachuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING  
; TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C10  
; CURRENT APPLICATION NUMBER: US/10/654,578  
; CURRENT FILING DATE: 2003-09-03  
; NUMBER OF SEQ ID NOS: 2009  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1352  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Cyclicized modulating agent comprising  
; OTHER INFORMATION: desmocolin-1 cell adhesion recognition sequence  
US-10-654-578-1352

Query Match 45.8%; Score 33; DB 17; Length 10;  
Best Local Similarity 60.0%; Pred. No. 5e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10  
||| |||  
Db 1 CGYATTADGC 10

RESULT 8  
US-08-821-739A-90  
; Sequence 90, Application US/08821739A  
; Publication No. US20020168374A1  
; GENERAL INFORMATION:  
; APPLICANT: Kubo, Ralph T.  
; APPLICANT: Grey, Howard M.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Celis, Esteban  
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses  
; FILE REFERENCE: 2060.005000A  
; CURRENT APPLICATION NUMBER: US/08/821,739A  
; CURRENT FILING DATE: 1999-03-20  
; PRIOR APPLICATION NUMBER: 60/013,833  
; PRIOR FILING DATE: 1996-03-21  
; PRIOR APPLICATION NUMBER: 08/589,107  
; PRIOR FILING DATE: 1996-07-12  
; PRIOR APPLICATION NUMBER: 08/451,913  
; PRIOR FILING DATE: 1995-05-26

; PRIOR APPLICATION NUMBER: 08/347,610  
; PRIOR FILING DATE: 1994-12-01  
; PRIOR APPLICATION NUMBER: 08/186,266  
; PRIOR FILING DATE: 1994-01-25  
; PRIOR APPLICATION NUMBER: 08/159,339  
; PRIOR FILING DATE: 1993-11-29  
; PRIOR APPLICATION NUMBER: 08/103,396  
; PRIOR FILING DATE: 1993-08-06  
; PRIOR APPLICATION NUMBER: 08/027,746  
; PRIOR FILING DATE: 1993-03-05  
; PRIOR APPLICATION NUMBER: 07/926,666  
; PRIOR FILING DATE: 1992-08-07  
; NUMBER OF SEQ ID NOS: 149  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 90  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-08-821-739A-90

Query Match 44.4%; Score 32; DB 8; Length 10;  
Best Local Similarity 83.3%; Pred. No. 6.8e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LTIWGC 10  
| ||||  
Db 2 LGIWGC 7

RESULT 9  
US-10-133-210-39  
; Sequence 39, Application US/10133210  
; Publication No. US20030103964A1  
; GENERAL INFORMATION:  
; APPLICANT: DeLisi, Charles  
; APPLICANT: Berzofsky, Jay  
; APPLICANT: Gulukota, Kamalakara  
; APPLICANT: Vaccaro, Dennis  
; APPLICANT: Weng, Zhiping  
; APPLICANT: Zhang, Chao  
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND  
; TITLE OF INVENTION: COMPOSITIONS THEREOF  
; FILE REFERENCE: BU-035AX  
; CURRENT APPLICATION NUMBER: US/10/133,210  
; CURRENT FILING DATE: 2002-04-26  
; NUMBER OF SEQ ID NOS: 281  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 39  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-133-210-39

Query Match 44.4%; Score 32; DB 14; Length 10;  
Best Local Similarity 83.3%; Pred. No. 6.8e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 LTIWGC 10  
| ||||  
Db 2 LGIWGC 7

RESULT 10  
US-10-133-210-69  
; Sequence 69, Application US/10133210  
; Publication No. US20030103964A1  
; GENERAL INFORMATION:  
; APPLICANT: DeLisi, Charles  
; APPLICANT: Berzofsky, Jay  
; APPLICANT: Gulukota, Kamalakara  
; APPLICANT: Vaccaro, Dennis

```
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 69
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-69

Query Match      44.4%; Score 32; DB 14; Length 10;
Best Local Similarity 83.3%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 LTIWGC 10
        |   |   |
Db       2 LGIWGC 7

RESULT 11
US-10-046-922-36
; Sequence 36, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 9
; TYPE: PRT
; ORGANISM: peptide
US-10-046-922-36

Query Match      43.1%; Score 31; DB 13; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
        |   |   |
Db       2 GYWDWTW 8

RESULT 12
US-09-572-404B-1454
; Sequence 1454, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 1454
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in p2RY5 at 139-148 and may interact with Sequen
```

```
; OTHER INFORMATION: in this patent.
US-09-572-404B-1454

Query Match      43.1%; Score 31; DB 10; Length 10;
Best Local Similarity 62.5%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GYWLTIW 9
        |   |   |
Db       1 GYWLTVIG 8

RESULT 13
US-08-821-739A-78
; Sequence 78, Application US/08821739A
; Publication No. US20020168374A1
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 2060.005000A
; CURRENT APPLICATION NUMBER: US/08/821,739A
; CURRENT FILING DATE: 1999-03-20
; PRIOR APPLICATION NUMBER: 60/013,833
; PRIOR FILING DATE: 1996-03-21
; PRIOR APPLICATION NUMBER: 08/589,107
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: 08/451,913
; PRIOR FILING DATE: 1995-05-26
; PRIOR APPLICATION NUMBER: 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: 08/186,266
; PRIOR FILING DATE: 1994-01-25
; PRIOR APPLICATION NUMBER: 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: 08/027,746
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: 07/926,666
; PRIOR FILING DATE: 1992-08-07
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 78
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-821-739A-78

Query Match      41.7%; Score 30; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 IWGC 10
        |   |   |
Db       1 IWGC 4

RESULT 14
US-09-832-723-104
; Sequence 104, Application US/09832723
; Patent No. US20020098524A1
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; APPLICANT: Chen, Yiyou
; APPLICANT: Murray, Christopher J.
; APPLICANT: Tijerina, Pilar
; TITLE OF INVENTION: METHODS FOR SELECTIVE TARGETING
; FILE REFERENCE: GC617-2
; CURRENT APPLICATION NUMBER: US/09/832,723
; CURRENT FILING DATE: 2001-04-11
```

; PRIOR APPLICATION NUMBER: US 60/197,259  
; PRIOR FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 117  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 104  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: peptides screened from a phage display random  
; OTHER INFORMATION: peptide library  
US-09-832-723-104

Query Match 41.7%; Score 30; DB 9; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.5e+06;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIW 8  
DB 1 CTLWPTFW 8

RESULT 15  
US-09-894-018-80  
; Sequence 80, Application US/09894018  
; Patent No. US20020119127A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMMUNE, Inc.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Chestnut, Robert  
; APPLICANT: Livingston, Brian  
; APPLICANT: Baker, Dennis  
; APPLICANT: Newman, Mark  
; APPLICANT: Brown, David  
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING  
; TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY  
; FILE REFERENCE: 39963-20033.00  
; CURRENT APPLICATION NUMBER: US/09/894,018  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: PCT/US00/35568  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/173,390  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 60/284,221  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 368  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 80  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligopeptide  
US-09-894-018-80

Query Match 41.7%; Score 30; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IWGC 10  
DB 1 IWGC 4

Search completed: December 29, 2004, 22:01:39  
Job time : 82 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 21:30:17 ; Search time 19 Seconds  
(without alignments)  
50.640 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 GGYWLTWGC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1102

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	33.3	10	S71868	glutathione transf
2	24	33.3	10	A35556	hypothetical prote
3	22	30.6	7	PT0586	T-cell receptor be
4	22	30.6	10	T17075	cytochrome-c oxida
5	21	29.2	10	E41946	T-cell receptor ga
6	20	27.8	5	JH0253	gut pentapeptide -
7	20	27.8	6	P41946	T-cell receptor ga
8	20	27.8	8	S13288	acylase - Kluvyvex
9	19	26.4	9	PT0324	Ig heavy chain CRD
10	19	26.4	10	PT0289	Ig heavy chain CRD
11	19	26.4	10	E49033	T-cell receptor ga
12	19	26.4	10	F49033	T-cell receptor ga
13	19	26.4	10	C41946	T-cell receptor ga
14	18	25.0	8	J50315	leucokinin V - Mad
15	18	25.0	10	PT0230	Ig heavy chain CDR
16	18	25.0	10	PH0923	T-cell receptor be
17	18	25.0	10	F33932	Ig mu chain J regi
18	18	25.0	10	S14943	UGA3 leader peptid
19	17	23.6	4	B53284	T-cell receptor be
20	17	23.6	6	PT0629	T-cell receptor be
21	17	23.6	6	PT0637	T-cell receptor be
22	17	23.6	6	A61068	locustakinin - mig
23	17	23.6	6	I79564	hypothetical TCL3
24	17	23.6	7	PT0628	T-cell receptor be
25	17	23.6	7	PT0642	T-cell receptor be
26	17	23.6	7	PT0722	T-cell receptor be
27	17	23.6	7	PT0728	T-cell receptor be
28	17	23.6	7	PX0008	glucuronosyltransf
29	17	23.6	7	B48394	major fat-globule

30	17	23.6	7	2	P00029	pev-kinin 1 - pena
31	17	23.6	7	2	S57274	triacylglycerol li
32	17	23.6	7	2	S33244	neuromodulatory pe
33	17	23.6	7	2	S33245	neuromodulatory pe
34	17	23.6	7	2	S33246	neuromodulatory pe
35	17	23.6	8	2	PT0724	T-cell receptor be
36	17	23.6	8	2	J50316	leucokinin VI - Ma
37	17	23.6	8	2	J50317	leucokinin VII - M
38	17	23.6	8	2	J50318	leucokinin VIII -
39	17	23.6	8	2	A31570	angiotensin-conver
40	17	23.6	9	2	A24244	adipokinetic hormo
41	17	23.6	9	2	PT0634	T-cell receptor be
42	17	23.6	9	2	PT0562	asperm-activating p
43	17	23.6	9	2	A60522	hypotrehalosemic h
44	17	23.6	10	2	B33995	hypertrehalosemic
45	17	23.6	10	2	S08997	

ALIGNMENTS

RESULT 1

S71868  
Glutathione transferase (EC 2.5.1.18) class mu 4 - pig (fragment)  
N:Alternate names: glutathione S-transferase class mu 4  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 19-Mar-1998 #sequence\_revision 13-Sep-1998 #text\_change 09-Jul-2004  
C:Accession: S71868

R:Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.

Biochem. J. 317, 879-884, 1996

A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospray

A:Reference number: S71864; MUID:96332484; PMID:8760377

A:Accession: S71868

A:Molecule type: protein

A:Residues: 1-10 <ROU>

A:Cross-references: UNIPROT:Q7M3E8

C:Comment: At least five species-independent classes of cytosolic glutathion transferases  
s mitochondrial form are known.

C:Complex: dimer

C:Function:

A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a v  
A:Pathway: detoxification; xenobiotics metabolism

A>Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism  
es of damage

C:Superfamily: glutathione transferase

C:Keywords: dimer; transferase

Query Match 33.3%; Score 24; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 9.9e+02;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYW 4

DB 4 GYW 6

RESULT 2

A35556  
hypothetical protein (ODC region) - human

C:Species: Homo sapiens (man)

C:Date: 21-Sep-1990 #sequence\_revision 21-Sep-1990 #text\_change 30-Sep-1993

C:Accession: A35556

R:Moshier, J.A.; Gilbert, J.D.; Skunca, M.; Dosesu, J.; Almodovar, K.M.; Luk, G.D.

J. Biol. Chem. 265, 4884-4892, 1990

A:Title: Isolation and expression of a human ornithine decarboxylase gene.

A:Reference number: A35556; MUID:90202959; PMID:2318672

A:Accession: A35556

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-10 <MOS>

A:Cross-references: GB:J05271

Query Match 33.3%; Score 24; DB 2; Length 10;

Best Local Similarity 75.0%; Pred. No. 9.9e+02;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGYW 4  
| |  
Db 5 CGAW 8

## RESULT 3

PT0586  
T-cell receptor beta chain V-D-J region (141-1CN) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0586; PT0592  
R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0586  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-7 <FEE>  
A;Experimental source: day 19 fetal thymus, strain BALB/c (clones 141-1CN and 141-1CD)  
C;Keywords: T-cell receptor

Query Match 30.6%; Score 22; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TIWG 9  
| | |  
Db 3 SING 6

## RESULT 4

TL17075  
cytochrome-c oxidase (EC 1.9.3.1) chain I - Chamaeleo fischeri mitochondrion (fragment)  
C;Species: mitochondrion Chamaeleo fischeri  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: TL17075  
R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Papenfuss, T.J.

J. Mol. Evol. 44, 660-674, 1997  
A;Title: Evolutionary shifts in three major structural features of the mitochondrial gene  
A;Reference number: Z18674; MUID:97315309; PMID:9169559  
A;Accession: TL17075

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA  
A;Residues: 1-10 <MAC>  
A;Cross-references: UNIPROT:O79912; EMBL:U82688; NID:G3603112; PID:G3603115; PIDN:AAC622

C;Genetics:

A;Genome: mitochondrion

A;Note: COI

C;Keywords: mitochondrion; oxidoreductase

Query Match 30.6%; Score 22; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WLTIW 8  
| | |  
Db 2 WLLRW 6

## RESULT 5

E41946  
T-cell receptor gamma chain (1a.9) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C;Accession: E41946  
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991  
A;Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma gene  
A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: E41946  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-10 <WHE>  
C;Keywords: T-cell receptor

Query Match 29.2%; Score 21; DB 2; Length 10;  
Best Local Similarity 40.0%; Pred. No. 2.8e+03;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYWL 5  
| | |  
Db 2 CAVWI 6

## RESULT 6

JH0253  
gut pentapeptide - Japanese eel  
C;Species: Anguilla japonica (Japanese eel)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C;Accession: JH0253  
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
A;Reference number: JH0253; MUID:92062113; PMID:1953755

A;Accession: JH0253

A;Molecule type: protein

A;Residues: 1-5 <UES>

A;Experimental source: gut

C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric  
, and of the circular muscle of the gastro-intestinal junction.

Query Match 27.8%; Score 20; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYW 4  
| |  
Db 1 GFW 3

## RESULT 7

F41946  
T-cell receptor gamma chain (1a.27) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999

C;Accession: F41946

R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991

A;Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma gene

A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: F41946

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-6 <WHE>

C;Keywords: T-cell receptor

Query Match 27.8%; Score 20; DB 2; Length 6;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYWL 5  
| | |  
Db 2 CAVWV 6

## RESULT 8

S19288  
acylase - Kluyvera cryocrescens

C;Species: Kluyvera cryocrescens

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S19288

R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.

Biochem. J. 280, 659-662, 1991  
A:Title: Chemical modification of serine at the active site of penicillin acylase from *R. Morita*, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.  
A:Reference number: S19288; MUID:92109664; PMID:1764029  
A:Accession: S19288  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-8 <MAR>  
A:Cross-references: UNIPROT:Q7M124

Query Match 27.8%; Score 20; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWL 5  
| | |  
DB 1 CNMW 5

## RESULT 9

PT0324  
Ig heavy chain CRD3 region (clone J2-106C) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0324  
R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0324  
A:Molecule type: DNA  
A:Residues: 1-9 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 26.4%; Score 19; DB 2; Length 9;  
Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
| | | |  
DB 3 GYGESYW 9

## RESULT 10

PT0289  
Ig heavy chain CRD3 region (clone 4-109) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C:Accession: PT0289  
R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J  
A:Reference number: PT0222; MUID:91108337; PMID:1899102  
A:Accession: PT0289  
A:Molecule type: DNA  
A:Residues: 1-10 <YAM>  
A:Experimental source: B lymphocyte  
C:Keywords: heterotetramer; immunoglobulin

Query Match 26.4%; Score 19; DB 2; Length 10;  
Best Local Similarity 33.3%; Pred. No. 5.4e+03;  
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 WLTIWG 9  
| | | |  
DB 4 WISMG 9

## RESULT 11

E49033  
T-cell receptor gamma chain V-D-J region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Dec-1993 #sequence\_revision 25-Aug-1995 #text\_change 21-Jul-2000

C:Accession: E49033; D49033  
R; Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.  
Eur. J. Immunol. 21, 2999-3007, 1991  
A:Title: Functionally distinct subsets of human gamma/delta T cells.  
A:Reference number: A49033; MUID:92083926; PMID:1684157  
A:Accession: E49033  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-10 <MOR>  
A:Cross-references: GB:S72587; NID:9240696; PIDN:AAB20630.1; PID:9240697  
A>Note: sequence extracted from NCBI backbone (NCBIN:72591, NCBIP:72595)  
A:Accession: D49033  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-10 <MOR2>  
A:Cross-references: GB:S72587; NID:9240696; PIDN:AAB20630.1; PID:9240697  
A>Note: sequence extracted from NCBI backbone (NCBIN:72587, NCBIP:72589)  
C:Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYW 4  
| | |  
DB 1 CALW 4

## RESULT 12

F49033  
T-cell receptor gamma chain V-D-J region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-Dec-1993 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
C:Accession: F49033  
R; Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.  
Eur. J. Immunol. 21, 2999-3007, 1991  
A:Title: Functionally distinct subsets of human gamma/delta T cells.  
A:Reference number: A49033; MUID:92083926; PMID:1684157  
A:Accession: F49033  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-10 <MOR>  
A:Cross-references: GB:S72605; NID:9240700; PIDN:AAB20632.1; PID:9240701  
A>Note: sequence extracted from NCBI backbone (NCBIN:72605, NCBIP:72606)  
C:Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 5.4e+03;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYW 4  
| | |  
DB 1 CALW 4

## RESULT 13

C41946  
T-cell receptor gamma chain (1t.60) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C:Accession: C41946  
R; Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991  
A:Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma ger  
A:Reference number: A41946; MUID:92049316; PMID:1658619  
A:Accession: C41946  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-10 <WHE>  
C:Keywords: T-cell receptor

Query Match 26.4%; Score 19; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 5.4e+03;

Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYW 4  
|  
Db 2 CAVW 5

RESULT 14  
JS0315  
leucokinin V - Madeira cockroach  
C;Species: Leucophaea maderae (Madeira cockroach)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: JS0315  
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
Comp. Biochem. Physiol. C 88, 27-30, 1987  
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic  
A;Reference number: JS0315  
A;Accession: JS0315  
A;Molecule type: protein  
A;Residues: 1-8 <HOL>  
A;Cross-references: UNIPROT:P19987  
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act  
C;Keywords: amidated carboxyl end; cephalomyotropic peptide  
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 25.0%; Score 18; DB 2; Length 8;  
Best Local Similarity 37.5%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GYMLTIWG 9  
| : ||  
Db 1 GSGFSSWG 8

RESULT 15  
PT0230  
Ig heavy chain CDR3 region (clone 1-118A) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996  
C;Accession: PT0230  
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
J. Exp. Med. 173, 395-407, 1991  
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
A;Reference number: PT0222; MUID:91108337; PMID:1899102  
A;Accession: PT0230  
A;Molecule type: DNA  
A;Residues: 1-10 <YAM>  
A;Experimental source: B lymphocyte  
C;Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 18; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 7.5e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LTIWG 9  
: ||:  
Db 3 ITIFG 7

Search completed: December 29, 2004, 21:42:54  
Job time : 19 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:27:57 ; Search time 100 Seconds  
(without alignments)  
57.537 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 GYWLTIWC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 2971

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30.5	42.4	10	1 LABA_JATMU	P13270 jatropha mu
2	27	37.5	10	2 Q8SHF6	Q8shf6 chamealeo m
3	26	36.1	8	2 Q70Y57	Q70y57 fuerstia af
4	26	36.1	8	2 CAD45547	Cad45547 fuerstia
5	24	33.3	10	2 Q7M3E8	Q7m3e8 sus scrofa
6	24	33.3	10	2 Q8SHN1	Q8shn1 bradypodion
7	24	33.3	10	2 Q6JL97	Q6jl97 neisseria g
8	24	33.3	10	2 AAS16521	Aas16521 neisseria
9	23.5	32.6	9	2 Q8SDB0	Q8sdb0 lepilemur s
10	23.5	32.6	9	2 Q8SDB8	Q8sdb8 lepilemur e
11	23.5	32.6	9	2 Q94NA9	Q94na9 daubentonla
12	23.5	32.6	9	2 Q94NB0	Q94nb0 microcebus
13	23.5	32.6	9	2 Q94NB1	Q94nb1 microcebus
14	23.5	32.6	9	2 Q94NB2	Q94nb2 microcebus
15	23.5	32.6	9	2 Q94XE6	Q94xe6 tectocoris
16	23	31.9	10	2 Q8SHC6	Q8shc6 furcifer be
17	22	30.6	10	2 Q79912	Q79912 chamealeo f
18	22	30.6	10	2 Q9G697	Q9g697 chamealeo d
19	22	30.6	10	2 Q8SH83	Q8sh83 brookesia t
20	22	30.6	10	2 Q8SH85	Q8sh85 brookesia t
21	22	30.6	10	2 Q8SH88	Q8sh88 brookesia t
22	22	30.6	10	2 Q8SH90	Q8sh90 brookesia s
23	22	30.6	10	2 Q8SH96	Q8sh96 brookesia p
24	22	30.6	10	2 Q8SHA2	Q8sha2 brookesia b
25	22	30.6	10	2 Q8SHA5	Q8sha5 brookesia a
26	22	30.6	10	2 Q8SHC9	Q8shc9 furcifer ba
27	22	30.6	10	2 Q8SHD2	Q8shd2 chamealeo w
28	22	30.6	10	2 Q8SHD5	Q8shd5 chamealeo s
29	22	30.6	10	2 Q8SHD8	Q8shd8 chamealeo r
30	22	30.6	10	2 Q8SHE1	Q8she1 chamealeo q
31	22	30.6	10	2 Q8SHE4	Q8she4 chamealeo q

32 22 30.6 10 2 Q8SHE7 Q8she7 chamealeo p  
33 22 30.6 10 2 Q8SHF3 Q8shf3 chamealeo m  
34 22 30.6 10 2 Q8SHF9 Q8shf9 chamealeo j  
35 22 30.6 10 2 Q8SHG5 Q8shg5 chamealeo h  
36 22 30.6 10 2 Q8SHG8 Q8shg8 chamealeo g  
37 22 30.6 10 2 Q8SHH1 Q8shh1 chamealeo f  
38 22 30.6 10 2 Q8SHH4 Q8shh4 chamealeo f  
39 22 30.6 10 2 Q8SHH7 Q8shh7 chamealeo f  
40 22 30.6 10 2 Q8SHI0 Q8shh0 chamealeo c  
41 22 30.6 10 2 Q8SHI3 Q8shh3 chamealeo c  
42 22 30.6 10 2 Q8SHI6 Q8shh6 chamealeo c  
43 22 30.6 10 2 Q8SHI9 Q8shh9 chamealeo c  
44 22 30.6 10 2 Q8SHJ2 Q8shj2 chamealeo a  
45 22 30.6 10 2 Q8SHJ5 Q8shj5 calumma par

## ALIGNMENTS

RESULT 1  
LABA\_JATMU  
ID LABA\_JATMU STANDARD; PRT; 10 AA.  
AC P13270;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Labaditin.  
OS Jatropha multifida (Physic nut).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Jatrophaceae;  
OC Jatropha.  
OX NCBI\_TaxID=3996;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Latex;  
RA Kosasi S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;  
RT "Labaditin, a novel cyclic decapeptide from the latex of Jatropha  
multifida L. (Euphorbiaceae). Isolation and sequence determination by  
RT means of two-dimensional NMR.";  
RL FEBS Lett. 256:91-96(1989).  
CC -!- FUNCTION: Labaditin is an active peptide which inhibits the  
CC classical pathway of complement activation in vitro. Activity  
CC seems to be based on an interaction with C1.  
CC -!- PTM: This is a cyclic peptide.  
CC -!- MISCELLANEOUS: Latex of this plant is used in folkloric medicine  
CC for treatment of infected wounds, skins infections and scabies.  
SQ Direct protein sequencing.  
KW SEQUENCE 10 AA; 1089 MW; D98AAD6362D1B362 CRC64;

Query Match 42.4%; Score 30.5; DB 1; Length 10;  
Best Local Similarity 62.5%; Pred. No. 5.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;  
QY 2 GYWLTIWC 9  
Db 2 GW-TVMG 8

RESULT 2  
Q8SHF6  
ID Q8SHF6 PRELIMINARY; PRT; 10 AA.  
AC Q8SHF6;  
DT 01-JUN-2002 (Tremblrel. 21, Created)  
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
GN Name=COI;  
OS Chamaeleo melleri (Meller's chameleon).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodactylia; Squamata; Iguania; Acrodonta; Chamaeleonidae; Chamaeleo.  
OX NCBI\_TaxID=179915;

```

RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=22169767; PubMed=12182400;
RA  Townsend T., Larson A.;
RT  "Molecular phylogenetics and mitochondrial genomic evolution in the
RT  chameleoneidae (Reptilia, Squamata).";
RL  Mol. Phylogenet. Evol. 23:22-36(2002).
RN  [2]
RP  SEQUENCE FROM N.A.
RA  Townsend T.M., Larson A.L.;
RL  Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF48755; AAL90547.1; -.
DR  GO; GO:0005739; C:mitochondrion; IEA.
KW  Mitochondrion.
FT  NON TER 10 10
SQ  SEQUENCE 10 AA; 1276 MW; 5E218E2733772727 CRC64;

Query Match 37.5%; Score 27; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 WLTW 8
Db 2 WLLW 6

RESULT 3
Q70Y57
ID Q70Y57 PRELIMINARY; PRT; 8 AA.
AC Q70Y57;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN Name=rps16;
OS Fuerstia africana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamnids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fierstia.
OX NCBI_TaxID=204226;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15019625;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 36.1%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TIWG 9
Db 2 TIWG 5

RESULT 4
CAD4547
ID CAD4547 PRELIMINARY; PRT; 8 AA.
AC CAD4547;
DT 14-MAR-2004 (TrEMBLrel. 27, Created)
DT 14-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).

```

```

GN RPS16.
OS Fuerstia africana.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamnids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fierstia.
OX NCBI_TaxID=204226;
RN [1]
RP SEQUENCE FROM N.A.
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505427; CAD45547.1; -.
KW Chloroplast; Ribosomal protein.
FT NON TER 1 1
FT NON TER 8 8
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 36.1%; Score 26; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 TIWG 9
Db 2 TIWG 5

RESULT 5
Q7M3E8
ID Q7M3E8 PRELIMINARY; PRT; 10 AA.
AC Q7M3E8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Glutathione transferase (EC 2.5.1.18) class mu 4 (Fragment).
OS Sus scrofa domestica (domestic pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sub.
OX NCBI_TaxID=9825;
RN [1]
RP SEQUENCE.
RA Rouimi P., Anglade P., Debrauwer L., Tulliez J.;
RT "Characterization of pig liver glutathione S-transferases using HPLC-
RT electrospray-ionization mass spectrometry.";
RL Biochem. J. 317:879-884(1996).
DR PIR; S71868; S71868.
DR GO; GO:0004364; F:glutathione transferase activity; IEA.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1223 MW; 5816395AB36B5877 CRC64;

Query Match 33.3%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYW 4
Db 4 GYW 6

RESULT 6
Q8SHN1
ID Q8SHN1 PRELIMINARY; PRT; 10 AA.
AC Q8SHN1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Bradypodion tavetanum (Dwarf Fischer's chameleon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC	Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
OC	Bradypodion.
OX	NCBI_TaxID=179888;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22169767; PubMed=12182400;
EX	Townsend T., Larson A.;
RT	"Molecular phylogenetics and mitochondrial genomic evolution in the
RT	chamaeleonidae (Reptilia, Squamata).";
RL	Mol. Phylogenet. Evol. 23:22-36(2002).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Townsend T.M., Larson A.L.;
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF448730; AAL90472.1; -.
DR	GO; GO:0005739; C:mitchondrion; IEA.
KW	Mitochondrion.
FT	NON TER 10 10
SQ	SEQUENCE 10 AA; 1327 MW; 5E2180C7336415B7 CRC64;
Query Match 33.3%; Score 24; DB 2; Length 10;	
Best Local Similarity 60.0%; Pred.No. 4.8e+03;	
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy	4 WLTIW 8
Db	:
	2 WLSRW 6
RESULT 7	
Q6JL97	
ID	PRELIMINARY; PRT; 10 AA.
AC	Q6JL97;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	NuOL (Fragment).
GN	Name=nuol;
OS	Neisseria gonorrhoeae.
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC	Neisseriaceae; Neisseria.
OX	NCBI_TaxID=485;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MS11;
RC	PubMed=15084227;
RA	Snyder L.A., Davies J.K., Saunders N.J.;
RT	"Microarray genotyping of key experimental strains of Neisseria
RT	gonorrhoeae reveals gene complement diversity and five new neisserial
RT	genes associated with Minimal Mobile Elements.";
RL	BMC Genomics 5:23-23(2004).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MS11;
RA	Snyder L.A.S., Davies J.K., Saunders N.J.;
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY386266; AAS16521.1; -.
FT	NON TER 1 1
SQ	SEQUENCE 10 AA; 1227 MW; BACCB286379DIA6 CRC64;
Query Match 33.3%; Score 24; DB 2; Length 10;	
Best Local Similarity 60.0%; Pred.No. 4.8e+03;	
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	
Qy	5 LTWG 9
Db	:
	3 MTFWG 7
RESULT 8	
AAS16521	
ID	PRELIMINARY; PRT; 10 AA.
AC	AAS16521;

Q85DB8  
 ID Q85DB8 PRELIMINARY; PRT; 9 AA.  
 AC Q85DB8;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Cytochrome oxidase subunit III (Fragment).  
 GN Name=COIII;  
 OS Lepilemur edwardsi (Milne-Edwards's sportive lemur).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Strepsirhini; Megaladapidae; Lepilemur.  
 OX NCBI\_TaxID=122230;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22631663; PubMed=12719521;  
 RA Pastorini J., Thalmann U., Martin R.D.;  
 RT "A molecular approach to comparative phylogeography of extant Malagasy lemurs.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).  
 DR EMBL; AF224595; AAK33644.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
 Query Match 32.6%; Score 23.5; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 QY 3 YWLTWG 9  
 Db ||||  
 5 YW---WG 8

RESULT 11  
 Q94NA9  
 ID Q94NA9 PRELIMINARY; PRT; 9 AA.  
 AC Q94NA9;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cytochrome oxidase subunit III (Fragment).  
 GN Name=COIII;  
 OS Daubentonia madagascariensis (Aye-aye).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Strepsirhini; Daubentonidae;  
 OC Daubentonia.  
 OX NCBI\_TaxID=31869;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21184272; PubMed=11286490;  
 RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
 RT "Molecular phylogeny of the lemur family Cheirogaleidae (Primates) based on mitochondrial DNA sequences.";  
 RL Mol. Phylogenet. Evol. 19:45-56(2001).  
 DR EMBL; AF224642; AAK70615.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
 Query Match 32.6%; Score 23.5; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 QY 3 YWLTWG 9  
 Db ||||  
 5 YW---WG 8

RESULT 12  
 Q94NB0  
 ID Q94NB0 PRELIMINARY; PRT; 9 AA.  
 AC Q94NB0;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cytochrome oxidase subunit III (Fragment).  
 GN Name=COIII;  
 OS Microcebus rufus (Brown mouse lemur).  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;  
 OC Microcebus.  
 OX NCBI\_TaxID=122232;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21184272; PubMed=11286490;  
 RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
 RT "Molecular phylogeny of the lemur family Cheirogaleidae (Primates) based on mitochondrial DNA sequences.";  
 RL Mol. Phylogenet. Evol. 19:45-56(2001).  
 DR EMBL; AF224636; AAK70595.1; -.  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
 Query Match 32.6%; Score 23.5; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 QY 3 YWLTWG 9  
 Db ||||  
 5 YW---WG 8

RESULT 13  
 Q94NB1  
 ID Q94NB1 PRELIMINARY; PRT; 9 AA.  
 AC Q94NB1;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cytochrome oxidase subunit III (Fragment).  
 GN Name=COIII;  
 OS Microcebus ravelobensis.  
 OC Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;  
 OC Microcebus.  
 OX NCBI\_TaxID=122231;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21184272; PubMed=11286490;  
 RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
 RT "Molecular phylogeny of the lemur family cheirogaleidae (primates)  
 based on mitochondrial DNA sequences.";  
 RL Mol. Phylogenet. Evol. 19:45-56(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22631663; PubMed=12719521;  
 RA Pastorini J., Thalmann U., Martin R.D.;  
 RT "A molecular approach to comparative phylogeography of extant Malagasy  
 lemurs.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).  
 DR EMBL; AF224630; AAK70571.1; -;  
 DR EMBL; AF224631; AAK70575.1; -;  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;  
 Query Match 32.6%; Score 23.5; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 QY 3 YWLTWIG 9  
 Db || || ||  
 5 YW---WG 8  
 RESULT 14  
 O94NB2 PRELIMINARY; PRT; 9 AA.  
 AC Q94NB2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Cytochrome oxidase subunit III (Fragment).  
 GN Names=COLII;  
 OS Microcebus murinus (Lesser mouse lemur).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Strepsirhini; Cheirogaleidae;  
 OC Microcebus.  
 OX NCBI\_TaxID=30608;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21184272; PubMed=11286490;  
 RA Pastorini J., Martin R.D., Ehresmann P., Zimmermann E., Forstner M.R.;  
 RT "Molecular phylogeny of the lemur family cheirogaleidae (primates)  
 based on mitochondrial DNA sequences.";  
 RL Mol. Phylogenet. Evol. 19:45-56(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22631663; PubMed=12719521;  
 RA Pastorini J., Thalmann U., Martin R.D.;  
 RT "A molecular approach to comparative phylogeography of extant Malagasy  
 lemurs.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:5879-5884(2003).  
 DR EMBL; AF224624; AAK70547.1; -;  
 DR EMBL; AF224625; AAK70551.1; -;  
 DR EMBL; AF224626; AAK70555.1; -;  
 DR EMBL; AF224627; AAK70559.1; -;  
 DR EMBL; AF224628; AAK70563.1; -;  
 DR EMBL; AF224629; AAK70567.1; -;  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 9 AA; 1160 MW; D5C563636B5045A2 CRC64;

Query Match 32.6%; Score 23.5; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 QY 3 YWLTWIG 9  
 Db || || ||  
 5 YW---WG 8  
 RESULT 15  
 O94XE6 PRELIMINARY; PRT; 9 AA.  
 AC Q94XE6;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Cytochrome c oxidase subunit III (Fragment).  
 GN Name=cox3;  
 OS Tectocoris diophthalmus (cotton harlequin bug).  
 OG Mitochondrion.  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;  
 OC Panheteroptera; Pentatomomorpha; Pentatomioidea; Pentatomidae;  
 OC Tectocoris.  
 OX NCBI\_TaxID=159956;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21396409; PubMed=11504862;  
 RA Shao R., Campbell N.J., Schmidt E.R., Barker S.C.;  
 RT "Increased rate of gene rearrangement in the mitochondrial genomes of  
 three orders of hemipteroid insects.";  
 RL Mol. Biol. Evol. 18:1828-1832(2001).  
 DR EMBL; AF335990; AAK55283.1; -;  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 9 AA; 1206 MW; A2C563636B5041A6 CRC64;  
 Query Match 32.6%; Score 23.5; DB 2; Length 9;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 3; Gaps 1;  
 QY 3 YWLTWIG 9  
 Db || || ||  
 5 YW---WG 8  
 Search completed: December 29, 2004, 21:41:52  
 Job time : 100 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: December 30, 2004, 12:55:07 ; Search time 69.6226 Seconds  
(without alignments)  
51.525 Million cell updates/sec

Title: US-10-046-922-35

Perfect score: 72

Sequence: 1 COYWLITWC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	10	5	ABP53932
2	54	75.0	10	5	ABP53931
3	50	69.4	10	5	ABP53968
4	47.5	66.0	304	7	ADC87481 Human GPC
5	47	65.3	25	7	ADC99638 Cancer-re
6	46	63.9	17	6	AAO26074 Fc region
7	46	63.9	17	6	ADJ50741 Human ser
8	46	63.9	136	8	ADM87650 Human EST
9	45	62.5	20	5	AAU90545 Insulin/i
10	45	62.5	129	2	AAV59880 Human nor
11	45	62.5	828	6	ABU49938 Protein e
12	44.5	61.8	1024	5	ABBO4861 LDL recep
13	44	61.1	149	8	ADP29850 Human sec
14	44	61.1	166	6	AAE31487 Human but
15	44	61.1	415	5	AAU91293 Human NOV
16	43	59.7	13	6	AAO26093 Fc region
17	43	59.7	13	8	ADJ50760 Human ser
18	43	59.7	454	5	ABP73979 Candida a
19	43	59.7	474	6	ABU30004 Protein e
20	43	59.7	492	7	ADC97318 E. faeciu
21	43	59.7	1084	8	ADL81869 P. aerugi
22	42.5	59.0	152	3	AAV94989 Human sec
23	42.5	59.0	152	5	ABB90081 Human pol
24	42.5	59.0	152	5	AAO17173 Human sec
25	42.5	59.0	152	5	ABG64784 Human alb

## ALIGNMENTS

### RESULT 1

ABP53932

ID ABP53932 standard; peptide; 10 AA.

AC ABP53932;

DT 09-JAN-2003 (first entry)

DE VEGFR-3 binding peptide SEQ ID NO:35.

KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulvular; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.

OS Homo sapiens.

OS Synthetic.

PN WO200257299-A2.

XX 25-JUL-2002.

XX 16-JAN-2002; 2002WO-IB000099.

XX 17-JAN-2001; 2001US-0262476P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (LICN ) LICENTIA LTD.

XX Alitalo K, Koivunen E, Kubo H;

XX WPI; 2002-691521/74.

XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
PT such as cancer and diseases of neovascularization.

XX Claim 13; Page 80; 149pp; English.

XX The present invention describes an isolated peptide (I) that binds to and  
CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
CC antidiabetic and vulvular activities, and can be used in gene therapy.  
CC Compositions and methods from the present invention are useful for  
CC diagnosing, evaluating and treating disorders mediated by the activity of  
CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

26	42.5	59.0	152	8	ADL78051	Adl78051 Albumin f
27	42.5	59.0	159	2	AAE66278	AAE66278 Therapeut
28	42.5	59.0	159	3	AAE12156	AAE12156 Hydrophob
29	42.5	59.0	159	4	AAE78581	AAE78581 Human pro
30	42.5	59.0	159	4	AAE73100	AAE73100 Human ang
31	42.5	59.0	159	5	AAO17198	AAO17198 Human sec
32	42.5	59.0	159	5	ABG64785	ABG64785 Human alb
33	42.5	59.0	159	8	ADL78052	Adl78052 Albumin f
34	42.5	59.0	159	8	ADN05188	Adn05188 Antipsori
35	42.5	59.0	161	4	AAE25822	AAE25822 Human pro
36	42.5	59.0	161	4	ABE12006	ABE12006 Human gli
37	42.5	59.0	161	4	AAE79565	AAE79565 Human pro
38	42.5	59.0	176	6	ABO07116	ABO07116 Novel hum
39	42.5	59.0	1024	5	ABO04863	ABO04863 LDL recep
40	42.5	59.0	1765	2	AAV16572	AAV16572 Type 5 so
41	42.5	59.0	1765	2	AAV41668	AAV41668 Rat senso
42	42.5	59.0	1765	2	AAV06596	AAV06596 Rat sodiu
43	42.5	59.0	1765	4	AAE20122	AAE20122 Rat sodiu
44	42.5	59.0	1765	4	AAE20123	AAE20123 Rat sodiu
45	42.5	59.0	1765	7	ADD32192	ADD32192 Rat Na v

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
 CC represents a specifically claimed VEGFR-3 binding peptide from the  
 CC present invention  
 CC  
 SQ Sequence 10 AA;  
 Query Match 100.0%; Score 72; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.0025;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CGYWLTIWGC 10  
 Db 1 CGYWLTIWGC 10  
 RESULT 2  
 ABP53931  
 ID ABP53931 standard; peptide; 10 AA.  
 XX  
 AC ABP53931;  
 XX  
 DT 09-JAN-2003 (first entry)  
 XX  
 DE VEGFR-3 binding peptide SEQ ID NO:34.  
 XX  
 KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
 KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
 KW vulnary; cell surface receptor; cancer; neovascularisation;  
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
 KW diabetes; PDGF; platelet derived growth factor.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "any amino acid"  
 FT Misc-difference 10 /note= "any amino acid"  
 FT  
 FT  
 FT  
 XX WO200257299-A2.  
 XX  
 XX 25-JUL-2002.  
 XX  
 XX 16-JAN-2002; 2002WO-IB000099.  
 XX  
 XX 17-JAN-2001; 2001US-0262476P.  
 XX  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX (LICN) LICENTIA LTD.  
 XX  
 XX Alitalo K, Koivunen E, Kubo H;  
 XX  
 XX WPI; 2002-691521/74.  
 XX  
 XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
 XX diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
 XX such as cancer and diseases of neovascularization.  
 XX  
 XX Claim 12; Page 80; 149pp; English.  
 XX  
 XX The present invention describes an isolated peptide (I) that binds to and  
 XX inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
 XX have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
 XX antidiabetic and vulnary activities, and can be used in gene therapy.  
 XX Compositions and methods from the present invention are useful for  
 XX diagnosing, evaluating and treating disorders mediated by the activity of  
 XX the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
 CC represents a specifically claimed VEGFR-3 binding peptide from the  
 CC present invention  
 CC  
 SQ Sequence 10 AA;  
 Query Match 75.0%; Score 54; DB 5; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 0.67;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GYWLTIWG 9  
 Db 2 GYWLTIWG 9  
 RESULT 3  
 ABP53968  
 ID ABP53968 standard; peptide; 10 AA.  
 XX  
 AC ABP53968;  
 XX  
 DT 09-JAN-2003 (first entry)  
 XX  
 DE VEGFR-3 binding peptide SEQ ID NO:73.  
 XX  
 KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
 KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
 KW vulnary; cell surface receptor; cancer; neovascularisation;  
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
 KW diabetes; PDGF; platelet derived growth factor.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT Misc-difference 5.7 /note= "X is any amino acid"  
 FT Misc-difference 9 /note= "X is any amino acid"  
 FT  
 FT  
 FT  
 XX WO200257299-A2.  
 XX  
 XX 25-JUL-2002.  
 XX  
 XX 16-JAN-2002; 2002WO-IB000099.  
 XX  
 XX 17-JAN-2001; 2001US-0262476P.  
 XX  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX (LICN) LICENTIA LTD.  
 XX  
 XX Alitalo K, Koivunen E, Kubo H;  
 XX  
 XX WPI; 2002-691521/74.  
 XX  
 XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
 XX diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
 XX such as cancer and diseases of neovascularization.  
 XX  
 XX Disclosure; Page 147; 149pp; English.  
 XX  
 XX The present invention describes an isolated peptide (I) that binds to and  
 XX inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
 XX have cytostatic, hepatotropic, antiinflammatory, hypotensive,  
 XX antidiabetic and vulnary activities, and can be used in gene therapy.  
 XX Compositions and methods from the present invention are useful for  
 XX diagnosing, evaluating and treating disorders mediated by the activity of  
 XX the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,

CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangiomas and diabetes. The present sequence  
 CC represents a VEGFR-3 binding peptide, which is given in the  
 CC exemplification of the present invention

XX  
 XX Sequence 10 AA;

Query Match 69.4%; Score 50; DB 5; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 2.3;  
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10  
 |||||  
 DB 1 CGYWXWXXWC 10

## RESULT 4

ADC87481  
 ID ADC87481 standard; protein; 304 AA.

XX  
 AC ADC87481;

XX 01-JAN-2004 (first entry)

XX Human GPCR protein SEQ ID NO:1934.

DE human; GPCR; guanosine triphosphate-binding protein coupled receptor;  
 KW gene therapy.

XX Homo sapiens.

XX EP1270724-A2.

XX 02-JAN-2003.

XX 18-JUN-2002; 2002EP-00013517.

XX 18-JUN-2001; 2001JP-00246789.

XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

XX Suwa M, Asai K, Akiyama Y, Aburatani H;

XX WPI; 2003-315783/31.

DR N-PSDB; ADC87480.

XX New polynucleotide, useful for preparing a composition for treating a  
 PT patient in need of increased or suppressed activity or expression of the  
 PT guanosine triphosphate-binding protein coupled receptor.

XX Claim 2; SEQ ID NO 1934; 28pp; English.

XX The invention relates to a novel polynucleotide encoding a guanosine  
 CC triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of  
 CC the invention may have a use in gene therapy. The polynucleotide and  
 CC polypeptide are useful for preparing a composition for treating a patient  
 CC in need of increased or suppressed activity or expression of the  
 CC guanosine triphosphate-binding protein coupled receptor. The protein  
 CC sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.

XX Sequence 304 AA;

Query Match 66.0%; Score 47.5; DB 7; Length 304;  
 Best Local Similarity 60.0%; Pred. No. 91;  
 Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWLTIWGC 10  
 |||||  
 DB 108 CGFW-AVWGC 116

## RESULT 5

ADC99638  
 ID ADC99638 standard; peptide; 25 AA.

XX  
 AC ADC99638;

XX 01-JAN-2004 (first entry)

XX Cancer-related Tie-1-binder peptide - SEQ ID 476.

DE cytostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras;  
 KW leptin; VEGF; vascular endothelial growth factor receptor; VEGF-R1;  
 KW VEGF-R2; VEGF-R3; FLT1; FMS-related tyrosine kinase 1; FLK1; KDR;  
 KW kinase insert domain protein receptor; EGFR; epidermal growth factor;  
 KW FGFR1; fibroblast growth factor; Tie-1.

XX Unidentified.

XX WO2003035839-A2.

XX 01-MAY-2003.

XX 24-OCT-2002; 2002WO-US034021.

XX 24-OCT-2001; 2001US-0345471P.

XX (DGI-B-) DGI BIOTECHNOLOGIES INC.

XX Pillutla RC, Briessette R, Spruyt M, Dedova O, Blume A;

PI Prendergast J, Goldstein N;

XX WPI; 2003-457332/43.

XX Selecting target and target binder pairs for preparing a composition for  
 PT treating cancer by mixing in a reaction vessel phage expressing  
 PT biological targets and phage expressing target binders.

XX Claim 26; SEQ ID NO 476; 172pp; English.

XX The invention relates to a novel method of selecting target and target  
 CC binder pairs comprising mixing in a reaction vessel phage expressing  
 CC biological targets and phage expressing target binders, each having  
 CC distinguishable selection markers and selecting target and target binder  
 CC pairs based on the selection markers. The molecules of the invention  
 CC demonstrate cytostatic activity whilst the method may be useful for  
 CC selecting target and target binder pairs for preparing a composition for  
 CC treating cancer. Furthermore, the method may be utilised during gene  
 CC therapy procedures. The current sequence is that of the cancer-related  
 CC Tie-1-binder peptide of the invention.

XX Sequence 25 AA;

Query Match 65.3%; Score 47; DB 7; Length 25;  
 Best Local Similarity 66.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 9  
 |||||  
 DB 5 CGYWGELMG 13

## RESULT 6

AAO26074  
 ID AAO26074 standard; peptide; 17 AA.

XX  
 AC AAO26074;

XX 03-APR-2003 (first entry)

XX Fc region binding peptide SEQ ID No 54.

XX

KW Immunoglobulin Fc region; binding; whole blood; plasma; transgenic milk;  
 KW antibody response; half-life; stability; circulatory system.  
 OS Unidentified.  
 XX WO200286070-A2.  
 XX 31-OCT-2002.  
 XX 18-APR-2002; 2002WO-US012492.  
 XX 18-APR-2001; 2001US-0284534P.  
 XX (DYAX-) DYAX CORP.  
 XX Rondon IJ, Wu Q, Ley AC, Stochl M, Ransohoff TC, Potter MD;  
 XX WPI; 2003-201220/19.  
 XX New polypeptides, useful as binding molecules for detecting, isolating or  
 PT purifying immunoglobulin Fc-region polypeptides present in a solution, or  
 PT for regulating or preventing an antibody response.  
 XX Claim 3; Page 76; 152pp; English.  
 XX The invention relates to novel isolated polypeptides comprising a  
 CC sequence that binds an immunoglobulin Fc region. The polypeptides are  
 CC useful as binding molecules for detecting, isolating or purifying  
 CC immunoglobulin Fc-region polypeptides present in a solution, e.g. whole  
 CC blood, plasma or transgenic milk. The Fc-region binding polypeptides are  
 CC also useful for regulating or preventing an antibody response, or for  
 CC increasing the half-life and over all stability of a therapeutic or  
 CC diagnostic compound that is administered to or enters the circulatory  
 CC system of an individual. This sequence represents an Fc region binding  
 CC peptide of the invention  
 XX SQ Sequence 17 AA;  
 Query Match 63.9%; Score 46; DB 6; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CGYWLTIWG 9  
 DB ||| |||  
 4 CGFWPRWG 12  
 RESULT 7  
 ADJ50741  
 ID ADJ50741 standard; peptide; 17 AA.  
 XX AC ADJ50741;  
 XX 06-MAY-2004 (first entry)  
 DT Human serum albumin binding peptide, Seq ID No 278.  
 DE human serum albumin; HSA; serum; blood; tumour; human.  
 XX Homo sapiens.  
 XX WO2003106493-A1.  
 XX 24-DEC-2003.  
 XX 16-JUN-2003; 2003WO-US018896.  
 XX 14-JUN-2002; 2002US-0388642P.  
 XX (DYAX-) DYAX CORP.  
 XX Sato AK, Dawson BM;  
 XX New isolated polynucleotides and polypeptides, useful for treating, e.g.

DR WPI; 2004-082161/08.  
 XX Evaluating sample comprising soluble serum protein by forming complex  
 PT comprising serum protein and physically associated compounds using  
 PT peptide ligand that specifically binds with proteins, which is separated  
 PT and evaluated.  
 XX Disclosure; SEQ ID NO 278; 191pp; English.  
 XX The invention relates to a method of evaluating sample by providing a  
 CC soluble serum protein (I), one or more compounds physically associated  
 CC with (I), and a (I)-binding agent that comprises a peptide that  
 CC specifically binds to (I), allowing the (I)-binding agent to bind to (I)  
 CC to form a complex including one or more compounds physically associated  
 CC with (I), separating the complex from one or more components of the  
 CC sample, and evaluating one or more of the physically associated  
 CC compounds. The sample comprises blood or serum, or is obtained from a  
 CC biopsy. The sample may also be obtained from a tumour or a region within  
 CC 5 mm of a tumour. The method is useful for detecting modulators that  
 CC modulate interaction of serum protein-binding compound and serum protein  
 CC and for identifying binding ligands for serum protein. The present  
 CC sequence represents a serum albumin-binding peptide identified using the  
 CC method of the invention.  
 XX SQ Sequence 17 AA;  
 Query Match 63.9%; Score 46; DB 8; Length 17;  
 Best Local Similarity 66.7%; Pred. No. 13;  
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CGYWLTIWG 9  
 DB ||| |||  
 4 CGFWPRWG 12  
 RESULT 8  
 ADM87650  
 ID ADM87650 standard; protein; 136 AA.  
 XX AC ADM87650;  
 XX 03-JUN-2004 (first entry)  
 DT Human EST derived amino acid sequence SEQ ID NO:743.  
 XX respiratory; cytostatic; antiarthritic; antiinflammatory;  
 KW gastrointestinal; antibacterial; immunosuppressive; antidiabetic;  
 KW antirheumatic; gene therapy; molecular weight marker; chromosome marker;  
 KW chromosome tag; genetic fingerprinting; nutritional supplement; cancer;  
 KW inflammatory condition; arthritis; inflammatory bowel disease;  
 KW Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;  
 KW graft versus host disease; human; expressed sequence tag; EST.  
 XX Homo sapiens.  
 XX WO2004009834-A2.  
 XX 29-JAN-2004.  
 XX 19-JUL-2002; 2002WO-US022858.  
 XX 21-JUL-2001; 2001US-0306971P.  
 XX 28-MAR-2002; 2002US-00112944.  
 XX (NUVE-) NUVELO INC.  
 XX Tang YT, Yang Y, Weng G, Zhang J, Ren F, Xue A, Wang J;  
 PI Wehrman T, Ghosh MJ, Wang D, Zhao QA, Wang Z;  
 XX WPI; 2004-143291/14.  
 DR N-PSDB; ADM87432.  
 XX New isolated polynucleotides and polypeptides, useful for treating, e.g.

PT cancer, lung or liver fibrosis, arthritis, inflammatory bowel disease,  
 PT Crohn's disease, rheumatoid arthritis, diabetes mellitus type 1 or graft  
 PT versus host disease.

XX Example 2; SEQ ID NO 743; 591pp; English.

CC The present invention describes an isolated polynucleotide (1): (a)  
 CC comprising a nucleotide sequence selected from SEQ ID NO:1-244; or (b)  
 CC which encodes a polypeptide with biological activity, where the  
 CC polynucleotide hybridizes to (i) under stringent hybridisation conditions  
 CC or has greater than 99% sequence identity with (1), (1) has respiratory,  
 CC cytotatic, antiarthritic, antinflammatory, gastrointestinal,  
 CC antibacterial, immunosuppressive, antidiabetic and antirheumatic  
 CC activities, and can be used in gene therapy. (1) can be used for  
 CC generating polynucleotides encoding chimeric or fusion proteins and  
 CC heterologous protein sequences. The polynucleotides can be used to  
 CC express recombinant protein for analysis, characterisation or therapeutic  
 CC use; as markers for tissues in which the corresponding protein is  
 CC preferentially expressed; as molecular weight markers on gels; as  
 CC chromosome markers or tags to identify chromosomes or to map related gene  
 CC positions; to compare with endogenous DNA sequences in patients to  
 CC identify potential genetic disorders; as probes to hybridise and discover  
 CC genes, related DNA sequences; as a source of information to derive PCR  
 CC primers for genetic fingerprinting; as a probe to subtract-out known  
 CC sequences in the process of discovering other novel polynucleotides; for  
 CC selecting and making oligomers for attachment to a gene chip or other  
 CC support, including for examination of expression patterns; to raise anti-  
 CC protein antibodies using DNA immunisation techniques; and as an antigen  
 CC to raise anti-DNA antibodies or elicit another immune response. The  
 CC polynucleotides and polypeptides can also be used as nutritional sources  
 CC or supplements, e.g. as a protein or amino acid supplement, as a carbon  
 CC source, as a nitrogen source or as a source of carbohydrates. The  
 CC polynucleotides and polypeptides can also be used treat cancer. The  
 CC compositions are useful for promoting better or faster closure of non-  
 CC healing wounds, for the generation and regeneration of tissues, for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues, and conditions resulting from  
 CC systemic cytokine damage. The compositions can also be used to treat  
 CC inflammatory conditions (e.g. arthritis, inflammatory bowel disease or  
 CC Crohn's disease), sepsis, rheumatoid arthritis, diabetes mellitus type 1  
 CC or graft versus host disease. The present sequence represents an  
 CC expressed sequence tag (EST) derived amino acid sequence from the present  
 CC invention. N.B. The sequences for this patent were obtained from the  
 CC USPTO web site from an equivalent US patent US20040048249A1.

XX Sequence 136 AA;

Query Match 63.9%; Score 46; DB 8; Length 136;  
 Best Local Similarity 60.0%; Pred. No. 73;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGVWLTWGC 10  
 Db 93 CGRWDLWGC 102

RESULT 9

AAU90545  
 ID AAU90545 standard; peptide; 20 AA.

XX AAU90545;

XX 18-JUN-2002 (first entry)

DE Insulin/insulin-like growth factor receptor-binding peptide #2501.

XX Cytostatic; antidiabetic; neuroprotective; cerebroprotective;

KW ophthalmological; insulin; receptor; gene therapy; diabetes;

KW insulin-like growth factor-1; IGF-1; tumour; prostate; breast;

KW diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy.

XX Synthetic.

OS

PN WO200172771-A2.

XX 04-OCT-2001.

XX 29-MAR-2000; 2000WO-US008528.

XX 29-MAR-2000; 2000WO-US008528.

XX (DGIB-) DGI BIOTECHNOLOGIES LLC.

PA (NOVO ) NOVO NORDISK AS.

XX Beasley J, Blume AJ, Schaeffer L, Pillutia R, Brandt J;

PI Brissette R, Spetzler J, Cheng W, Ostergaard S, Mandecki WS;

XX Hansen PH, Ravera M, Hsiao K;

DR WPI; 2002-025774/03.

PT Modulating insulin activity in mammalian cells, for treating e.g.  
 PT diabetes and tumors, comprises using peptides that bind to insulin or  
 PT insulin-like growth factor receptors.

XX Disclosure; Fig 8-3; 390pp; English.

CC The invention relates to a method of modulating insulin activity in  
 CC mammalian cells by administering a peptide that binds the insulin  
 CC receptor (IR). A composition containing a peptide, optionally expressed  
 CC from gene therapy vectors, that binds to Site 1 of IR and an insulin  
 CC agonist are useful for treating diabetes. Also, peptides that are  
 CC antagonists of the insulin-like growth factor-1 (IGF-1) receptor are  
 CC useful for treating insulin-like growth factor-1 (IGF-1) receptor  
 CC (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1  
 CC receptor agonists are useful for treating neurological diseases,  
 CC including stroke and diabetic neuropathy. The peptides are also useful in  
 CC screening for compounds that bind to IR or IGF-1 receptor, potential  
 CC therapeutics and research reagents. AAU8034-AAU90957 represent IR and/or  
 CC IGF-1 receptor-binding peptides and related amino acid sequences of the  
 CC invention

XX Sequence 20 AA;

Query Match 62.5%; Score 45; DB 5; Length 20;  
 Best Local Similarity 60.0%; Pred. No. 20;  
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CGVWLTWGC 10  
 Db 8 CGAWPTWNC 17

RESULT 10

AAU59880

ID AAU59880 standard; protein; 129 AA.

XX AAU59880;

XX 19-JAN-2000 (first entry)

XX Human normal uterus tissue derived protein 43.

XX Human; uterus; cancer; treatment; anticancer; cytostatic; gene therapy;  
 KW EST; expressed sequence tag.

XX Homo sapiens.

XX DE19817946-A1.

XX 21-OCT-1999.

XX 17-APR-1998; 98DE-01017946.

XX 17-APR-1998; 98DE-01017946.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

```

XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilareky C, Dahl B;
PI WPI; 1999-591956/51.
XX N-PSDB; AAZ41339.
XX
XX New nucleic acid sequences expressed in normal uterine tissues, and
PT derived polypeptides, for treatment of uterine cancer and identification
PT of therapeutic agents.
XX
XX Claim 23; Page 138; 154pp; German.
XX
XX This invention describes novel cDNA sequences (A) highly expressed in
CC normal uterine tissue which can have anticancer and cytostatic activity
CC and can be used for gene therapy. (A) are used (i) for recombinant
CC expression of polypeptides (B) and (ii) to isolate complete genes. (B)
CC are used (i) to identify agents suitable for treatment of uterine cancer;
CC (ii) directly for treating this form of cancer (including expression from
CC gene therapy vectors) and (iii) for generation of specific antibodies.
CC (A) are identified by assembling ESTs (expressed sequence tags) from a
CC particular tissue type before comparison of expression patterns. This
CC allows a significantly longer fragment of the gene to be revealed, so
CC should reduce the number of failures associated with the fact that ESTs
CC from different libraries may represent different parts of the same
CC unknown gene, distorting the estimated frequency of occurrence in a
CC particular tissue. AAY59838-Y59892 represent protein fragments encoded by
CC the human uterine tissue derived cDNA fragments represented in AAZ41325-
CC Z41385
XX
XX Sequence 129 AA;
SQ
Query Match 62.5%; Score 45; DB 2; Length 129;
Best Local Similarity 62.5%; Pred. No. 96;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CGYWLTIW 8
Db 32 CSHWLTW 39
| : ||| : |
| : ||| : |

RESULT 11
ABU49938
ID ABU49938 standard; protein; 828 AA.
XX
XX AC ABU49938;
XX
XX 19-JUN-2003 (first entry)
XX
XX Protein encoded by Prokaryotic essential gene #35465.
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
XX Yersinia pestis.
XX
XX WO200277183-A2.
XX
XX 03-OCT-2002.
XX
XX 21-MAR-2002; 2002WO-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
XX
XX 06-SEP-2001; 2001US-00948993.
XX
XX 25-OCT-2001; 2001US-0342923P.
XX
XX 08-FEB-2002; 2002US-00072851.
XX
XX 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI; 2003-029926/02.
XX
XX N-PSDB; ACA53808.
XX
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 77862; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 828 AA;
SQ
Query Match 62.5%; Score 45; DB 6; Length 828;
Best Local Similarity 58.3%; Pred. No. 4.6e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
Qy 1 CGYWLTI--WGC 10
Db 372 CGLWLELLSGWC 383
| : ||| : |
| : ||| : |

RESULT 12
ABB04861
ID ABB04861 standard; protein; 1024 AA.
XX
XX AC ABB04861;
XX
XX 13-MAR-2002 (first entry)
XX
XX LDL receptor binding protein Na channel brain 3 SEQ ID NO:84.
XX
XX Low density lipoprotein receptor binding protein; signal transduction;
XX LDL receptor binding protein; LDL receptor signalling pathway.
XX
XX Synthetic.
XX
XX WO200184159-A2.
XX
XX 08-NOV-2001.
XX
XX 24-APR-2001; 2001WO-US013214.
XX
XX 01-MAY-2000; 2000US-00562737.
XX
XX

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PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Herz J, Gotthardt M;  
XX  
DR WPI; 2002-082855/11.  
XX  
PT Detecting stress that alters interaction of LDL receptor binding  
PT polypeptide with LDL receptor interaction domain, comprises detecting  
PT difference in stress-biased and unbiased interaction of peptide and  
PT domain in a system.  
XX  
PS Disclosure; Page 148-150; 200pp; English.  
XX  
CC The present invention describes a method for detecting a stress that  
CC alters a functional interaction of a low density lipoprotein (LDL)  
CC receptor binding protein (I) with an LDL receptor interaction domain  
CC (II). The method involves introducing a predetermined stress into a  
CC system which provides a stress-biased physical interaction of (I) with  
CC (II), where in the absence of the stress, the system provides an unbiased  
CC interaction of (I) and (II), and detecting the stress-biased interaction  
CC of (I) and (II), where a difference between BI and UI indicates that the  
CC stress alters the interaction of (I) and (II). (I) is selected from  
CC SEMCAP-1, JIP-1, PSD-95, JIP-2, Talin, OMP25, CAPON, PIP4, 5 Kinase, Na  
CC channel brain 3, Min1, ICAP-1 and APC subunit 10. The method is useful  
CC for detecting a stress that alters functional interaction of LDL receptor  
CC binding polypeptide with LDL receptor interaction domain. The method is  
CC useful for detecting and modulating signal transduction through LDL  
CC receptors. AB04778 to AB04909 represent LDL receptor binding proteins  
CC which are used in the exemplification of the present invention  
XX  
SQ Sequence 1024 AA;  
  
Query Match 61.8%; Score 44.5; DB 5; Length 1024;  
Best Local Similarity 54.5%; Pred. No. 6.5e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;  
  
QY 1 CGWYL-TWGC 10  
||:|:|:|:  
Db 892 CGHWIETMWC 902  
  
RESULT 13  
ID ADP29850 standard; protein; 149 AA.  
XX  
AC ADP29850;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human secreted protein SEQ ID #617.  
XX  
KW Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;  
KW cancer; inflammatory; immune; human secreted protein.  
XX  
OS Homo sapiens.  
XX  
PN WO2004035732-A2.  
XX  
PD 29-APR-2004.  
XX  
PF 28-AUG-2003; 2003WO-US026780.  
XX  
PR 29-AUG-2002; 2002US-0406576P.  
PR 29-AUG-2002; 2002US-0406579P.  
PR 29-AUG-2002; 2002US-0406585P.  
PR 29-AUG-2002; 2002US-0406588P.  
PR 29-AUG-2002; 2002US-0406608P.  
PR 29-AUG-2002; 2002US-0406611P.  
PR 29-AUG-2002; 2002US-0406612P.  
PR 29-AUG-2002; 2002US-0406616P.  
PR 29-AUG-2002; 2002US-0406640P.  
PR 29-AUG-2002; 2002US-0406642P.  
PR 29-AUG-2002; 2002US-0406646P.  
  
29-AUG-2002; 2002US-0406653P.  
29-AUG-2002; 2002US-0406655P.  
29-AUG-2002; 2002US-0406666P.  
17-SEP-2002; 2002US-0410946P.  
17-SEP-2002; 2002US-0410947P.  
17-SEP-2002; 2002US-0410948P.  
17-SEP-2002; 2002US-0410949P.  
17-SEP-2002; 2002US-0410953P.  
17-SEP-2002; 2002US-0410957P.  
17-SEP-2002; 2002US-0410958P.  
17-SEP-2002; 2002US-0410959P.  
17-SEP-2002; 2002US-0410960P.  
17-SEP-2002; 2002US-0410961P.  
17-SEP-2002; 2002US-0410962P.  
17-SEP-2002; 2002US-0411019P.  
17-SEP-2002; 2002US-0411022P.  
17-SEP-2002; 2002US-0411023P.  
17-SEP-2002; 2002US-0411024P.  
17-SEP-2002; 2002US-0411032P.  
17-SEP-2002; 2002US-0411035P.  
17-SEP-2002; 2002US-0411037P.  
17-SEP-2002; 2002US-0411041P.  
17-SEP-2002; 2002US-0411045P.  
17-SEP-2002; 2002US-0411048P.  
17-SEP-2002; 2002US-0411052P.  
17-SEP-2002; 2002US-0411055P.  
17-SEP-2002; 2002US-0411073P.  
17-SEP-2002; 2002US-0411082P.  
17-SEP-2002; 2002US-0411101P.  
17-SEP-2002; 2002US-0411111P.  
18-APR-2003; 2003US-0463700P.  
18-APR-2003; 2003US-0463708P.  
18-APR-2003; 2003US-0463716P.  
18-APR-2003; 2003US-0463732P.  
02-MAY-2003; 2003US-0467199P.  
02-MAY-2003; 2003US-0467201P.  
02-MAY-2003; 2003US-0467203P.  
02-MAY-2003; 2003US-0467230P.  
19-MAY-2003; 2003US-0471306P.  
22-MAY-2003; 2003US-0471336P.  
22-MAY-2003; 2003US-0472420P.  
22-MAY-2003; 2003US-0472430P.  
09-JUN-2003; 2003US-0476609P.  
08-JUL-2003; 2003US-0485218P.  
08-JUL-2003; 2003US-0485223P.  
08-JUL-2003; 2003US-0485224P.  
08-JUL-2003; 2003US-0485325P.  
14-JUL-2003; 2003US-0486446P.  
15-JUL-2003; 2003US-0486480P.  
15-JUL-2003; 2003US-0486891P.  
08-AUG-2003; 2003US-0486960P.  
08-AUG-2003; 2003US-0493341P.  
08-AUG-2003; 2003US-0493370P.  
08-AUG-2003; 2003US-0493573P.  
08-AUG-2003; 2003US-0493577P.  
  
(FIVE-) FIVE PRIME THERAPEUTICS INC.  
PA  
XX  
XX Williams LT, Chu K, Lee B, Hestir K, Beaurang PA, Behrens D;  
PI Halenbeck RF, Huang MM, Kothakota S, Linnemann T;  
PI Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;  
XX  
XX WPI; 2004-348438/32.  
DR  
XX  
XX New nucleic acid molecule for diagnosing, preventing or treating diseases  
PT such as proliferative (e.g. cancer), inflammatory, immune, metabolic,  
PT genetic, bacterial and viral diseases.  
XX  
PS Claim 1; SEQ ID NO 1848; 428pp; English.  
XX  
CC The present invention relates to an isolated nucleic acid molecule

CC encoding a polypeptide which is believed to be cytostatic,  
 CC anti-inflammatory, immunosuppressive, antibacterial and virucidal. The  
 CC composition and methods are useful for diagnosing, preventing and  
 CC treating diseases such as proliferative (e.g. cancer), inflammatory,  
 CC immune, metabolic, genetic, bacterial and viral diseases. The present  
 CC sequence represents a human secreted protein. The present sequence is  
 CC available on WIPWEB and is not in the specification.  
 XX  
 SQ Sequence 149 AA;

Query Match 61.1%; Score 44; DB 8; Length 149;  
 Best Local Similarity 62.5%; Pred. No. 1.5e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGYWLTIW 8  
 Db 95 CHFWLTVW 102  
 | : ||| : |

RESULT 14  
 AAEE31487  
 ID AAE31487 standard; protein; 166 AA.  
 XX AC AAE31487;  
 XX AC  
 XX DT 24-FEB-2003 (first entry)  
 XX DE Human butyrophilin 2/3 protein.  
 XX KW Human; B7-H1.2 protein; Butyrophilin 2/3 protein; transplant rejection;  
 KW immunological condition; graft-versus-host disease; allergy; asthma;  
 KW inflammatory bowel disease; sepsis; Alzheimer's disease; atherosclerosis;  
 KW T-cell mediated inflammation; autoimmune disease; multiple sclerosis;  
 KW systemic lupus erythematosus; autoimmune demyelination; Grave's disease;  
 KW psoriasis; autoimmune diabetes; diabetic neuropathy; HIV infection;  
 KW rheumatoid arthritis; human immunodeficiency virus; immunosuppressive;  
 KW gene therapy; infection; virucide.  
 XX KW  
 OS Homo sapiens.  
 XX PN WO200279474-A2.  
 XX PD 10-OCT-2002.  
 XX PF 08-JAN-2002; 2002WO-US000590.  
 XX PR 08-JAN-2001; 2001US-0260617P.  
 PR 19-JAN-2001; 2001US-0262737P.  
 PR 07-JAN-2002; 2002US-00260617.  
 XX PA (IMMV ) IMMUNEX CORP.  
 XX PI Baum PR, Dubose RF, Wiley SR;  
 XX WPI; 2003-046816/04.  
 XX DR New B7-H1.2 or Butyrophilin 2/3 polypeptide of the human B7 polypeptide  
 PT family, useful for treating an immunological condition e.g. transplant  
 PT rejection.  
 XX PS Example 1; Page 64-65; 99pp; English.  
 XX CC The invention relates to B7-H1.2 or Butyrophilin 2/3 polypeptides of  
 CC human B7 polypeptide family and polynucleotides encoding such proteins.  
 CC Sequences of the invention are useful for treating an immunological  
 CC conditions (e.g., transplant rejection, graft-versus-host disease,  
 CC allergy, asthma, inflammatory bowel disease, sepsis), diseases that are  
 CC caused or exacerbated by T-cell mediated inflammation (e.g., Alzheimer's  
 CC disease or atherosclerosis), autoimmune diseases (e.g., systemic lupus  
 CC erythematosus, autoimmune demyelination, Grave's disease, psoriasis,  
 CC multiple sclerosis, autoimmune diabetes, diabetic neuropathy, rheumatoid  
 CC arthritis), bacterial or viral infections such as human immunodeficiency  
 CC virus (HIV) infection, delayed reconstitution of T-cells, defects in T-

CC cell or accessory cell function or congenital immunodeficiencies. They  
 CC are also used in gene therapy. The present sequence is human butyrophilin  
 CC consensus protein  
 XX Sequence 166 AA;  
 SQ

Query Match 61.1%; Score 44; DB 6; Length 166;  
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YMLTIWGC 10  
 Db 127 YMEVWGC 134  
 || : |||

RESULT 15  
 AAU91293  
 ID AAU91293 standard; protein; 415 AA.  
 XX AC AAU91293;  
 XX DT 18-JUN-2002 (first entry)  
 XX DE Human NOV8 protein.  
 XX KW Human; NOVX; gene therapy; cardiomyopathy; atherosclerosis; diabetes;  
 KW cell signal processing; metabolic pathway modulation; inflammation;  
 KW autoimmune disorder; scleroderma; transplantation; allergy;  
 KW systemic lupus erythematosus; haemophilia; Alzheimer's disease;  
 KW graft versus host disease; Lesch-Nyhan syndrome; periodontitis;  
 KW pancreatitis; musculoskeletal disorder; Parkinson's disease;  
 KW Huntington's disease; behavioural disorder; pain; obesity; wound healing;  
 KW neurodegenerative disorder; neuropsychiatric disorder; hypertension;  
 KW growth disorder; reproductive disorder; lung disease.  
 XX KW  
 OS Homo sapiens.  
 XX PN WO200216600-A2.  
 XX PD 28-FEB-2002.  
 XX PF 27-AUG-2001; 2001WO-US026518.  
 XX PR 25-AUG-2000; 2000US-0227800P.  
 PR 25-AUG-2000; 2000US-0228205P.  
 PR 25-AUG-2000; 2000US-0228324P.  
 PR 30-AUG-2000; 2000US-0228997P.  
 PR 30-AUG-2000; 2000US-0229185P.  
 PR 01-SEP-2000; 2000US-0229780P.  
 PR 01-SEP-2000; 2000US-0229848P.  
 PR 01-SEP-2000; 2000US-0229850P.  
 PR 22-JAN-2001; 2001US-0263377P.  
 PR 31-JAN-2001; 2001US-0265518P.  
 PR 15-MAR-2001; 2001US-0276451P.  
 PR 27-MAR-2001; 2001US-0279196P.  
 PR 24-AUG-2001; 2001US-00939398.  
 XX PA (CURA-) CURAGEN CORP.  
 XX PI Gerlach V, Macdougall JR, Smithson G, Stone DJ, Ellerman K;  
 PI Spytek KA, Zerkusen BD, Rastelli L, Verney CAM, Patturajan M;  
 PI Tchernev VT, Padigaru M, Taupier RJ;  
 XX WPI; 2002-292064/33.  
 DR N-PSDB; ABK55577.  
 XX PT New isolated cytoplasmic, nuclear, membrane bound and secreted  
 PT polypeptides, termed NOVX, useful for treating inflammation, autoimmune  
 PT disorders, haemophilia, Lesch-Nyhan syndrome, pancreatitis,  
 PT musculoskeletal disorders.  
 XX Claim 1; Page 108; 245pp; English.  
 XX

CC The invention relates to an isolated cytoplasmic, nuclear, membrane bound  
 CC or secreted polypeptide, designated NOVX (actually NOV1, 2a, 2b, 3a, 3b,  
 CC 4, 5a, 5b, 5c, 5d, 5e, 5f, 5g, 5h, 5i, 6, 7 and 8), a variant of NOVX, a  
 CC mature form, or a variant of the mature form of NOVX. Also included are a  
 CC polynucleotide encoding NOVX (or its complement), a vector comprising the  
 CC polynucleotide, a cell comprising the vector, an anti-NOVX antibody,  
 CC determining the presence of NOVX in a sample using the antibody,  
 CC determining the presence of NOVX polynucleotide in a sample using a probe  
 CC which binds to NOVX polynucleotide, identifying an agent which binds to  
 CC NOVX (including modulators of NOVX). NOVX, the polynucleotide and the  
 CC antibody are useful for diagnosing, treating or preventing a NOVX-  
 CC associated disorder selected from cardiomyopathy, atherosclerosis,  
 CC diabetes, a disorder related to cell signal processing and metabolic  
 CC pathway modulation, inflammation, autoimmune disorders, scleroderma,  
 CC transplantation, allergies, systemic lupus erythematosus, haemophilia,  
 CC graft versus host disease, Alzheimer's disease, stroke, Lesch-Nyhan  
 CC syndrome, periodontitis, pancreatitis, musculoskeletal disorders, pain,  
 CC Parkinson's disease, Huntington's disease, behavioural disorders, pain,  
 CC neurodegenerative and neuropsychiatric disorders, hypertension, wound  
 CC healing, obesity, growth and reproductive disorders, lung diseases and  
 CC many other diseases and disorders listed in the specification. NOVX, the  
 CC polynucleotide and the antibody are useful in screening assays, detection  
 CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),  
 CC predictive medicine (e.g., diagnostic assays, prognostic assays,  
 CC monitoring clinical trials and pharmacogenomic), and in methods of  
 CC treatment (e.g., therapeutic and prophylactic). NOVX is useful as  
 CC immunogen to produce antibodies immunospecific for NOVX, as vaccines to  
 CC screen for potential agonist and antagonist compounds, and as bait  
 CC protein in a two-hybrid or three-hybrid assay. The polynucleotide is  
 CC useful in gene therapy, to express NOVX, to detect NOVX mRNA or a genetic  
 CC lesion in a NOVX gene, and to modulate NOVX activity. The vector is  
 CC useful for producing non-human transgenic animals. The antibody is useful  
 CC for isolating, and purifying NOVX and to monitor protein levels in tissue  
 CC as part of a clinical testing procedure. The present sequence represents  
 CC a NOVX protein

XX  
 SQ Sequence 415 AA;

Query Match 61.1%; Score 44; DB 5; Length 415;  
 Best Local Similarity 62.5%; Pred. No. 3.5e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGYWLTIW 8

Db 95 CHEWLTVW 102

Search completed: December 30, 2004, 13:07:53  
 Job time : 72.6226 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:59:07 ; Search time 23.0189 Seconds  
(without alignments)  
28.810 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
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2: /cgn2.6/prodata/1/iaa/5B COMB.pep.\*  
3: /cgn2.6/prodata/1/iaa/6A COMB.pep.\*  
4: /cgn2.6/prodata/1/iaa/6B COMB.pep.\*  
5: /cgn2.6/prodata/1/iaa/PCTUS COMB.pep.\*  
6: /cgn2.6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44.5	61.8	1024	4	US-09-562-737-84
2	43	59.7	492	4	US-09-107-532A-6945
3	42.5	59.0	1024	4	US-09-562-737-86
4	42.5	59.0	1765	4	US-09-354-147C-2
5	42.5	59.0	1765	4	US-09-354-147C-3
6	42	58.3	161	4	US-09-325-932A-187
7	42	58.3	273	4	US-09-270-767-46926
8	42	58.3	1498	4	US-09-792-616-9
9	42	58.3	1503	4	US-09-792-616-3
10	41	56.9	222	4	US-09-071-035-408
11	41	56.9	229	4	US-09-134-000C-3630
12	41	56.9	264	4	US-09-540-236-2978
13	41	56.9	266	4	US-09-071-035-406
14	40.5	56.2	1024	4	US-09-562-737-81
15	40.5	56.2	1024	4	US-09-562-737-87
16	40.5	56.2	1835	3	US-08-836-325-15
17	40.5	56.2	1835	4	US-09-457-571-15
18	40.5	56.2	1836	4	US-10-162-012-24
19	40.5	56.2	1869	3	US-08-836-325-16
20	40.5	56.2	1969	4	US-09-457-571-16
21	40.5	56.2	1976	3	US-09-024-020B-9
22	40.5	56.2	1976	3	US-09-425-043-9
23	40.5	56.2	1977	4	US-09-976-594-757
24	40.5	56.2	1977	4	US-09-919-039-367
25	40.5	56.2	1978	3	US-09-024-020B-3
26	40.5	56.2	1978	3	US-09-425-043-3
27	40.5	56.2	1984	3	US-08-836-325-10

28	40.5	56.2	1984	4	US-09-457-571-10	Sequence 10, Appl
29	40.5	56.2	1988	3	US-09-024-020B-4	Sequence 4, Appl
30	40.5	56.2	1988	3	US-09-425-043-4	Sequence 4, Appl
31	40.5	56.2	1989	3	US-08-836-325-11	Sequence 11, Appl
32	40.5	56.2	1989	3	US-08-836-325-12	Sequence 12, Appl
33	40.5	56.2	1989	4	US-09-457-571-11	Sequence 11, Appl
34	40.5	56.2	1989	4	US-09-457-571-12	Sequence 12, Appl
35	40.5	56.2	2005	3	US-08-836-325-7	Sequence 7, Appl
36	40.5	56.2	2005	4	US-09-457-571-7	Sequence 7, Appl
37	40.5	56.2	2016	3	US-09-634-920-4	Sequence 4, Appl
38	40.5	56.2	2016	4	US-09-514-907A-2	Sequence 2, Appl
39	40.5	56.2	2016	4	US-09-896-994-2	Sequence 2, Appl
40	40.5	56.2	2016	4	US-09-840-125-4	Sequence 4, Appl
41	40	55.6	362	1	US-08-415-751-6	Sequence 6, Appl
42	40	55.6	668	4	US-09-248-796A-19350	Sequence 19350, A
43	39.5	54.9	73	4	US-09-513-999C-4541	Sequence 4541, Ap
44	39	54.2	430	4	US-09-443-041A-18	Sequence 18, Appl
45	39	54.2	450	4	US-09-443-041A-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1  
US-09-562-737-84  
; Sequence 84, Application US/09562737  
; Patent No. 6428967  
; GENERAL INFORMATION:  
; APPLICANT: Herz, Joachim  
; APPLICANT: Gotthardt, Michael  
; TITLE OF INVENTION: LDL Receptor Signaling Pathways  
; FILE REFERENCE: UTSW0708  
; CURRENT APPLICATION NUMBER: US/09/562,737  
; CURRENT FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 84  
; TYPE: PRT  
; LENGTH: 1024  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Sequence  
US-09-562-737-84

Query Match 61.8%; Score 44.5; DB 4; Length 1024;  
Best Local Similarity 54.5%; Pred No. 1.6e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;  
  
QY 1 CGYWL-TIWGC 10  
|||:|:|  
Db 892 CGHWIETWDC 902  
  
RESULT 2  
US-09-107-532A-6945  
; Sequence 6945, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD/ROM ISO9660  
; COMPUTER: PC

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/ OPERATING SYSTEM: <Unknown>
/ SOFTWARE: ASCII
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/107.532A
/ FILING DATE: 30-Jun-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/085,598
/ FILING DATE: 14 May 1998
/ APPLICATION NUMBER: 60/051571
/ FILING DATE: July 2, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Ariniello, Pamela Deneke
/ REGISTRATION NUMBER: 40,489
/ REFERENCE/DOCKET NUMBER: GTC-012
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (781)893-5007
/ TELEFAX: (781)893-8277
/ INFORMATION FOR SEQ ID NO: 6945:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 492 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: YES
/ ORIGINAL SOURCE:
/ ORGANISM: Enterococcus faecium
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (B) LOCATION 1...492
/ SEQUENCE DESCRIPTION: SEQ ID NO: 6945:
US-09-107-532A-6945

Query Match 59.7%; Score 43; DB 4; Length 492;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GYMLTIW 8
Db 112 GYMLTCW 118

RESULT 3
US-09-562-737-86
/ Sequence 86, Application US/09562737
/ Patent No. 6428967
/ GENERAL INFORMATION:
/ APPLICANT: Herz, Joachim
/ TITLE OF INVENTION: LDL Receptor Signaling Pathways
/ FILE REFERENCE: UTSW0708
/ CURRENT APPLICATION NUMBER: US/09/562,737
/ CURRENT FILING DATE: 2000-05-01
/ NUMBER OF SEQ ID NOS: 132
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 86
/ LENGTH: 1024
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-562-737-86

Query Match 59.0%; Score 42.5; DB 4; Length 1024;
Best Local Similarity 63.6%; Pred. No. 3.1e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10
Db 892 CGEWLEITWDC 902

RESULT 4
US-09-354-147C-2
/ Sequence 2, Application US/09354147C
/ Patent No. 6573067
/ GENERAL INFORMATION:
/ APPLICANT: Dib-Hajj, Sulayman
/ TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
/ FILE REFERENCE: 44574-5004-01-US
/ CURRENT APPLICATION NUMBER: US/09/354,147C
/ CURRENT FILING DATE: 1999-07-16
/ PRIOR APPLICATION NUMBER: US 60/072,990
/ PRIOR FILING DATE: 1998-01-29
/ PRIOR APPLICATION NUMBER: US 60/109,402
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: PCT/US99/02008
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 1765
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (652)...(1334)
/ OTHER INFORMATION: Xaa at position 652 is Leu; Xaa at position 1334 is Asn
/ OTHER INFORMATION: or Lys. Xaa's result from n's in SEQ ID NO: 1.
US-09-354-147C-2

Query Match 59.0%; Score 42.5; DB 4; Length 1765;
Best Local Similarity 54.5%; Pred. No. 5.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10
Db 754 CGEWIENMGC 764

RESULT 5
US-09-354-147C-3
/ Sequence 3, Application US/09354147C
/ Patent No. 6573067
/ GENERAL INFORMATION:
/ APPLICANT: Dib-Hajj, Sulayman
/ TITLE OF INVENTION: Modulation of Sodium Channels in Dorsal Root Ganglia
/ FILE REFERENCE: 44574-5004-01-US
/ CURRENT APPLICATION NUMBER: US/09/354,147C
/ CURRENT FILING DATE: 1999-07-16
/ PRIOR APPLICATION NUMBER: US 60/072,990
/ PRIOR FILING DATE: 1998-01-29
/ PRIOR APPLICATION NUMBER: US 60/109,402
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: PCT/US99/02008
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 1765
/ TYPE: PRT
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ OTHER INFORMATION: putative amino acid seq. of rat NaN
US-09-354-147C-3

Query Match 59.0%; Score 42.5; DB 4; Length 1765;
Best Local Similarity 54.5%; Pred. No. 5.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 CGYWL-TIWGC 10
Db 754 CGEWIENMGC 764
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RESULT 6
US-09-325-932A-187
; Sequence 187, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 187
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-325-932A-187
Query Match      58.3%; Score 42; DB 4; Length 161;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 GYWLTIWC 10
      |||| : ||
Db      100 GYWLNSGC 108

RESULT 7
US-09-270-767-46926
; Sequence 46926, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46926
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-46926
Query Match      58.3%; Score 42; DB 4; Length 273;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGYWLTIW 8
      |||| : ||
Db      266 CGYWATIF 273

RESULT 8
US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498

; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9
Query Match      58.3%; Score 42; DB 4; Length 1498;
Best Local Similarity 71.4%; Pred. No. 5.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
      |||| : ||
Db      960 GYWLSLW 966

RESULT 9
US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; APPLICANT: University of Hawaii
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; TITLE OF INVENTION: Pseudoxanthoma Elasticum
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-616-3
Query Match      58.3%; Score 42; DB 4; Length 1503;
Best Local Similarity 71.4%; Pred. No. 5.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 GYWLTIW 8
      |||| : ||
Db      965 GYWLSLW 971

RESULT 10
US-09-071-035-408
; Sequence 408, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gil H. Choi
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 408:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 222 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-071-035-408

Query Match 56.9%; Score 41; DB 4; Length 222;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
| | | | |  
DB 179 GTWITLWG 186

RESULT 11  
US-09-134-000C-3630  
Sequence 3630, Application US/09134000C  
Patent No. 6617156  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
FILE REFERENCE: 032796-032  
CURRENT APPLICATION NUMBER: US/09/134,000C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/055,778  
PRIOR FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3630  
LENGTH: 229  
TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-3630

Query Match 56.9%; Score 41; DB 4; Length 229;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
| | | | |  
DB 203 GTWITLWG 210

RESULT 12  
US-09-540-236-2978  
Sequence 2978, Application US/09540236  
Patent No. 6673910  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR  
FILE REFERENCE: 2709.2005-001  
CURRENT APPLICATION NUMBER: US/09/540,236  
CURRENT FILING DATE: 2000-04-04  
NUMBER OF SEQ ID NOS: 3840  
SEQ ID NO 2978  
LENGTH: 264  
TYPE: PRT  
ORGANISM: M.catarrhalis  
US-09-540-236-2978

Query Match 56.9%; Score 41; DB 4; Length 264;  
Best Local Similarity 75.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIW 8  
| | | | |  
DB 200 CGAWLGIW 207

## RESULT 13

US-09-071-035-406  
Sequence 406, Application US/09071035  
Patent No. 6448043  
GENERAL INFORMATION:  
APPLICANT: Gil H. Choi  
TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
NUMBER OF SEQUENCES: 496  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071,035  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: A. Anders Brookes  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PB369P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8504  
TELEFAX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 406:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 266 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-071-035-406

Query Match 56.9%; Score 41; DB 4; Length 266;  
Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIWG 9  
| | | | |  
DB 203 GTWITLWG 210

## RESULT 14

US-09-562-737-81  
Sequence 81, Application US/09562737  
Patent No. 6428967  
GENERAL INFORMATION:  
APPLICANT: Herz, Joachim  
APPLICANT: Gotthardt, Michael  
TITLE OF INVENTION: LDL Receptor Signaling Pathways  
FILE REFERENCE: UTM0708  
CURRENT APPLICATION NUMBER: US/09/562,737  
CURRENT FILING DATE: 2000-05-01  
NUMBER OF SEQ ID NOS: 132  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 81  
LENGTH: 1024  
TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Sequence  
US-09-562-737-81

Query Match 56.2%; Score 40.5; DB 4; Length 1024;  
Best Local Similarity 54.5%; Pred. No. 5.8e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10  
|||:|:|  
Db 892 CGEWIGTMWDC 902

RESULT 15  
US-09-562-737-87  
; Sequence 87, Application US/09562737  
; Patent No. 6428967  
; GENERAL INFORMATION:  
; APPLICANT: Herz, Joachim  
; APPLICANT: Gotthardt, Michael  
; TITLE OF INVENTION: LDL Receptor Signaling Pathways  
; FILE REFERENCE: UTSW0708  
; CURRENT APPLICATION NUMBER: US/09/562,737  
; CURRENT FILING DATE: 2000-05-01  
; NUMBER OF SEQ ID NOS: 132  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 87  
; LENGTH: 1024  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Sequence  
US-09-562-737-87

Query Match 56.2%; Score 40.5; DB 4; Length 1024;  
Best Local Similarity 54.5%; Pred. No. 5.8e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10  
|||:|:|  
Db 892 CGEWIGTMWDC 902

Search completed: December 30, 2004, 13:19:20  
Job time : 24.0189 secs

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# OM protein - protein search, using sw model

Run on: December 30, 2004, 13:08:04 ; Search time 74.5283 Seconds  
(without alignments)  
48.267 Million cell updates/sec

Title: US-10-046-922-35

Perfect score: 72

Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09D\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	10	13	US-10-046-922-35
2	54	75.0	10	13	Sequence 35, Appl
3	50	69.4	10	13	Sequence 34, Appl
4	47.5	66.0	304	14	US-10-046-922-73
5	47.5	66.0	304	14	Sequence 73, Appl
6	47.5	66.0	304	14	Sequence 2288, Ap
7	47.5	66.0	304	14	Sequence 1934, Ap
8	47.5	66.0	304	14	Sequence 476, Ap
9	46	63.9	17	14	Sequence 125253,
10	46	63.9	17	14	Sequence 54, Appl
11	45	62.5	828	15	US-10-125-869A-54
12	44.5	61.8	1024	14	Sequence 278, Ap
13	44	61.1	103	16	Sequence 743, Ap
					Sequence 77862, A
					Sequence 84, Appl
					Sequence 181150,

14	44	61.1	161	16	US-10-767-701-54778	Sequence 54778, A
15	43	59.7	13	14	US-10-125-868A-73	Sequence 73, Appl
16	43	59.7	13	15	US-10-462-262-297	Sequence 297, App
17	43	59.7	291	14	US-10-369-493-19313	Sequence 19313, A
18	43	59.7	454	14	US-10-032-585-7816	Sequence 7816, Ap
19	43	59.7	459	16	US-10-437-963-160191	Sequence 160191, A
20	43	59.7	474	15	US-10-282-122A-57928	Sequence 57928, A
21	43	59.7	671	16	US-10-437-963-190740	Sequence 190740, A
22	42.5	59.0	152	11	US-09-833-245-1533	Sequence 1533, Ap
23	42.5	59.0	152	15	US-10-264-237-2457	Sequence 2457, Ap
24	42.5	59.0	159	11	US-09-833-245-1534	Sequence 1534, Ap
25	42.5	59.0	161	15	US-10-276-774-2376	Sequence 2376, Ap
26	42.5	59.0	161	15	US-10-296-115-1337	Sequence 1337, Ap
27	42.5	59.0	176	14	US-10-161-927-10	Sequence 10, Appl
28	42.5	59.0	1024	14	US-10-211-962-86	Sequence 86, Appl
29	42.5	59.0	1765	14	US-10-388-470-2	Sequence 2, Appl
30	42.5	59.0	1765	14	US-10-388-470-3	Sequence 3, Appl
31	42	58.3	90	11	US-09-864-408A-8146	Sequence 8146, Ap
32	42	58.3	161	14	US-10-219-220-187	Sequence 187, App
33	42	58.3	1498	10	US-09-792-616-9	Sequence 9, Appl
34	42	58.3	1498	16	US-10-764-328-9	Sequence 9, Appl
35	42	58.3	1503	10	US-09-792-616-3	Sequence 3, Appl
36	42	58.3	1503	16	US-10-764-328-3	Sequence 3, Appl
37	41.5	57.6	122	15	US-10-108-260A-2641	Sequence 2641, Ap
38	41.5	57.6	620	14	US-10-369-493-119	Sequence 119, App
39	41	56.9	14	14	US-10-125-869A-114	Sequence 114, App
40	41	56.9	14	15	US-10-462-262-338	Sequence 338, App
41	41	56.9	34	9	US-09-864-761-43458	Sequence 43458, A
42	41	56.9	57	15	US-10-424-599-179308	Sequence 179308,
43	41	56.9	78	17	US-10-425-115-204642	Sequence 204642,
44	41	56.9	82	15	US-10-424-599-240891	Sequence 240891,
45	41	56.9	104	17	US-10-425-115-332065	Sequence 332065,

## ALIGNMENTS

RESULT 1  
US-10-046-922-35  
; Sequence 35, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Ailitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Isolated peptide  
US-10-046-922-35

Query Match 100.0%; Score 72; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.0026;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10  
|||||  
Db 1 CGYWLTIWGC 10

RESULT 2  
US-10-046-922-34  
; Sequence 34, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Ailitalo, Kari  
; APPLICANT: Koivunen, Erkki

; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 34  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: isolated peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (10)..(10)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-34

Query Match 75.0%; Score 54; DB 13; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.72;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9  
|||||||  
Db 2 GYWLTIWG 9

RESULT 3  
US-10-046-922-73  
; Sequence 73, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Allitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 73  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: peptide library  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (5)..(7)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-73

Query Match 69.4%; Score 50; DB 13; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.5;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CGYWLTIWGC 10  
|||||  
Db 1 CGYWLTIWGC 10

RESULT 4  
US-10-017-161-2288  
; Sequence 2288, Application US/10017161  
; Publication No. US20030143668A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA

; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 084335/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: JP 2001/246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2288  
; LENGTH: 304  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (73)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (79)..(83)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (85)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (89)..(91)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (96)..(97)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (101)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (107)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (118)..(119)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (121)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (123)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (162)  
; OTHER INFORMATION: Variable amino acid  
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; NAME/KEY: MOD\_RES  
; LOCATION: (178)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (194)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (210)..(211)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (219)  
; OTHER INFORMATION: Variable amino acid

; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (256)..(289)  
; OTHER INFORMATION: Variable amino acid  
US-10-017-161-2288

Query Match 66.0%; Score 47.5; DB 14; Length 304;  
Best Local Similarity 60.0%; Pred. No. 88;  
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWLTIWGC 10  
Db 108 CGFW-AVMGC 116  
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RESULT 5  
US-10-292-798-1934  
; Sequence 1934, Application US/10292798  
; Publication No. US2003023583A1  
; GENERAL INFORMATION:  
; APPLICANT: SUMA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 084335/166  
; CURRENT APPLICATION NUMBER: US/10/292,798  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/017,161  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: JP 2001-246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2070  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1934  
; LENGTH: 304  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (73)..(73)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (80)..(83)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (89)..(91)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (96)..(97)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (101)..(101)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (107)..(107)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (118)..(119)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (121)..(121)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (123)..(123)

; OTHER INFORMATION: Variable amino acid  
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; NAME/KEY: MOD\_RES  
; LOCATION: (178)..(178)  
; OTHER INFORMATION: Variable amino acid  
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; NAME/KEY: MOD\_RES  
; LOCATION: (210)..(211)  
; OTHER INFORMATION: Variable amino acid  
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; NAME/KEY: MOD\_RES  
; LOCATION: (219)..(219)  
; OTHER INFORMATION: Variable amino acid  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: (256)..(289)  
; OTHER INFORMATION: Variable amino acid  
US-10-292-798-1934

Query Match 66.0%; Score 47.5; DB 14; Length 304;  
Best Local Similarity 60.0%; Pred. No. 88;  
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWLTIWGC 10  
Db 108 CGFW-AVMGC 116  
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RESULT 6  
US-10-280-066-476  
; Sequence 476, Application US/10280066  
; Publication No. US20030180718A1  
; GENERAL INFORMATION:  
; APPLICANT: Pillutla, Renuka C.  
; APPLICANT: Brissette, Renee  
; APPLICANT: Spruyt, Michael  
; APPLICANT: Dedova, Olga  
; APPLICANT: Blume, Arthur J.  
; APPLICANT: Prendergast, John  
; APPLICANT: Goldstein, Neil I.  
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BINDI  
; FILE REFERENCE: 2598-4009US1  
; CURRENT APPLICATION NUMBER: US/10/280,066  
; CURRENT FILING DATE: 2002-10-24  
; PRIOR APPLICATION NUMBER: 60/345,471  
; PRIOR FILING DATE: 2001-10-24  
; NUMBER OF SEQ ID NOS: 537  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 476  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: Eschericia coli  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; OTHER INFORMATION: Tiel-20C-3-D116  
US-10-280-066-476

Query Match 65.3%; Score 47; DB 14; Length 25;  
Best Local Similarity 66.7%; Pred. No. 13;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 9  
Db 5 CGYWGELWG 13  
|||:|:|

RESULT 7  
US-10-437-963-125253  
; Sequence 125253, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.

```
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 125253
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27915C.1.pep
US-10-437-963-125253

Query Match      65.3%; Score 47; DB 16; Length 63;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CGYWLTIWGC 10
      ||::|||
Db      37 CGHYLKAWGC 46

RESULT 8
US-10-125-869A-54
; Sequence 54, Application US/10125869A
; Publication No. US20030195671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Qi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ransohoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR Fc-REGION
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-54

Query Match      63.9%; Score 46; DB 14; Length 17;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CGYWLTIWGC 9
      ||::|||
Db      4 CGFWPRWIG 12

RESULT 9
US-10-462-262-278
; Sequence 278, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
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; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 278
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin binding polypeptide
US-10-462-262-278

Query Match      63.9%; Score 46; DB 15; Length 17;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CGYWLTIWGC 9
      ||::|||
Db      4 CGFWPRWIG 12

RESULT 10
US-10-112-944-743
; Sequence 743, Application US/10112944
; Publication No. US20040048249A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Weng, Gezhi
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyang
; APPLICANT: Xue, Aidong J.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrul
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: Pt_FL_genes Version 5.0
; SEQ ID NO 743
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(136)
; OTHER INFORMATION: Xaa = any amino acid or symbol as shown in the table 8 as set forth
```

OTHER INFORMATION: in Example 2  
US-10-112-944-743

Query Match 63.9%; Score 46; DB 15; Length 136;  
Best Local Similarity 60.0%; Pred. No. 73;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10  
|||:|:|  
DB 93 CGRWDLWGC 102

## RESULT 11

US-10-282-122A-77862  
; Sequence 77862, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zvekind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 77862

; LENGTH: 828

; TYPE: PRT

; ORGANISM: Yersinia pestis

US-10-282-122A-77862

Query Match 62.5%; Score 45; DB 15; Length 828;  
Best Local Similarity 58.3%; Pred. No. 4.3e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGYWLTI--WGC 10  
|||:|:|  
DB 372 CGLWLELLSWGC 383

## RESULT 12

US-10-211-962-84

; Sequence 84, Application US/10211962  
; Publication No. US20030082640A1

; GENERAL INFORMATION:

; APPLICANT: Herz, Joachim

; APPLICANT: Gotthardt, Michael

; TITLE OF INVENTION: LDL Receptor Signaling Pathways

; FILE REFERENCE: UTSW0708

; CURRENT APPLICATION NUMBER: US/10/211,962

; CURRENT FILING DATE: 2002-08-01

; PRIOR APPLICATION NUMBER: US/09/562,737

; PRIOR FILING DATE: 2000-05-01

; NUMBER OF SEQ ID NOS: 132

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 84

; LENGTH: 1024

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: Sequence

US-10-211-962-84

Query Match 61.8%; Score 44.5; DB 14; Length 1024;  
Best Local Similarity 54.5%; Pred. No. 6e+02; 3; Mismatches 1; Indels 1; Gaps 1;  
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10  
|||:|:|  
DB 892 CGHWIETWDC 902

## RESULT 13

US-10-437-963-181150

; Sequence 181150, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 181150

; LENGTH: 103

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_78451C.1.pap

US-10-437-963-181150

Query Match 61.1%; Score 44; DB 16; Length 103;  
Best Local Similarity 50.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 YWLTIWGC 10  
|||:|:|  
DB 19 WWSVWGC 26

## RESULT 14

US-10-767-701-54778

; Sequence 54778, Application US/10767701

; Publication No. US20040172684A1

; GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(53535)B  
; CURRENT APPLICATION NUMBER: US/10/767,701  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 54778  
; LENGTH: 161  
; TYPE: PRT  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 14593586.pep  
US-10-767-701-54778

Query Match 61.1%; Score 44; DB 16; Length 161;  
Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGYWLTIW 8  
Db 150 CGYWLKEP 157

RESULT 15  
US-10-125-869A-73  
; Sequence 73, Application US/10125869A  
; Publication No. US20030199671A1  
; GENERAL INFORMATION:  
; APPLICANT: Rondon, Isaac Jesus  
; APPLICANT: Wu, Qi-Long  
; APPLICANT: Ley, Arthur C.  
; APPLICANT: Stochl, Mark  
; APPLICANT: Ransohoff, Thomas C.  
; APPLICANT: Potter, M. Daniel (deceased)  
; TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION  
; TITLE OF INVENTION: POLYPEPTIDES  
; FILE REFERENCE: 3421.1006-001  
; CURRENT APPLICATION NUMBER: US/10/125,869A  
; CURRENT FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: 60/284,534  
; PRIOR FILING DATE: 2001-04-18  
; NUMBER OF SEQ ID NOS: 200  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 73  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Fc region binding polypeptide  
US-10-125-869A-73

Query Match 59.7%; Score 43; DB 14; Length 13;  
Best Local Similarity 62.5%; Pred. No. 27;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GYWLTIWG 9  
Db 1 GYWCNVWG 8

Search completed: December 30, 2004, 13:50:01  
Job time : 75.5283 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:58:17 ; Search time 11.5094 Seconds  
(without alignments)  
83.598 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGYWLTINGC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	63.9	218	2 S76385	hypothetical prote
2	45	62.5	828	2 AD0412	ATP-dependent heli
3	43.5	60.4	1923	2 T30902	sodium channel sca
4	42.5	59.0	1765	2 T42388	sodium channel alp
5	42	58.3	72	2 S30980	gene 35 protein -
6	42	58.3	441	2 C95307	probable transport
7	42	58.3	1502	2 T42216	multidrug resistan
8	41.5	57.6	620	2 F70439	oxaloacetate decar
9	41	56.9	307	2 T48166	hypothetical prote
10	41	56.9	391	2 PC4117	replication protei
11	41	56.9	419	2 E90446	permease [imported
12	41	56.9	739	2 T29407	hypothetical prote
13	40.5	56.2	200	2 T49108	sodium channel alp
14	40.5	56.2	1681	2 A55138	sodium channel mNa
15	40.5	56.2	1882	2 A45380	sodium channel pro
16	40.5	56.2	1820	1 CHBE	sodium channel alp
17	40.5	56.2	1835	2 I54323	sodium channel alp
18	40.5	56.2	1836	2 I64893	sodium channel alp
19	40.5	56.2	1836	2 J90648	sodium channel alp
20	40.5	56.2	1836	2 I51964	sodium channel alp
21	40.5	56.2	1840	1 CHRTM1	sodium channel pro
22	40.5	56.2	1951	2 S00320	sodium channel pro
23	40.5	56.2	1976	2 I56555	sodium channel pro
24	40.5	56.2	1977	2 S54771	sodium channel alp
25	40.5	56.2	1983	2 A60054	sodium channel pro
26	40.5	56.2	2005	2 A46269	sodium channel alp
27	40.5	56.2	2005	2 B25019	sodium channel pro
28	40.5	56.2	2009	2 A25019	sodium channel pro
29	40.5	56.2	2016	2 A38195	sodium channel pro

30	40.5	56.2	2019	2 A33996	sodium channel pro
31	40.5	56.2	2049	2 T43161	sodium channel pro
32	40	55.6	142	2 C34903	ig heavy chain pro
33	40	55.6	339	2 F97190	phenylalanyl-tRNA
34	40	55.6	359	2 F95406	probable ABC trans
35	40	55.6	425	2 B71038	probable Na+/H+-ex
36	40	55.6	508	2 C95282	probable ABC trans
37	40	55.6	2344	2 S64740	genome polyprotein
38	39.5	54.9	298	2 AH0289	probable aldo/keto
39	39.5	54.9	345	1 JH0185	D-amino-acid oxida
40	39.5	54.9	347	1 OXPGDA	D-amino-acid oxida
41	39.5	54.9	347	1 S01340	D-amino-acid oxida
42	39.5	54.9	347	1 JX0132	D-amino-acid oxida
43	39	54.2	376	2 AF1978	hypothetical prote
44	39	54.2	392	2 A53580	neurexin III beta
45	39	54.2	426	2 B53580	neurexin III beta

ALIGNMENTS

RESULT 1

S76385  
hypothetical protein - Synechocystis sp. (strain PCC 6803)  
C:Species: Synechocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S76385  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996  
A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S76385  
A>Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-218 <KAN>  
A:Cross-references: UNIPROT:Q55705; EMBL:D64000; GB:AB001339; NID:g1001484; PIDN:BAAL023;  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Superfamily: probable alkaline phosphatase yngC

Query Match

Best Local Similarity 63.9%; Score 46; DB 2; Length 218;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTING 9  
DB 73 CGYVWGRWG 81

RESULT 2

AD0412  
ATP-dependent helicase [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: AD0412  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchall, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001  
A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AD0412  
A>Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-828 <KUR>  
A:Cross-references: UNIPROT:Q82BL4; GB:AL590842; PIDN:CAC92624.1; PID:g15981320; GSPDB:G C:Superfamily: ATP-dependent RNA helicase, HrpB type

Query Match

Score 62.5%; DB 2; Length 828;

Best Local Similarity 58.3%; Pred. No. 36;  
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGYWLTI--WGC 10  
||| : |||  
Db 372 CGLWLELLSWGC 383

RESULT 3  
T30902  
sodium channel SCAP1 alpha chain - California sea hare  
C;Species: Aplysia californica (California sea hare)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T30902  
R;Dyer, J.R.; Johnston, W.L.; Castellucci, V.F.; Dunn, R.J.  
DNA Cell Biol. 16, 347-356, 1997  
A;Title: Cloning and tissue distribution of the Aplysia Na+ channel alpha-subunit cDNA.  
A;Reference number: Z20929; MUID: 97238630; PMID: 9115644  
A;Accession: T30902  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1993 <DYE>  
A;Cross-references: UNIPROT:P90670; EMBL:U66915; NID:gl842249; PIDN:AAC474  
C;Superfamily: sodium channel protein

Query Match 60.4%; Score 43.5; DB 2; Length 1993;  
Best Local Similarity 54.5%; Pred. No. 1.3e+02;  
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10  
||| : |||  
Db 942 CGEWIESMWGC 952

RESULT 4  
T42388  
sodium channel alpha chain - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T42388  
R;Dib-Hajj, S.D.; Tyrell, L.; Black, J.A.; Waxman, S.G.  
Proc. Natl. Acad. Sci. U.S.A. 95, 8963-8968, 1998  
A;Title: NaV, a novel voltage-gated Na channel, is expressed preferentially in peripheral  
A;Reference number: Z22149; MUID: 98338024; PMID: 9671787  
A;Accession: T42388  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1765 <DIB>  
A;Cross-references: UNIPROT:O88457; EMBL:AF059030; NID:g3372614; PID:g3372615; PIDN:AAC4  
A;Experimental source: strain Sprague-Dawley; dorsal root ganglia  
A;Note: preferentially expressed in sensory neurons within dorsal root ganglia and trigem  
C;Superfamily: sodium channel protein

Query Match 59.0%; Score 42.5; DB 2; Length 1765;  
Best Local Similarity 54.5%; Pred. No. 1.6e+02;  
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10  
||| : |||  
Db 754 CGEWIENMWGC 764

RESULT 5  
S30980  
gene 35 protein - Mycobacterium phage L5  
C;Species: Mycobacterium phage L5  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C;Accession: S30980  
R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.  
Mol. Microbiol. 7, 407-417, 1993  
A;Title: Superinfection immunity of mycobacteriophage L5: applications for genetic trans  
A;Reference number: S30949; MUID: 93211283; PMID: 8459767  
A;Accession: S30980

A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-72 <DON>  
A;Cross-references: UNIPROT:Q05245; EMBL:Z18946; NID:gl5859; PIDN:CMA79411.1; PID:gl5891  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992  
C;Genetics:  
A;Gene: 35

Query Match 58.3%; Score 42; DB 2; Length 72;  
Best Local Similarity 62.5%; Pred. No. 12;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIW 8  
||| : |||  
Db 50 CGWMLPW 57

RESULT 6  
C95307  
probable transport protein SMA0684 [imported] - Sinorhizobium meliloti (strain 1021) mag  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: C95307  
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bower  
.; Kallman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.  
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001  
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti  
A;Reference number: A93262; MUID: 21396509; PMID: 11481432  
A;Accession: C95307  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-441 <KUR>  
A;Cross-references: UNIPROT:Q92ZT6; GB:AE006469; PIDN:AAK65021.1; PID:gl4523451; GSPDB:GN  
A;Experimental source: strain 1021, megaplasmid pSymA  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-Hubler  
peia, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A;Authors: Kahn, D.; Kahn, M.L.; Kallman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure  
heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A;Reference number: A96039; MUID: 21368234; PMID: 11474104  
A;Contents: annotation  
C;Genetics:  
A;Gene: SMA0684  
A;Genome: plasmid  
C;Superfamily: L-lysine transport protein

Query Match 58.3%; Score 42; DB 2; Length 441;  
Best Local Similarity 71.4%; Pred. No. 58;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
||| : |||  
Db 92 GYWISW 98

RESULT 7  
T42216  
multidrug resistance-associated protein homolog MLP-1 - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T42216  
R;Hirohashi, T.; Suzuki, H.; Ito, K.; Ogawa, K.; Kume, K.; Shimizu, T.; Sugiyama, Y.  
Mol. Pharmacol. 53, 1068-1075, 1998  
A;Title: Hepatic expression of multidrug resistance-associated protein-like proteins main  
A;Reference number: Z22081; MUID: 98279136; PMID: 9614210  
A;Accession: T42216  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-1502 <HIR>  
A;Cross-references: UNIPROT:O88269; EMBL:AB010466; NID:g3242457; PIDN:BAA28954.1; PID:g3  
A;Experimental source: strain Sprague-Dawley; liver

C:Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

Query Match 58.3%; Score 42; DB 2; Length 1502;  
Best Local Similarity 71.4%; Pred. No. 1.7e+02;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GYWLTIW 8  
DB 964 GYWLTLW 970

RESULT 8  
F70439  
oxaloacetate decarboxylase alpha chain - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
C:Accession: F70439  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; MUID:98196566; PMID:9537320  
A:Accession: F70439  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-620 <AQF>  
A:Cross-references: UNIPROT:O67544; GB:AE000747; NID:G2983944; PIDN:AAC07497.1; PID:G298  
A:Experimental source: strain VFS  
C:Genetics:  
A:Gene: oadA  
C:Superfamily: Klebsiella pneumoniae oxaloacetate decarboxylase alpha chain; lipoyl/biot  
F:540-613/Domain: lipoyl/biotin-binding homology <LPB>  
F:579/Binding site: biotin (Lys) (covalent) #status predicted

Query Match 57.6%; Score 41.5; DB 2; Length 620;  
Best Local Similarity 60.0%; Pred. No. 93;  
Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWLTIW 9  
DB 38 CGFWLEWVG 47

RESULT 9  
T48166  
hypoetical protein T1008.150 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: T48166  
R:Bevan, M.; Pohl, T.; Weizenecker, T.; Bancroft, I.; Mewes, H.W.; Lemcke, K.; Mayer, K.  
submitted to the Protein Sequence Database, March 2000  
A:Reference number: Z24486  
A:Accession: T48166  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-307 <BEV>  
A:Cross-references: UNIPROT:Q9M030; EMBL:AL161746  
A:Experimental source: cultivar Columbia; BAC clone T1008  
C:Genetics:  
A:Map position: 5  
A:Introns: 31/3; 66/2; 114/3; 149/2; 232/2; 284/1  
A>Note: T1008.150

Query Match 56.9%; Score 41; DB 2; Length 307;  
Best Local Similarity 50.0%; Pred. No. 60;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10  
DB 186 CSFVVSINGC 195

RESULT 10

PC4117  
replication protein homolog - Pyrococcus sp. (fragment)  
N:Alternate names: hypoetical 391 protein  
C:Species: Pyrococcus sp.  
C:Date: 07-Feb-1996 #sequence\_revision 19-Apr-1996 #text\_change 17-May-1996  
C:Accession: PC4117  
R:Rashid, N.; Morikawa, M.; Imanaka, T.  
Gene 166, 139-143, 1995  
A:Title: An abnormally acidic TATA-binding protein from a hyperthermophilic archaeon.  
A:Reference number: JC4514; MUID:96105215; PMID:8529878  
A:Accession: PC4117  
A:Molecule type: DNA  
A:Residues: 1-391 <RAS>  
A:Cross-references: DDBJ:D50018

Query Match 56.9%; Score 41; DB 2; Length 391;  
Best Local Similarity 85.7%; Pred. No. 74;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YWLTIW 9  
DB 155 YWLTEWG 161

RESULT 11  
E90446  
permease [imported] - Sulfolobus solfataricus  
C:Species: Sulfolobus solfataricus  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C:Accession: E90446  
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-y  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A:Description: Sulfolobus solfataricus complete genome.  
A:Reference number: A99139  
A:Accession: E90446  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-419 <KUR>  
A:Cross-references: UNIPROT:Q97VB7; GB:AE006641; NID:G13816037; PIDN:AAK42828.1; GSPDB:G  
C:Genetics:  
A:Gene: SSO2718

Query Match 56.9%; Score 41; DB 2; Length 419;  
Best Local Similarity 62.5%; Pred. No. 78;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTIW 9  
DB 365 GFWETLW 372

RESULT 12  
T29407  
hypoetical protein C16C8.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
C:Accession: T29407  
R:Waterston, R.; Le, T.T.; Gattung, S.  
submitted to the EMBL Data Library, November 1996  
A:Description: The sequence of C. elegans cosmid C16C8.  
A:Reference number: Z20617  
A:Accession: T29407  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-739 <WAT>  
A:Cross-references: EMBL:U80452; PIDN:AAB37863.1; GSPDB:GN000020; CESP:C16C8.2  
A:Experimental source: strain Bristol N2; clone C16C8  
C:Genetics:  
A:Gene: CESP:C16C8.2  
A:Map position: 2  
A:Introns: 68/2; 179/3; 253/1; 275/3; 327/2; 365/3; 397/1; 428/2; 463/3; 629/1; 668/2; 7

C;Superfamily: myeloperoxidase; myeloperoxidase homology

Query Match 56.9%; Score 41; DB 2; Length 739;  
 Best Local Similarity 60.0%; Pred. No. 1.3e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CGYWLTIWGC 10  
 |||||  
 Db 118 CGFWATIREC 127

#### RESULT 13

I48108  
 sodium channel alpha subunit - long-tailed hamster (fragment)  
 C;Species: Cricetus longicaudatus (long-tailed hamster)  
 C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
 C;Accession: I48108  
 R;Lalik, P.H.; Krafte, D.S.; Ciccarelli, R.B.  
 Am. J. Physiol. 264, 803-809, 1993  
 A;Title: Characterization of endogenous Sodium channel gene expressed in chinese hamster  
 A;Reference number: I48107

A;Accession: I48108  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-200 <RES>  
 A;Cross-references: UNIPROT:Q60464; GB:M87541; NID:g191069; PIDN:AAA36979.1; PID:g553840  
 C;Genetics:  
 A;Gene: choi  
 C;Superfamily: sodium channel protein  
 C;Keywords: duplication

Query Match 56.2%; Score 40.5; DB 2; Length 200;  
 Best Local Similarity 54.5%; Pred. No. 49;  
 Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10  
 |||||  
 Db 26 CGEWETIWDG 36

#### RESULT 14

A55138  
 sodium channel mRNA2.3, voltage-gated - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C;Accession: A55138  
 R;Felipe, A.; Knittle, T.J.; Doyle, K.L.; Tamkun, M.M.  
 J. Biol. Chem. 269, 30125-30131, 1994  
 A;Title: Primary structure and differential expression during development and pregnancy  
 A;Reference number: A55138; MUID:95074002; PMID:7982916  
 A;Accession: A55138  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-1681 <PEL>  
 A;Cross-references: UNIPROT:Q62467; GB:L36179; NID:g609544; PIDN:AAA66192.1; PID:g806397  
 C;Superfamily: sodium channel protein

Query Match 56.2%; Score 40.5; DB 2; Length 1681;  
 Best Local Similarity 54.5%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10  
 |||||  
 Db 686 CGEWETIWDG 696

#### RESULT 15

A45380  
 sodium channel protein alpha chain hNav2.1 - human  
 C;Species: Homo sapiens (man)  
 C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C;Accession: A45380  
 R;George Jr., A.L.; Knittle, T.J.; Tamkun, M.M.

Proc. Natl. Acad. Sci. U.S.A. 89, 4893-4897, 1992  
 A;Title: Molecular cloning of an atypical voltage-gated sodium channel expressed in human  
 A;Reference number: A45380; MUID:92279233; PMID:1317577  
 A;Accession: A45380  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-1682 <GEO>  
 A;Cross-references: UNIPROT:Q01118; GB:M91556; NID:g189046; PIDN:AAA59899.1; PID:g189047  
 A;Experimental source: heart  
 A;Note: sequence extracted from NCBI backbone (NCBIP:104344)  
 C;Superfamily: sodium channel protein  
 C;Keywords: glycoprotein; membrane protein; phosphoprotein; sodium channel; voltage-gated

Query Match 56.2%; Score 40.5; DB 2; Length 1682;  
 Best Local Similarity 54.5%; Pred. No. 3.1e+02;  
 Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10  
 |||||  
 Db 686 CGEWETIWDG 696

Search completed: December 30, 2004, 13:17:13  
 Job time : 12.6761 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:57:52 ; Search time 92.2641 Seconds  
(without alignments)  
62.362 Million cell updates/sec

Title: US-10-046-922-35  
Perfect score: 72  
Sequence: 1 CGYWLTIWGC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	63.9	218	1 Y232_SYNY3	Q55705 synchocyst
2	45	62.5	828	1 Q8ZBL4	Q8ZBL4 versinia pe
3	45	62.5	853	2 Q8D1A7	Q8D1A7 versinia pe
4	45	62.5	853	2 AAS60566	AAS60566 versinia
5	43.5	60.4	1993	2 P90670	P90670 aplysia cal
6	43	59.7	168	2 Q6H022	Q6H022 fremyella d
7	43	59.7	221	2 Q74JK6	Q74JK6 lactobacill
8	43	59.7	221	2 AAS08923	AAS08923 lactobaci
9	43	59.7	501	2 Q6C574	Q6C574 varrowia li
10	43	59.7	646	2 Q8DKD6	Q8DKD6 synchococ
11	43	59.7	733	2 Q8H2N7	Q8H2N7 oryza sativ
12	43	59.7	1084	2 Q7WY20	Q7WY20 pseudomonas
13	42.5	59.0	152	2 Q96AC0	Q96AC0 homo sapien
14	42.5	59.0	159	2 Q6RW13	Q6RW13 homo sapien
15	42.5	59.0	159	2 Q9NRW9	Q9NRW9 homo sapien
16	42.5	59.0	159	2 Q96PL4	Q96PL4 homo sapien
17	42.5	59.0	159	2 AAR25556	AAR25556 homo sapi
18	42.5	59.0	263	2 Q7YIF1	Q7YIF1 cryptospori
19	42.5	59.0	1765	2 Q88457	Q88457 rattus norv
20	42	58.3	72	1 VG35_BPML5	VG35_BPML5 mycobacteri
21	42	58.3	133	2 Q855L3	Q855L3 mycobacteri
22	42	58.3	284	2 Q6MC01	Q6MC01 parachlamyd
23	42	58.3	284	2 CAF23898	CAF23898 parachlam
24	42	58.3	343	2 Q94FS2	Q94FS2 cajanus caj
25	42	58.3	389	2 Q83151	Q83151 tropheryma
26	42	58.3	441	2 Q922T6	Q922T6 rhizobium m
27	42	58.3	452	2 Q83G14	Q83G14 tropheryma
28	42	58.3	472	1 RBL_NITVU	RBL_NITVU nitrobacter
29	42	58.3	473	2 Q9XD76	Q9XD76 nitrobacter
30	42	58.3	473	2 Q9XD77	Q9XD77 nitrobacter
31	42	58.3	473	2 Q8VQ84	Q8VQ84 nitrosospir

32 42 58.3 1308 2 Q8T6H2  
33 42 58.3 1498 1 MRP6\_MOUSE  
34 42 58.3 1502 1 MRP6\_RAT  
35 42 58.3 1503 1 MRP6\_HUMAN  
36 41.5 57.6 122 2 Q8N1Z5  
37 41.5 57.6 620 2 Q67544  
38 41 56.9 266 2 Q82285  
39 41 56.9 307 2 Q9M030  
40 41 56.9 376 2 Q6CBE4  
41 41 56.9 398 2 Q8IUD8  
42 41 56.9 413 2 Q9HKA9  
43 41 56.9 419 2 Q97VB7  
44 41 56.9 432 2 Q6NUR0  
45 41 56.9 432 2 AAH59368

## ALIGNMENTS

RESULT 1  
Y232\_SYNY3  
ID Y232\_SYNY3 STANDARD; PRT; 218 AA.  
AC Q55705;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE Hypothetical protein slr0232.  
DE Hypothetical protein slr0232.  
GN OrderedLocusNames=slr0232;  
OS Synchocystis sp. (strain PCC 6803).  
OC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.  
OX NCBI\_TaxID=1148;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96127529; PubMed=8590279;  
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,  
RA Sugita M., Tabata S.,  
RT "Sequence analysis of the genome of the unicellular cyanobacterium  
RT Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb  
RT region from map positions 64% to 92% of the genome.";  
RL DNA Res. 2:153-166(1995).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -!- SIMILARITY: Belongs to the deda family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to license@isb-sib.ch).  
EMBL; D64000; BAA10237.1; -  
PIR; S76385; S76385.  
DR InterPro; IPR000252; Deda.  
DR Pfam; PF00597; Deda; 1.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 218 AA; 23781 MW; C04B5D7B7BA7F863 CRC64;

Query Match 63.9%; Score 46; DB 1; Length 218;  
Best Local Similarity 66.7%; Pred. No. 50;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CGYWLTIWGC 9  
DB 73 CGYWLTVRWG 81  
||||: ||  
CGYWLTVRWG 81

RESULT 2  
Q8ZBL4  
ID Q8ZBL4 PRELIMINARY; PRT; 828 AA.  
AC Q8ZBL4;  
DT 01-MAR-2002 (TremblRel. 20, Created)  
DT 01-MAR-2002 (TremblRel. 20, Last sequence update)

```

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ATP-dependent helicase.
GN Name=hrpB; OrderedLocusNames=YPO3394;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis; DOI=10.1038/35097083;
RX MEDLINE=21470413; PubMed=11586360; Titball R.W., Holden M.T.G.,
RA Parkhill J., Wren B.W., Thomson N.R., Churcher C.M., Mungall K.L.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feitwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds S., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR ENBL; A414156; CAC92824.1; -.
DR PIR; AD0412; AD0412.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0008026; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR010225; DEAD box HrpB.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR007502; Helicase_dom.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF04408; HA2; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR PIRSF; PIRSF005496; ATP_hel_hrpB; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR TIGRFAMS; TIGR01970; DEAH_box_HrpB; 1.
KW ATP-binding. Complete proteome; Helicase; Hydrolase.
SQ SEQUENCE 828 AA; 91982 MW; 3A11F8883D5E583 CRC64;

Query Match 62.5%; Score 45; DB 2; Length 828;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGWLTIT--WGC 10
Db 372 CGLWLELLSWG 383

RESULT 3
Q8D1A7 PRELIMINARY; PRT; 853 AA.
ID Q8D1A7 Q74XU2;
AC Q8D1A7; Q74XU2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Helicase, ATP-dependent.
GN Name=hrpB; OrderedLocusNames=YPO291, Y0794;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
```

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RL J. Bacteriol. 184:4601-4611(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=91001 / Biovar Mediaevalis;
RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
RA Yang R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AE013681; AAM84381.1; -.
DR GO; GO:0008026; F:ATP binding; IEA.
DR GO; GO:0005524; F:ATP-dependent helicase activity; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR010225; DEAD box HrpB.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR007502; Helicase_dom.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF04408; HA2; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR PIRSF; PIRSF005496; ATP_hel_hrpB; 1.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELIC; 1.
DR TIGRFAMS; TIGR01970; DEAH_box_HrpB; 1.
KW ATP-binding; Helicase; Hydrolase.
SQ SEQUENCE 853 AA; 95004 MW; B3DB738A18665B42 CRC64;

Query Match 62.5%; Score 45; DB 2; Length 853;
Best Local Similarity 58.3%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGWLTIT--WGC 10
Db 397 CGLWLELLSWG 408

RESULT 4
AAS60566 PRELIMINARY; PRT; 853 AA.
ID AAS60566
AC AAS60566
DT 24-MAR-2004 (TrEMBLrel. 27, Created)
DT 24-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 04-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE Helicase, ATP-dependent.
GN HRPB OR YPO291.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=91001 / Biovar Mediaevalis;
RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
RA Yang R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AE017128; AAS60566.1; -.
KW Helicase.
SQ SEQUENCE 853 AA; 95004 MW; B3DB738A18665B42 CRC64;

Query Match 62.5%; Score 45; DB 2; Length 853;
Best Local Similarity 58.3%; Pred. No. 2.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 CGWLTIT--WGC 10
Db 397 CGLWLELLSWG 408
```

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RESULT 5
P90670
ID P90670 PRELIMINARY; PRT; 1993 AA.
AC P90670;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAY-2004 (TREMBLrel. 26, Last annotation update)
DE Sodium channel alpha-subunit SCAP1.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidaea;
OC Aplysioidae; Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Nervous system;
RX MEDLINE=97238630; PubMed=9115644;
RA Dyer J.R., Johnston W.L., Castellucci V.F., Dunn R.J.;
RT "Cloning and tissue distribution of the Aplysia Na+ channel alpha-
subunit cDNA.";
RL DNA Cell Biol. 16:347-356(1997).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to the sodium channel family.
DR EMBL; U66915; AAC7457.1; -.
DR PIR; T30902; T30902.
DR HSSP; P04775; 1BYV.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0001518; C:voltage-gated sodium channel complex; IEA.
DR GO; GO:0005263; F:cation channel activity; IEA.
DR GO; GO:0005248; F:voltage-gated sodium channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR GO; GO:0006814; P:sodium ion transport; IEA.
DR InterPro; IPR001682; Ca/Na pore.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M-channel_nlg.
DR InterPro; IPR001696; Na_channel.
DR InterPro; IPR010526; Na_trans_assoc.
DR Pfam; PF00520; Ion_trans; 4.
DR Pfam; PF06512; Na_trans_assoc; 1.
DR PRINTS; PR00170; NACHANNEL.
DR Ion transport; Ionic channel; Sodium channel; Transmembrane;
KW Transport; Voltage-gated channel.
KW SEQUENCE 1993 AA; 225896 MW; 33E174B9BF07E1A7 CRC64;

Query Match 60.4%; Score 43.5; DB 2; Length 1993;
Best Local Similarity 54.5%; Pred. No. 8.9e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
Db 942 CGEWIESMWGC 952

RESULT 6
Q6H022
ID Q6H022 PRELIMINARY; PRT; 168 AA.
AC Q6H022;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Fremyella diplophron (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Microchaetaceae; Fremyella.
OX NCBI_TaxID=1197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FD33;
RA Stowe-Evans E.L., Ford J., Kehoe D.M.;
RT "Genomic DNA Microarray Analysis: Identification of New Genes
Regulated by Light Color in the Cyanobacterium Fremyella
diplophron.";

Query Match 60.4%; Score 43.5; DB 2; Length 1993;
Best Local Similarity 54.5%; Pred. No. 8.9e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CGYWL-TIWGC 10
Db 942 CGEWIESMWGC 952

RESULT 7
Q74JK6
ID Q74JK6 PRELIMINARY; PRT; 221 AA.
AC Q74JK6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hemolysin-like protein.
GN OrderedLocusNames=LJ1101;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 533;
RX PubMed=14966310;
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwielen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
Lactobacillus johnsonii NCC 533.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
DR EMBL; AE017203; AAS08923.1; -.
DR InterPro; IPR004254; HlyVIII_related.
DR InterPro; IPR005744; HlyVIII.
DR Pfam; PF03006; HlyVIII; 1.
DR TIGRFAMs; TIGR01065; hlyVIII; 1.
DR Complete proteome.
KW Complete proteome.
KW SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 221;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTVWG 9
Db 172 GFWLLVWG 179

RESULT 8
AAS08923
ID AAS08923 PRELIMINARY; PRT; 221 AA.
AC AAS08923;
DT 02-MAR-2004 (TREMBLrel. 27, Created)
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
DE Hemolysin-like protein.
GN LJ1101.
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]

```

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RP SEQUENCE FROM N.A.
RC STRAIN=NCC 533;
RX PubMed=14966310;
RA Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwielen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
RT Lactobacillus johnsonii NCC 533.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
DR EMBL; AE017203; AAS08923.1; -.
SQ SEQUENCE 221 AA; 24721 MW; 1DBC78FF9810E152 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 221;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTVWG 9
Db 172 GFWLLVWG 179

RESULT 9
Q6C574
ID Q6C574 PRELIMINARY; PRT; 501 AA.
AC Q6C574;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chromosome E of strain CLB99 of Yarrowia lipolytica.
GN ORFNames=YALI0E204719;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLB99;
RG GENOLEVURES;
RA DuJon B., Sherman D., Fischer G., Durrans P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anhouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boistrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye P., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikoleki M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellens S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLB99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382131; CAG79783.1; -.
SQ SEQUENCE 501 AA; 56411 MW; 91F08EF5A63C60FB CRC64;

Query Match 59.7%; Score 43; DB 2; Length 501;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GYWLTVWG 10
Db 157 GYWLTVWG 165

RESULT 10
Q8DKD6

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ID Q8DKD6 PRELIMINARY; PRT; 646 AA.
AC Q8DKD6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T110923 protein.
GN OrderedLocusNames=t110923;
OS Synechococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=32046;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=22225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A., Nakazaki N.,
RA Shimpō S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
RT Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
DR EMBL; AP005372; BAC08475.1; -.
DR GO; GO:0003824; P: catalytic activity; IEA.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
KW Complete proteome.
SQ SEQUENCE 646 AA; 71071 MW; 56CSA74F76652D56 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 646;
Best Local Similarity 62.5%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 YWLTWGC 10
Db 415 YWINRWGC 422

RESULT 11
Q8H2N7
ID Q8H2N7 PRELIMINARY; PRT; 733 AA.
AC Q8H2N7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein OJ138_B05.118;
GN Names=OJ138_B05.118;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005486; BAC16197.1; -.
DR Gramene; Q8H2N7; -.
DR InterPro; IPR007658; DUF594.
DR Pfam; PF04578; DUF594; 1.
KW Hypothetical protein.
SQ SEQUENCE 733 AA; 82939 MW; E95884DAD1DC2AC9 CRC64;

Query Match 59.7%; Score 43; DB 2; Length 733;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YWLTWGC 9
Db 328 YWLTWGC 334

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RESULT 12
Q7WY20 PRELIMINARY; PRT; 1084 AA.
AC Q7WY20;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Kc8C.
GN Name=rc8C; ORFNames=RL038;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC SUBM=PA14;
RX PubMed=14983043;
RA He J., Baldini R.L., Dezziel E., Saucier M., Zhang Q., Liberati N.T.,
RT Lee D., Urbach J., Goodman H.M., Rahme L.G.;
RT "The broad host range pathogen Pseudomonas aeruginosa strain PA14
RT carries two pathogenicity islands harboring plant and animal virulence
RT genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2530-2535(2004).
CC -1- SIMILARITY: Contains 1 histidine kinase domain.
DR EMBL; AY273869; AAP84165.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0000156; F:two-component response regulator activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0000160; F:two-component signal transduction system (p. . .); IEA.
DR InterPro; IPR003594; ATPbind ATPase.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kinA_N.
DR InterPro; IPR008207; Hpt.
DR InterPro; IPR000014; PAS.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HATPase_c; 1.
DR Pfam; PF0512; HisKA; 1.
DR Pfam; PF01627; Hpt; 1.
DR Pfam; PF00072; Response_reg; 1.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00388; HisKA; 1.
DR SMART; SM00091; PAS; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS50109; HIS_KIN; 1.
DR PROSITE; PS50894; HPT; 1.
DR PROSITE; PS50110; RESPONSE_REGULATORY; 1.
DR Kinase; Phosphorylation; Sensory transduction; Transferase.
KW KINASE
SQ SEQUENCE 1084 AA; 119129 MW; C953FDD2F273BF1B CRC64;

Query Match 59.7%; Score 43; DB 2; Length 1084;
Best Local Similarity 66.7%; Pred. No. 66+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GYWLTIWGC 10
DB 750 GAWLXWGC 758

RESULT 13
Q96AC0 PRELIMINARY; PRT; 152 AA.
AC Q96AC0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AGTRAP protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Query Match 59.0%; Score 42.5; DB 2; Length 159;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins B.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dapkin L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017328; AAH17328.1; -.
DR InterPro; IPR009436; AGTRAP.
DR Pfam; PF06396; AGTRAP; 1.
SQ SEQUENCE 152 AA; 16669 MW; 637C01214175C3C9 CRC64;

Query Match 59.0%; Score 42.5; DB 2; Length 152;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 2 GYWLTIWGC 10
DB 14 GHWLLTWGC 23

RESULT 14
QGRW13 PRELIMINARY; PRT; 159 AA.
AC Q6RW13;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Angiotensin II receptor-associated protein.
GN Name=AGTRAP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA Rajkumar N., Yi Q., Nickerson D.A.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY488088; AAR25556.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR009436; AGTRAP.
DR Pfam; PF06396; AGTRAP; 1.
KW Receptor.
SQ SEQUENCE 159 AA; 17419 MW; 7E1D5C7E79AE6BC5 CRC64;

Query Match 59.0%; Score 42.5; DB 2; Length 159;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

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Qy 2 GYW-LTIWGC 10  
|:| |||  
Db 14 GHWLLTTWGC 23

RESULT 15

Q9NRW9 PRELIMINARY; PRT; 159 AA.  
AC Q9NRW9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ATRAP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Kidney;  
RA Ye R.D., He R.;  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF165187; AAF89547.1; -.  
DR Genew; HGNC:13539; AGTRAP.  
DR InterPro; IPR009436; AGTRAP.  
DR Pfam; PF06396; AGTRAP; 1.  
SQ SEQUENCE 159 AA; 17518 MW; 7E012C7E79AE6BC5 CRC64;

Query Match 59.0%; Score 42.5; DB 2; Length 159;  
Best Local Similarity 70.0%; Pred. No. 1.2e+02;  
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 2 GYW-LTIWGC 10  
|:| |||  
Db 14 GHWLLTTWGC 23

Search completed: December 30, 2004, 13:16:10  
Job time : 94.2641 secs

	1	32	84.2	7	5	ABP53964	VEGFR-3 b
2	31	81.6	7	3	AA76794	Somatostata	
3	31	81.6	7	5	ABP53418	Backbone	
4	26	68.4	6	2	AA893713	Cyclo[-Ty	
5	25	65.8	7	3	AA76792	Somatostata	
6	25	65.8	7	5	ABP53416	Backbone	
7	24	63.2	4	8	ADJ38912	AID target	
8	24	63.2	5	2	AA76079	Mab 55-1	
9	24	63.2	5	3	AA732257	Light cha	
10	24	63.2	5	8	ADM10172	Human pro	
11	24	63.2	5	8	ADM10201	Human pro	
12	24	63.2	6	2	AA880643	Receptor	
13	24	63.2	6	5	AAU83934	Tyrosine	
14	24	63.2	6	6	ABJ37222	Rhodopsin	
15	24	63.2	6	6	ABJ37226	Rhodopsin	
16	24	63.2	6	6	ABJ37224	Rhodopsin	
17	24	63.2	6	8	ABG75386	C melo se	
18	24	63.2	7	2	AA808140	Neurokinin	
19	24	63.2	7	2	AA62543	Fibronect	
20	24	63.2	7	3	AA76793	Somatostata	
21	24	63.2	7	3	AAU78246	Clonorchis	
22	24	63.2	7	3	AAU77087	Clonorchis	
23	24	63.2	7	4	AAm44768	H11 bindi	
24	24	63.2	7	4	AAm44793	H11 bindi	
25	24	63.2	7	5	AAU81571	Enterokin	

CC antidiabetic and vulnery activities, and can be used in gene therapy.  
 CC .Compositions and methods from the present invention are useful for  
 CC diagnosing, evaluating and treating disorders mediated by the activity of  
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangionas and diabetes. The present sequence  
 CC represents a specifically claimed VEGFR-3 binding peptide from the  
 CC present invention  
 XX  
 SQ Sequence 7 AA;

Query Match 84.2%; Score 32; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. NO. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
 |||||  
 DB 1 GYWXXXW 7

RESULT 2  
 AAY76794  
 ID AAY76794 standard; peptide; 7 AA.

XX  
 AC AAY76794;

XX  
 DT 20-APR-2000 (first entry)

XX  
 DE Somatostatin analogue peptide 3181.

XX Somatostatin analogue; therapy; cyclic peptide; autoimmune disease;  
 KW endocrine disorder; cancer; diabetic-associated complication; diagnosis;  
 KW gastrointestinal disorder; inflammatory disease; pancreatitis;  
 KW atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor;  
 KW hormone-secreting tumour; hormone-dependent tumour; diarrhoea;  
 KW vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 3

FT Modified-site 7 /note= "D-form residue"

FT /note= "Trp-NH2"

XX WO9965508-A1.

XX 23-DEC-1999.

XX 15-JUN-1999; 99WO-IL000329.

XX 19-JUN-1998; 98US-00100360.

XX 02-DEC-1998; 98US-00203389.

XX (PEPT-) PEPTOR LTD.

XX Hornik V, Afargan MM, Gellerman G;

XX WPI; 2000-136888/12.

XX Cyclized somatostatin analogs for inhibiting growth hormone secretion  
 PT from anterior pituitary and as antiproliferative agents for the treatment  
 PT of tumors.

XX Example 11; Page 61; 82pp; English.

XX This sequence represents a somatostatin analogue of the invention. The  
 CC invention relates to a backbone cyclised somatostatin analogue that has  
 CC one building unit containing a nitrogen atom of the peptide backbone  
 CC connected to a bridging group comprising an amide, thioether, thioester

CC or disulphide. At least one building unit is connected via a bridging  
 CC group to form a cyclic structure with a moiety selected from a second  
 CC building unit, side chain of or N-terminal amino acid residue. A  
 CC composition containing the analogue may be used for preventing disorders  
 CC such as cancer, autoimmune diseases, endocrine disorders, diabetic-  
 CC associated complications, gastrointestinal disorders, inflammatory  
 CC diseases, pancreatitis, atherosclerosis, restenosis and post-surgical  
 CC pain. It may also be used for diagnosing cancer. The backbone cyclic  
 CC analogue is used for imaging the existence of metastases. Somatostatin  
 CC analogues can be used for the treatment of patients with hormone-secreting  
 CC and hormone-dependent tumours. They reduce diarrhoea through the  
 CC inhibition of vasoactive intestinal peptide (VIP) secretion and by direct  
 CC effect on intestinal secretion. Somatostatin analogues selective to type  
 CC 2 and 5 receptors may be used for treatment of non-insulin dependent  
 CC diabetes mellitus. They are useful for the prevention of atherosclerosis  
 CC and restenosis. The analogues are metabolically stable, selective in  
 CC their in-vivo activities and safe  
 XX  
 SQ Sequence 7 AA;

Query Match 81.6%; Score 31; DB 3; Length 7;  
 Best Local Similarity 57.1%; Pred. NO. 1.7e+06;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
 |||||  
 DB 1 GYWKVCW 7

RESULT 3  
 ABP53418

ID ABP53418 standard; peptide; 7 AA.

XX AC ABP53418;

XX 19-NOV-2002 (first entry)

XX Backbone cyclised somatostatin analogue PTR 3181.

XX Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;  
 KW somatostatin release inhibiting factor; somatostatin receptor subtype;  
 KW synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer;  
 KW antidiabetic; antiinflammatory; somatostatin receptor ligand;  
 KW atherosclerosis; autoimmune disease; diabetic-associated complication;  
 KW endocrine disorder; inflammation; gastrointestinal disorder; restenosis;  
 KW pancreatitis; post-surgical pain.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminally modified with Fmoc  
 (fluorenylmethoxycarbonyl)"

FT Misc-difference 3

FT /note= "D form residue"

FT Modified-site 7 /note= "amidated"

XX US2002052315-A1.

XX 02-MAY-2002.

XX 13-DEC-2000; 2000US-00734583.

XX 19-JUN-1998; 98US-00100360.

XX 02-DEC-1998; 98US-00203389.

XX 15-JUN-1999; 99WO-IL000329.

XX (HORN/) HORNIK V.

XX (AFAR/) AFARGAN M M.

XX (GELL/) GELLERMAN G.

XX Hornik V, Afargan MM, Gellerman G;  
 PI

XX WPI; 2002-681319/73.  
 XX New backbone cyclized somatostatin analogs are e.g. useful in the  
 PT treatment of atherosclerosis, autoimmune diseases and cancers.  
 XX  
 XX Example 12; Page 21; 30pp; English.  
 XX  
 CC The present invention describes backbone cyclised somatostatin analogues  
 CC (I) that incorporates at least one building unit containing one nitrogen  
 CC atom of the peptide backbone connected to a bridging group (comprising an  
 CC amide, thioether, thioester or disulfide) where at least one building  
 CC unit is connected via the bridging group to form a cyclic structure with  
 CC a moiety selected from the group consisting of a second building unit,  
 CC the side chain of an amino acid residue of the sequence or the N-terminal  
 CC amino acid residue. (I) has antiarteriosclerotic, immunosuppressive,  
 CC cytostatic, antidiabetic, antiinflammatory and analgesic activities, and  
 CC can be used as a somatostatin receptor ligand. (I) are useful in the  
 CC treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-  
 CC associated complications, endocrine disorders, inflammation,  
 CC gastrointestinal disorders, pancreatitis, post-surgical pain, and  
 CC restenosis. (I) can also be used in the diagnosis of cancer, by imaging  
 CC the existence of metastases, it being labeled with a detectable probe.  
 CC The present sequence represents a backbone cyclised somatostatin analogue  
 CC from the present invention  
 XX  
 XX Sequence 7 AA;  
 SQ  
 Query Match 81.6%; Score 31; DB 5; Length 7;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+06;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GYWXWV 7  
 ||| |  
 Db 1 GYWKVCM 7  
 RESULT 4  
 AAR93713  
 ID AAR93713 standard; peptide; 6 AA.  
 XX  
 AC AAR93713;  
 XX  
 XX 10-MAY-1996 (first entry)  
 DT  
 XX  
 DE Cyclo(-Tyr-trp-Leu-Arg-Gly-Trp-).  
 XX  
 XX neurokinin A antagonist; tachykinin; respiratory disease; asthma;  
 KW analgesic; cyclic.  
 KW  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /note= "not an N-terminal amino acid, but condensed with  
 FT Trp(6) to form a cyclic peptide"  
 FT Misc-difference 2  
 FT /note= "D-form residue"  
 FT Modified-site 6  
 FT /note= "not a C-terminal amino acid, but condensed with  
 FT Tyr(1) to form a cyclic peptide"  
 FT  
 XX W09521187-A1.  
 PN  
 XX  
 XX 10-AUG-1995.  
 PD  
 XX  
 XX 10-JAN-1995; 95WO-US000296.  
 PF  
 XX  
 XX 03-FEB-1994; 94US-00191571.  
 PR  
 XX (RICH ) MERRELL DOW PHARM INC.  
 PA  
 XX Owen TJ, Kudlacz EM, Buck SH, Harbeson SL;

XX WPI; 1995-336695/43.  
 XX New cyclic peptide derivs. - are neurokinin A and tachykinin antagonists  
 PT useful e.g. for treating asthma or as analgesics.  
 XX  
 XX Claim 8; Page 69; 82pp; English.  
 PS  
 XX The patent describes novel cyclic hexapeptide and octapeptide compounds  
 CC which are antagonists of neurokinin A and which are useful medically as  
 CC analgesics and for treating respiratory diseases such as asthma. The  
 CC present sequence represents a specifically preferred example of the new  
 CC peptide  
 XX  
 SQ Sequence 6 AA;  
 Query Match 68.4%; Score 26; DB 2; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 YWXXXW 7  
 ||| |  
 Db 1 YWLRCW 6  
 RESULT 5  
 AAY76792  
 ID AAY76792 standard; peptide; 7 AA.  
 XX  
 AC AAY76792;  
 XX  
 XX 20-APR-2000 (first entry)  
 DT  
 XX  
 DE Somatostatin analogue peptide 3177.  
 XX  
 XX Somatostatin analogue; therapy; cyclic peptide; autoimmune disease;  
 KW endocrine disorder; cancer; diabetic-associated complication; diagnosis;  
 KW gastrointestinal disorder; inflammatory disease; pancreatitis;  
 KW atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor;  
 KW hormone-secreting tumour; hormone-dependent tumour; diarrhoea;  
 KW vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.  
 KW  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 3  
 FT /note= "D-form residue"  
 FT Modified-site 7  
 FT /note= "Trp-NH2"  
 FT  
 XX W09965508-A1.  
 PN  
 XX  
 XX 23-DEC-1999.  
 PD  
 XX  
 XX 15-JUN-1999; 99WO-IL000329.  
 PF  
 XX  
 XX 19-JUN-1998; 98US-00100360.  
 PR  
 XX 02-DEC-1998; 98US-00203389.  
 PR  
 XX (PEPT-) PEPTOR LTD.  
 PA  
 XX  
 XX Hornik V, Afargan MM, Gellerman G;  
 PI  
 XX WPI; 2000-136888/12.  
 DR  
 XX Cyclized somatostatin analogs for inhibiting growth hormone secretion  
 PT from anterior pituitary and as antiproliferative agents for the treatment  
 PT of tumors.  
 PT  
 XX Example 11; Page 61; 82pp; English.  
 PS  
 XX This sequence represents a somatostatin analogue of the invention. The  
 CC invention relates to a backbone cyclised somatostatin analogue that has

CC one building unit containing a nitrogen atom of the peptide backbone  
 CC connected to a bridging group comprising an amide, thioether, thioester  
 CC or disulphide. At least one building unit is connected via a bridging  
 CC group to form a cyclic structure with a moiety selected from a second  
 CC building unit, side chain of or N-terminal amino acid residue. A  
 CC composition containing the analogue may be used for preventing disorders  
 CC such as cancers, autoimmune diseases, endocrine disorders, diabetic-  
 CC associated complications, gastrointestinal disorders, inflammatory  
 CC diseases, pancreatitis, atherosclerosis, restenosis and post-surgical  
 CC pain. It may also be used for diagnosing cancer. The backbone cyclic  
 CC analogue is used for imaging the existence of metastases. Somatostatin  
 CC analogues can be used for the treatment of patients with hormone-secreting  
 CC and hormone-dependent tumours. They reduce diarrhoea through the  
 CC inhibition of vasoactive intestinal peptide (VIP) secretion and by direct  
 CC effect on intestinal secretion. Somatostatin analogues selective to type  
 CC 2 and 5 receptors may be used for treatment of non-insulin dependent  
 CC diabetes mellitus. They are useful for the prevention of atherosclerosis  
 CC and restenosis. The analogues are metabolically stable, selective in  
 CC their in-vivo activities and safe  
 XX  
 SQ Sequence 7 AA;

Query Match 65.8%; Score 25; DB 3; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
 ||| |  
 Db 2 YWKVCW 7

RESULT 6  
 ABP53416  
 ID ABP53416 standard; peptide; 7 AA.  
 XX  
 AC ABP53416;  
 XX  
 DT 19-NOV-2002 (first entry)  
 XX  
 DE Backbone cyclised somatostatin analogue PTR 3177.

XX Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;  
 KW somatostatin release inhibiting factor; somatostatin receptor subtype;  
 KW synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer;  
 KW antidiabetic; antiinflammatory; somatostatin receptor ligand;  
 KW atherosclerosis; autoimmune disease; diabetic-associated complication;  
 KW endocrine disorder; inflammation; gastrointestinal disorder; restenosis;  
 KW pancreatitis; post-surgical pain.  
 XX  
 OS Synthetic.

FH Key Location/Qualifiers  
 FT Misc-difference 3 /note= "D form residue"  
 FT FT  
 FT Modified-site 7 /note= "amidated"  
 FT FT

XX US2002052315-A1.  
 XX  
 XX 02-MAY-2002.  
 XX  
 XX 13-DEC-2000; 2000US-00734583.  
 XX  
 XX 19-JUN-1998; 98US-00100360.  
 XX  
 XX 02-DEC-1998; 98US-00203389.  
 XX  
 XX 15-JUN-1999; 99WO-IL000329.

XX (HORN/) HORNIK V.  
 PA (AFAR/) AFARGAN M M.  
 PA (GELL/) GELLERMAN G.  
 XX

PI Hornik V, Afargan MM, Gellerman G;  
 XX

DR WPI; 2002-681319/73.

XX New backbone cyclised somatostatin analogs are e.g. useful in the  
 PT treatment of atherosclerosis, autoimmune diseases and cancers.

XX Example 12; Page 21; 30pp; English.

XX The present invention describes backbone cyclised somatostatin analogues  
 CC (I) that incorporates at least one building unit containing one nitrogen  
 CC atom of the peptide backbone connected to a bridging group (comprising an  
 CC amide, thioether, thioester or disulfide) where at least one building  
 CC unit is connected via the bridging group to form a cyclic structure with  
 CC a moiety selected from the group consisting of a second building unit,  
 CC the side chain of an amino acid residue of the sequence or the N-terminal  
 CC amino acid residue. (I) has antiarteriosclerotic, immunosuppressive, and  
 CC cytostatic, antidiabetic, antiinflammatory and analgesic activities, and  
 CC can be used as a somatostatin receptor ligand. (I) are useful in the  
 CC treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-  
 CC associated complications, endocrine disorders, inflammation,  
 CC gastrointestinal disorders, pancreatitis, post-surgical pain, and  
 CC restenosis. (I) can also be used in the diagnosis of cancer, by imaging  
 CC the existence of metastases, it being labeled with a detectable probe.  
 CC The present sequence represents a backbone cyclised somatostatin analogue  
 CC from the present invention  
 XX

SQ Sequence 7 AA;

Query Match 65.8%; Score 25; DB 5; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
 ||| |  
 Db 2 YWKVCW 7

RESULT 7  
 ADJ38912  
 ID ADJ38912 standard; peptide; 4 AA.

XX ADJ38912;

XX 06-MAY-2004 (first entry)

DT AID target hotspot motif peptide, SEQ ID 9.

DE  
 XX Anti-HIV; Cytostatic; Immunostimulant; Gene Therapy; Vaccine;  
 KW HIV TAT protein transduction domain; human; CEM15; hemagglutinin domain;  
 KW AID; activation induced deaminase; enzyme.  
 XX

OS Unidentified.

XX WO2004013160-A2.

PN 12-FEB-2004.

XX 05-AUG-2003; 2003WO-US024458.

XX 05-AUG-2002; 2002US-0401293P.

PR 21-OCT-2002; 2002US-0419982P.

XX (UVRP ) UNIV ROCHESTER.

XX Smith HC, Sowden MP, Dewhurst S, Kim B, Wedekind J;

XX WPI; 2004-169321/16.

XX New chimeric protein useful for treating human immunodeficiency virus  
 PT infection in a subject, comprises protein transduction domain and a  
 PT cytidine deaminase domain.

XX Disclosure; SEQ ID NO 9; 240pp; English.

XX

CC The present invention relates to chimeric proteins (I) which comprise a  
 CC protein transduction domain and a deaminase domain. In (I), the protein  
 CC transduction domain is chosen from poly-arginine, poly-lysine peptide,  
 CC third alpha-helix of Antennapedia homeodomain protein, HSV-1 virion  
 CC protein (VP)22, HIV-1 Vpr and HIV TAT protein. The deaminase domain  
 CC comprises CEM15 or Activation Induced Deaminase (AID). (I) further  
 CC comprises an epitope tag which is a hemagglutinin or a polyhistidine tag,  
 CC and a polypeptide domain that enhances solubility of (I). (I) further  
 CC comprises a third polypeptide comprising a cytoplasmic localization  
 CC protein (e.g. chicken muscle pyruvate kinase) or its fragment which  
 CC enhances localization of the chimeric protein to the cytoplasm. (I) is  
 CC useful for interrupting HIV infectivity which involves contacting an HIV-  
 CC infected cell or a cell prior to HIV infection with (I) to allow delivery  
 CC of (I) into the cell, where (I) binds with vif to interrupt HIV  
 CC infectivity, for treating a subject with an HIV infection or at risk for  
 CC an HIV infection which involves administering (I) to the subject, where  
 CC the administration step is dose-dependent or transient. (I) is also  
 CC useful for treating a subject for hyper-IgM syndrome which involves  
 CC administering (I) to a subject exhibiting hyper-IgM syndrome, where (I)  
 CC taken up by B lymphocyte cells induces antibody production sufficient to  
 CC treat the hyper-IgM syndrome. (I) is useful for treating a subject for B  
 CC lymphocyte cell lymphoma which involves administering (I) to a subject  
 CC exhibiting B lymphocyte cell lymphoma, where (I) is taken up by cancerous  
 CC B lymphocyte cells, and inhibits blunt cell growth, thus treating the  
 CC lymphoma. (I) is also useful for treating conditions such as cancer and  
 CC infectious diseases. The present sequence was used to illustrate the  
 CC invention.

XX Sequence 4 AA;

Query Match 63.2%; Score 24; DB 8; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
 Db |||  
 2 GYW 4

RESULT 8

AAR76079  
 ID AAR76079 standard; peptide; 5 AA.

XX AC AAR76079;

XX DT 25-MAR-2003 (revised)  
 XX DT 21-NOV-1995 (first entry)

XX DE MAB 55.1 heavy chain CDRI.

XX KW Antigen binding structure; complementarity determining region; CDR;  
 KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;  
 KW monoclonal antibody; MAB; immunotherapy; therapy; diagnosis;  
 KW transgenic animal; transgenic plant; antibody engineering;  
 KW humanized antibody; immunotoxin.

XX OS Mus sp.

XX FN WO9515382-A1.

XX PD 08-JUN-1995.

XX PF 29-NOV-1994; 94WO-GB002610.

XX PR 03-DEC-1993; 93GB-00024819.

XX PR 03-JUN-1994; 94GB-00011089.

XX PA (ZENE) ZENECA LTD.

XX PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;  
 PI Blakey DC;

XX DR WPI; 1995-215262/28.

XX Antigen binding structures containing CDR's recognising the CA55.1  
 PT antigen - produced by hybridomas and host cells, for use in the diagnosis  
 PT and therapy of cancer.  
 XX Claim 2; Page 96; 121pp; English.  
 XX An antigen binding structure is based on the CDRs (given in AAR76078- 84)  
 CC of the heavy and light chains of MAB 55.1 (SCACC 93081901), which  
 CC recognises the colorectal tumor-associated antigen CA55.1. It is  
 CC optionally humanized and in the form F(ab')<sub>2</sub>, F(ab)', Fab, Fv, scFv or V-  
 CC min, and is produced in transgenic animals or plants. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)

XX Sequence 5 AA;

Query Match 63.2%; Score 24; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
 Db |||  
 1 GYW 3

RESULT 9

AAY32257  
 ID AAY32257 standard; peptide; 5 AA.

XX AC AAY32257;

XX DT 15-FEB-2000 (first entry)

XX DE Light chain CDR H1 of mouse anti-CD23 MAB C11.

XX KW CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;  
 KW monoclonal antibody; chimeric antibody; humanised antibody;  
 KW complementarity determining region; CDR; autoimmune disease;  
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;  
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;  
 KW urticaria; nephrotic syndrome; glomerulonephritis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;  
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;  
 KW graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy;  
 KW therapy.

XX OS Mus musculus.

XX FN WO958679-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001434.

XX PR 09-MAY-1998; 98GB-00009839.

XX PA (GLAXO) GLAXO GROUP LTD.

XX PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

XX DR WPI; 2000-053101/04.  
 XX N-PSDB; AAZ34742.

XX Cell receptor specific antibodies useful for treating e.g. arthritis,  
 PT diabetes, multiple sclerosis and psoriasis.  
 XX Claim 1; Page 40; 81pp; English.

XX This sequence represents complementarity determining region 1 (CDR H1)  
 CC of the heavy chain of murine anti-CD23 (PCERII) monoclonal antibody C11  
 CC (see also AAY32263). The invention provides altered antibodies, such as  
 CC chimeric or humanised antibodies, which comprise sufficient of the amino  
 CC acid sequences of C11 light and heavy chain CDRs (see AAY32254-59) to

CC render them capable of binding to the CD23 type II molecule expressed on  
 CC haematopoietic cells. The antibodies are used to block soluble CD23  
 CC formation for treatment of arthritis, lupus erythematosus, Hashimoto's  
 CC thyroiditis, multiple sclerosis, diabetes, uveitis, dermatitis,  
 CC psoriasis, urticaria, nephrotic syndrome, glomerulonephritis,  
 CC inflammatory bowel disease, ulcerative colitis, Crohn's disease,  
 CC Sjogren's syndrome, allergies, allergic asthma, intrinsic asthma, acute  
 CC asthmatic exacerbation, rhinitis, eczema, graft-versus-host disease,  
 CC COPD, insulinitis, bronchitis (particularly chronic bronchitis) or diabetes  
 CC (particularly type 1 diabetes), and B-cell malignancies (claimed). They  
 CC are also useful for studying interactions between CD23 and various  
 CC ligands and determining the binding agents  
 XX

SQ Sequence 5 AA;

Query Match 63.2%; Score 24; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
 ||||  
 Db 1 GYW 3

RESULT 10

ID ADM10172  
 XX ADM10172 standard; peptide; 5 AA.

AC ADM10172;

XX 20-MAY-2004 (first entry)

DE Human proteome unique recognition sequence (URS) seqid 496.

XX soluble peptide analyte; unique recognition sequence; URS;  
 KW protein detection; clinical diagnosis; environmental diagnosis;  
 KW drug discovery; protein sequencing; pathogen detection; toxin detection;  
 KW anthrax toxin; small pox toxin; cholera toxin;  
 KW packaged protein detection array; protein expression profile;  
 KW drug screening; protein characterisation; disease prognosis;  
 KW pathologic cell profiling; proteome epitope tag; human; proteome.

XX Homo sapiens.

XX US2004038307-A1.

XX 26-FEB-2004.

XX 12-MAY-2003; 2003US-00436549.

XX 10-MAY-2002; 2002US-0379626P.

PR 01-JUL-2002; 2002US-0393137P.

PR 01-JUL-2002; 2002US-0393197P.

PR 01-JUL-2002; 2002US-0393211P.

PR 01-JUL-2002; 2002US-0393223P.

PR 01-JUL-2002; 2002US-0393233P.

PR 01-JUL-2002; 2002US-0393235P.

PR 01-JUL-2002; 2002US-0393280P.

PR 04-DEC-2002; 2002US-0430948P.

PR 13-DEC-2002; 2002US-0433319P.

XX (ENGE-) ENGNEOS INC.

XX Lee FD, Meng X, Chan JW, Zhang S, Benkovic SJ;

XX WPI; 2004-327083/30.

XX Detecting proteins comprises providing solution of soluble peptide  
 XX analytes, contacting solution with capture agents capable of interacting  
 PT with unique recognition sequence of protein and detecting binding between  
 PT agents and analytes.

XX Claim 60; SEQ ID NO 496; 134pp; English.

XX The invention describes a method of detecting proteins in sample. The  
 CC method comprises: providing a solution of soluble peptide analytes  
 CC produced by denaturation and/or cleavage of several sample proteins, and  
 CC optionally, labeling the collection of peptides by a detectable part;  
 CC contacting the solution with one or more capture agent(s), where each of  
 CC the capture agent(s) is able to specifically recognise and interact with  
 CC a unique recognition sequence (URS) of a reference protein; and detecting  
 CC the binding between one or more of the capture agent(s) and the peptide  
 CC analytes, where the detection of binding between a capture agent and a  
 CC peptide analyte indicates the presence of the reference protein in the  
 CC several of sample proteins. Also described are; and a method of  
 CC quantifying proteins in a biological sample; a method of simultaneously  
 CC detecting several specific proteins in a multi-protein sample. The method  
 CC of the invention is used in clinical or environmental diagnosis, drug  
 CC discovery, protein sequencing and for the detection of a pathogen or  
 CC toxins (such as anthrax toxin, small pox toxin, and cholera toxin). A  
 CC packaged protein detection array is useful for: quantifying various forms  
 CC of post-translationally modified proteins in a biological sample;  
 CC screening large libraries of natural or synthetic compounds to identify  
 CC competitors of natural or non-natural ligands for the capture agent,  
 CC which may be of diagnostic, prognostic, therapeutic or scientific  
 CC interest; and to study the relationship between a subject protein  
 CC expression profile and that subjects response to a foreign compound or  
 CC drug. The methods of assaying differential protein expression are useful  
 CC in the identification and validation of new potential drug targets as  
 CC well as for drug screening. The capture agents are useful for protein  
 CC characterisation, for screening, making prognosis of disease outcomes and  
 CC providing treatment modality suggestion based on the profiling of the  
 CC pathologic cells, prognosis of the outcome of a normal lesion and  
 CC susceptibility of lesions to malignant transformation. The methods  
 CC described are useful for identifying and/or detecting a specific organism  
 CC based on the organisms proteome epitope tag. This is the amino acid  
 CC sequence of a human proteome unique recognition sequence (URS).

XX Sequence 5 AA;

Query Match 63.2%; Score 24; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
 ||||  
 Db 1 GYW 3

RESULT 11

ID ADM10201  
 XX ADM10201 standard; peptide; 5 AA.

AC ADM10201;

XX 20-MAY-2004 (first entry)

DE Human proteome unique recognition sequence (URS) seqid 525.

XX soluble peptide analyte; unique recognition sequence; URS;  
 KW protein detection; clinical diagnosis; environmental diagnosis;  
 KW drug discovery; protein sequencing; pathogen detection; toxin detection;  
 KW anthrax toxin; small pox toxin; cholera toxin;  
 KW packaged protein detection array; protein expression profile;  
 KW drug screening; protein characterisation; disease prognosis;  
 KW pathologic cell profiling; proteome epitope tag; human; proteome.

XX Homo sapiens.

XX US2004038307-A1.

XX 26-FEB-2004.

XX 12-MAY-2003; 2003US-00436549.

XX 10-MAY-2002; 2002US-0379626P.

PR 01-JUL-2002; 2002US-0393137P.  
 PR 01-JUL-2002; 2002US-0393197P.  
 PR 01-JUL-2002; 2002US-0393211P.  
 PR 01-JUL-2002; 2002US-0393223P.  
 PR 01-JUL-2002; 2002US-0393233P.  
 PR 01-JUL-2002; 2002US-0393235P.  
 PR 01-JUL-2002; 2002US-0393280P.  
 PR 04-DEC-2002; 2002US-0430948P.  
 PR 13-DEC-2002; 2002US-0433319P.  
 XX (ENGE-) ENGENSEOS INC.  
 XX  
 XX Lee FD, Meng X, Chan JW, Zhang S, Benkovic SJ;  
 PI  
 XX WPI; 2004-327083/30.  
 DR  
 XX  
 PT Detecting proteins comprises providing solution of soluble peptide  
 PT analytes, contacting solution with capture agents capable of interacting  
 PT with unique recognition sequence of protein and detecting binding between  
 PT agents and analytes.  
 XX  
 PS Claim 60; SEQ ID NO 525; 134pp; English.  
 XX  
 CC The invention describes a method of detecting proteins in sample. The  
 CC method comprises: providing a solution of soluble peptide analytes  
 CC produced by denaturation and/or cleavage of several sample proteins, and  
 CC optionally, labeling the collection of peptides by a detectable part;  
 CC contacting the solution with one or more capture agent(s), where each of  
 CC the capture agent(s) is able to specifically recognise and interact with  
 CC a unique recognition sequence (URS) of a reference protein; and detecting  
 CC the binding between one or more of the capture agent(s) and the peptide  
 CC analytes, where the detection of binding between a capture agent and a  
 CC peptide analyte indicates the presence of the reference protein in the  
 CC several of sample proteins. Also described are; and a method of  
 CC quantifying proteins in a biological sample; a method of simultaneously  
 CC detecting several specific proteins in a multi-protein sample. The method  
 CC of the invention is used in clinical or environmental diagnosis, drug  
 CC discovery, protein sequencing and for the detection of a pathogen or  
 CC toxins (such as anthrax toxin, small pox toxin, and cholera toxin). A  
 CC packaged protein detection array is useful for: quantifying various forms  
 CC of post-translationally modified proteins in a biological sample;  
 CC screening large libraries of natural or synthetic compounds to identify  
 CC competitors of natural or non-natural ligands for the capture agent,  
 CC which may be of diagnostic, prognostic, therapeutic or scientific  
 CC interest; and to study the relationship between a subject protein  
 CC expression profile and that subjects response to a foreign compound or  
 CC drug. The methods of assaying differential protein expression are useful  
 CC in the identification and validation of new potential drug targets as  
 CC well as for drug screening. The capture agents are useful for protein  
 CC characterisation, for screening, making prognosis of disease outcomes and  
 CC providing treatment modality suggestion based on the profiling of the  
 CC pathologic cells, prognosis of the outcome of a normal lesion and  
 CC susceptibility of lesions to malignant transformation. The methods  
 CC described are useful for identifying and/or detecting a specific organism  
 CC based on the organisms proteome epitope tag. This is the amino acid  
 CC sequence of a human proteome unique recognition sequence (URS).  
 XX  
 SQ Sequence 5 AA;  
 Query Match 63.2%; Score 24; DB 8; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYW 3  
 Db |||  
 2 GYW 4  
 RESULT 12  
 AAR80643  
 ID AAR80643 standard; peptide; 6 AA.  
 XX  
 AC AAR80643;

XX 25-MAR-2003 (revised)  
 DT 05-MAR-1996 (first entry)  
 XX  
 DE Receptor binding peptide used in a new isolation method.  
 XX  
 KW Protease; vaccine; isolation; diagnosis; receptor; bacteriophage;  
 KW oligonucleotide library.  
 XX  
 OS Synthetic.  
 XX  
 PN USS432018-A.  
 XX  
 PD 11-JUL-1995.  
 XX  
 PF 20-JUN-1991; 91US-00718577.  
 XX  
 PR 20-JUN-1990; 90US-00541108.  
 XX  
 PA (AFPY-) APFYMAX TECHNOLOGIES NV.  
 XX  
 PI Barrett RW, Cwirla SE, Dower WJ;  
 XX  
 XX WPI; 1995-254429/33.  
 DR  
 XX Identification of phage encoding a substrate for a specific protease -  
 PT useful for identification of peptide(s) potentially useful as vaccines,  
 PT therapeutic or diagnostic agents.  
 XX  
 PS Example 3; Col 29; 28pp; English.  
 XX  
 CC AAR80638-R80659 are peptides identified using a new method of peptide  
 CC detection which involves the use of a pre-selected receptor to which the  
 CC peptides bind. The peptides are isolated by screening libraries which may  
 CC be very large. The dissociation rate of the individual peptides can be  
 CC obtained as a measure of the amt. of receptor that binds to each isolate  
 CC as a function of time. The method is used to identify peptides that are  
 CC potentially useful as vaccines or as therapeutic or diagnostic agents,  
 CC i.e. able to bind the pre-selected receptor and act as an agonist or  
 CC antagonist. The new method enables peptides to be isolated without prior  
 CC knowledge of their ligand or receptor structure. (Updated on 25-MAR-2003  
 CC to correct PF field.)  
 XX  
 SQ Sequence 6 AA;  
 Query Match 63.2%; Score 24; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GYW 3  
 Db |||  
 2 GYW 4  
 RESULT 13  
 AAR83934  
 ID AAR83934 standard; peptide; 6 AA.  
 XX  
 AC AAR83934;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE Tyrosine recombinase inhibitory peptide #37.  
 XX  
 KW Tyrosine recombinase; antibacterial; cytostatic; cell growth modulator;  
 KW site-specific DNA recombinase; type I DNA topoisomerase; tumour;  
 KW tyrosine recombinase; cancer; Holliday junction.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200198540-A2.  
 XX  
 PD 27-DEC-2001.

```
XX 21-JUN-2001; 2001WO-US020046.
PF
XX
PR 22-JUN-2000; 2000US-00602087.
XX
XX (UYSA-) UNIV SAN DIEGO STATE FOUND.
XX
XX Segall A, Pinilla C;
XX WPI; 2002-114591/15.
DR
XX
XX
XX Identifying cell growth modulators for inhibiting cancer cell growth in
PT humans, involves assessing and comparing activity of site-specific
PT recombinase or type I DNA topoisomerase in presence/absence of test
PT substance.
XX
XX Claim 39; Page 90; 115pp; English.
PS
XX
XX The method relates to a method of identifying a modulator of cell growth,
CC comprising assessing and comparing the activities of site-specific DNA
CC recombinase (I) or type I DNA topoisomerase (II) in presence and absence
CC of a test substance. A difference in activity of (I) and (II) assessed in
CC the presence and absence of the test substance indicates that the test
CC substance modulates cell growth. The identified cell growth modulator,
CC preferably an inhibitor of (I) or (II), is useful for inhibiting cell
CC growth in a subject, preferably a human. The inhibitor inhibits (I) which
CC is preferably tyrosine recombinase or type I DNA topoisomerase in humans
CC having or suspected of having tumour or cancer, where the method further
CC involves administering an effective of antitumour or anticancer agent or
CC treatment; or who are, or are suspected of being infected by a bacterium,
CC in which case the inhibitor inhibits Holliday junction intermediate
CC resolution activity of tyrosine recombinase. The method further involves
CC administering an effective amount of antibiotic or antibacterium
CC treatment. AAU83898-AAU83991 represents tyrosine recombinase inhibitory
CC peptides of the invention
XX
XX Sequence 6 AA;
SQ
Query Match 63.2%; Score 24; DB 5; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 YWXXXW 7
DB 1 YWCYWW 6
RESULT 14
ABJ37222
ID ABJ37222 standard; peptide; 6 AA.
XX
AC ABJ37222;
XX
XX 08-MAY-2003 (first entry)
XX
XX Rhodopsin related G-protein coupled receptor binding site peptide #98.
XX
XX Compound library; microenvironment; G-protein Coupled Receptor; GPCR;
XX Rhodopsin.
XX
XX Unidentified.
XX
XX WO2003004147-A2.
XX
XX 16-JAN-2003.
XX
XX 05-JUL-2002; 2002WO-GB003094.
XX
XX Rhodopsin related G-protein coupled receptor binding site peptide #102.
XX
XX Compound library; microenvironment; G-protein Coupled Receptor; GPCR;
XX Rhodopsin.
XX
XX Unidentified.
XX
XX WO2003004147-A2.
XX
XX 16-JAN-2003.
XX
XX 05-JUL-2002; 2002WO-GB003094.
XX
XX 06-JUL-2001; 2001GB-00016570.
XX
XX (BIOF-) BIOFOCUS PLC.
XX
XX Crossley R, Rose VS, Stevens AP;
XX WPI; 2003-221549/21.
XX
XX Producing compound library, by generating biological target model using
PT target sequence information, defining microenvironments interacting with
PT ligand and motifs interacting with microenvironment, and assembling
PT motifs.
XX
XX Disclosure; Fig 1; 39pp; English.
PS
XX
XX The invention relates to a novel method for producing a compound library.
CC The novel method involves reducing a biological target into a group of
CC one or more amino acids required for interaction with a ligand, to
CC generate a model of the biological target, using the model to define a
CC microenvironment in the biological target capable of interacting with the
CC ligand, defining motifs which interact with the microenvironment, and
CC assembling the motifs to generate a compound library for screening. The
CC novel method is useful to produce compound libraries for screening
CC natural ligands such as peptides and proteins or for producing chemical
CC compounds based on drug motifs for screening. This sequence represents a
CC peptide of a G-protein Coupled Receptor (GPCR) relating to Rhodopsin,
CC which relates to the novel compound library production method of the
CC invention
XX
XX Sequence 6 AA;
SQ
Query Match 63.2%; Score 24; DB 6; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYW 3
DB 4 GYW 6
RESULT 15
ABJ37226
ID ABJ37226 standard; peptide; 6 AA.
XX
AC ABJ37226;
XX
XX 08-MAY-2003 (first entry)
XX
XX Rhodopsin related G-protein coupled receptor binding site peptide #102.
XX
XX Compound library; microenvironment; G-protein Coupled Receptor; GPCR;
XX Rhodopsin.
XX
XX Unidentified.
XX
XX WO2003004147-A2.
XX
XX 16-JAN-2003.
XX
XX 05-JUL-2002; 2002WO-GB003094.
XX
XX 06-JUL-2001; 2001GB-00016570.
XX
XX (BIOF-) BIOFOCUS PLC.
XX
XX Crossley R, Rose VS, Stevens AP;
XX WPI; 2003-221549/21.
XX
XX Producing compound library, by generating biological target model using
PT target sequence information, defining microenvironments interacting with
PT ligand and motifs interacting with microenvironment, and assembling
PT motifs.
XX
XX Disclosure; Fig 1; 39pp; English.
PS
XX
XX The invention relates to a novel method for producing a compound library.
CC The novel method involves reducing a biological target into a group of
```

CC one or more amino acids required for interaction with a ligand, to  
CC generate a model of the biological target, using the model to define a  
CC microenvironment in the biological target capable of interacting with the  
CC ligand, defining motifs which interact with the microenvironment, and  
CC assembling the motifs to generate a compound library for synthesis. The  
CC novel method is useful to produce compound libraries for screening. The  
CC natural ligands such as peptides and proteins or for producing chemical  
CC compounds based on drug motifs for screening. This sequence represents a  
CC peptide of a G-protein Coupled Receptor (GPCR) relating to Rhodopsin,  
CC which relates to the novel compound library production method of the  
XX invention  
SQ Sequence 6 AA;

Query Match 63.2%; Score 24; DB 6; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GYW 3  
DB 4 GYW 6

Search completed: December 29, 2004, 22:04:19  
Job time : 156 secs

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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:56:54 ; Search time 36 Seconds  
(without alignments)  
12.895 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYXXXXXW 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 58200

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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4: /cgn2.6/prodata/1/iaa/6B COMB.pep:\*  
5: /cgn2.6/prodata/1/iaa/PCUS COMB.pep:\*  
6: /cgn2.6/prodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	63.2	5	US-08-353-400-27	Sequence 27, Appl
2	24	63.2	5	US-08-753-750B-38	Sequence 38, Appl
3	24	63.2	5	5185431-15	Patent No. 5185431
4	24	63.2	6	US-07-718-577-6	Sequence 6, Appl
5	24	63.2	7	US-07-973-235A-30	Sequence 30, Appl
6	24	63.2	7	US-08-443-640-16	Sequence 16, Appl
7	24	63.2	7	US-08-462-720-30	Sequence 30, Appl
8	24	63.2	7	US-09-388-788-2	Sequence 2, Appl
9	24	63.2	7	US-09-069-827A-94	Sequence 94, Appl
10	24	63.2	7	US-09-563-222C-53	Sequence 53, Appl
11	22	57.9	6	US-08-446-345-12	Sequence 12, Appl
12	22	57.9	6	US-08-951-260A-2	Sequence 2, Appl
13	22	57.9	6	US-08-884-569A-11	Sequence 11, Appl
14	22	57.9	6	US-08-884-569A-14	Sequence 14, Appl
15	22	57.9	6	US-09-430-626A-2	Sequence 2, Appl
16	22	57.9	6	US-09-361-096A-46	Sequence 46, Appl
17	22	57.9	6	US-09-743-492A-5	Sequence 5, Appl
18	22	57.9	6	US-10-243-687-2	Sequence 2, Appl
19	22	57.9	7	US-08-652-971-5	Sequence 5, Appl
20	22	57.9	7	US-08-991-258A-5	Sequence 5, Appl
21	22	57.9	7	US-08-769-399-5	Sequence 2, Appl
22	22	57.9	7	US-08-991-953A-5	Sequence 5, Appl
23	21	55.3	5	5217869-38	Patent No. 5217869
24	21	55.3	7	US-09-082-279B-653	Sequence 653, App
25	21	55.3	7	US-09-315-304B-653	Sequence 653, App
26	21	55.3	7	US-09-315-304B-1579	Sequence 1579, App
27	21	55.3	7	US-09-350-325-39	Sequence 39, Appl

28	21	55.3	7	4	US-09-834-784-653	Sequence 653, App
29	21	55.3	7	4	US-09-515-965A-653	Sequence 653, App
30	21	55.3	7	4	US-09-350-641C-653	Sequence 653, App
31	21	55.3	7	4	US-09-350-641C-1579	Sequence 1579, App
32	21	55.3	7	4	US-09-350-841A-653	Sequence 653, App
33	20	52.6	5	2	US-08-480-434-22	Sequence 22, Appl
34	20	52.6	5	2	US-08-480-434-31	Sequence 31, Appl
35	20	52.6	5	2	US-08-053-451B-22	Sequence 22, Appl
36	20	52.6	5	2	US-08-053-451B-31	Sequence 31, Appl
37	20	52.6	5	6	5217869-8	Patent No. 5217869
38	20	52.6	5	6	5217869-14	Patent No. 5217869
39	20	52.6	6	1	US-07-718-577-2	Sequence 2, Appl
40	20	52.6	6	1	US-07-718-577-10	Sequence 10, Appl
41	20	52.6	6	1	US-07-973-235A-29	Sequence 29, Appl
42	20	52.6	6	1	US-08-487-006-67	Sequence 67, Appl
43	20	52.6	6	1	US-08-487-006-88	Sequence 88, Appl
44	20	52.6	6	2	US-08-462-720-29	Sequence 29, Appl
45	20	52.6	6	2	US-08-488-659A-67	Sequence 67, Appl

## ALIGNMENTS

RESULT 1  
US-08-353-400-27  
; Sequence 27, Application US/08353400  
; Patent No. 5665357  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 37  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION NUMBER: US/08/353,400  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9324819.3  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9411089.7  
; FILING DATE: 03-JUN-1994  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-353-400-27

Query Match 63.2%; Score 24; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 1 GYW 3

RESULT 2  
US-08-753-750B-38  
; Sequence 38, Application US/08753750B  
; Patent No. 6610506  
; GENERAL INFORMATION:  
; APPLICANT: Lo, Reggie Y.C.  
; APPLICANT: Schryvers, Anthony B.  
; APPLICANT: Potter, Andrew A.  
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF

```
; TITLE OF INVENTION: PASTEURILLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PASTSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Pasteurella haemolytica
US-08-753-750B-38

Query Match          63.2%; Score 24; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYW 3
        |||
Db      3 GYW 5

RESULT 3
5185431-15
;PATENT NO. 5185431
; APPLICANT: YOSHIMATSU, KENTARO;SHIKATA, YASUSHI;TANAKA, ISAO;
; HASEGAWA, YOSHIKAZU;SETO, TOSHIO;OSAWA, TOSHIO
; TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392,841
; FILING DATE: 11-AUG-1989
; SEQ ID NO:15;
; LENGTH: 5
5185431-15

Query Match          63.2%; Score 24; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYW 3
        |||
Db      2 GYW 4

RESULT 4
US-07-718-577-6
; Sequence 6, Application US/07718577
; Patent No. 5432018
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Cwiria, Steven E.
; APPLICANT: Barrett, Ronald W.
; TITLE OF INVENTION: PEPTIDE LIBRARY AND
; TITLE OF INVENTION: SCREENING SYSTEMS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Stuart Street
; STREET: Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/07/718,577
; FILING DATE: 19910620
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/541,108
; FILING DATE: 20-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-25-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-718-577-6

Query Match          63.2%; Score 24; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GYW 3
        |||
Db      2 GYW 4

RESULT 5
US-07-973-235A-30
; Sequence 30, Application US/07973235A
; Patent No. 5491130
; GENERAL INFORMATION:
; APPLICANT: David D. Roberts, et al.
; TITLE OF INVENTION: Peptide Inhibitors of Fibronection and
; TITLE OF INVENTION: Related Collagen-Binding Proteins
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,235A
; FILING DATE: 19921110
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert L. Price
; REGISTRATION NUMBER: 22,695
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)684-1111
; TELEFAX: (703)684-1124
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: AMINO ACIDS
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-973-235A-30

Query Match          63.2%; Score 24; DB 1; Length 7;
Best Local Similarity 42.9%; Pred. No. 3.8e+05;
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Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
| | |  
Db 1 GWSKSW 7

## RESULT 6

US-08-443-640-16  
; Sequence 16, Application US/08443640  
; Patent No. 5691140  
; GENERAL INFORMATION:  
; APPLICANT: NOREN, CHRISTOPHER J.  
; APPLICANT: EVANS, PAUL D.  
; TITLE OF INVENTION: BIDIRECTIONAL IN VITRO TRANSCRIPTION  
; TITLE OF INVENTION: VECTORS UTILIZING A SINGLE RNA POLYMERASE FOR BOTH  
; TITLE OF INVENTION: DIRECTIONS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NEW ENGLAND BIOLABS, INC  
; STREET: 32 TOZER ROAD  
; CITY: BEVERLY  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 01915  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/443,640  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILLIAMS, GREGORY D.  
; REGISTRATION NUMBER: 30901  
; REFERENCE/DOCKET NUMBER: NEB-102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508) 927-5054  
; TELEFAX: (508) 927-1705  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-443-640-16

Query Match 63.2%; Score 24; DB 1; Length 7;  
Best Local Similarity 42.9%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
| | |  
Db 1 GWSKSW 7

## RESULT 7

US-08-462-720-30  
; Sequence 30, Application US/08462720  
; Patent No. 5849701  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, David D.  
; APPLICANT: Kruttsch, Henry C.  
; APPLICANT: Sipes, John M.  
; APPLICANT: Guo, Neng-hua  
; APPLICANT: Negre, Eric  
; TITLE OF INVENTION: Peptide Inhibitors of Fibronectin and  
; TITLE OF INVENTION: Related Collagen-Binding Proteins  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/462,720  
FILING DATE: 05-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 015280-0231100US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-462-720-30

Query Match 63.2%; Score 24; DB 2; Length 7;  
Best Local Similarity 42.9%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
| | |  
Db 1 GWSKSW 7

## RESULT 8

US-09-388-788-2  
; Sequence 2, Application US/09388788  
; Patent No. 6429359  
; GENERAL INFORMATION:  
; APPLICANT: LAMPPA, GAYLE  
; TITLE OF INVENTION: PRODUCTION OF CELLULOSE IN PLASTIDS OF TRANSGENIC  
; TITLE OF INVENTION: PLANTS  
; FILE REFERENCE: 21459/90301  
; CURRENT APPLICATION NUMBER: US/09/388,788  
; CURRENT FILING DATE: 1999-09-02  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein  
; OTHER INFORMATION: Construct  
US-09-388-788-2

Query Match 63.2%; Score 24; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYX 3  
| | |  
Db 5 GYW 7

## RESULT 9

US-09-069-827A-94

```

RESULT 10
:
: US-09-563-222C-53
: Sequence 53, Application US/09563222C
: Patent No. 6696620
: GENERAL INFORMATION:
:
: APPLICANT: EPICYTE PHARMACEUTICALS, INC.
:
: APPLICANT: HIAFT, ANDREW C.
:
: APPLICANT: HEIN, MICHAEL B.
:
: TITLE OF INVENTION: IMMUNOGLOBULIN BINDING
:
: FILE REFERENCE: 068904-0501
:
: CURRENT APPLICATION NUMBER: US/09/563,222C
:
: CURRENT FILING DATE: 2000-05-02
:
: PRIOR APPLICATION NUMBER: PCT/US01/14349
:
: PRIOR FILING DATE: 2001-05-02
:

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Qy	2	YWXXXW	7
		:	
Db	1	FWXXMW	6

RESULT 12  
US-08-951-260A-2  
; Sequence 2, Application US/08951260A  
; Patent No. 6004791  
; GENERAL INFORMATION:  
; APPLICANT: Aoki, Naohito  
; APPLICANT: Ullrich, Axel  
; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20  
; TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: FastSeq for Windows 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/951,260A  
; FILING DATE: October 16, 1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/030,860  
; FILING DATE: No. 6004791 September 13, 1996  
; APPLICATION NUMBER: PCT/1897/00946  
; FILING DATE: June 17, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warburg, Richard J.  
; REGISTRATION NUMBER: 32,327  
; REFERENCE/DOCKET NUMBER: 227/004  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:  
; OTHER INFORMATION: "Xaa" in positions 3 and 5 stand  
; OTHER INFORMATION: for an unspecified amino acid.  
US-08-951-260A-2

Query Match 57.9%; Score 22; DB 3; Length 6;  
Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
: || ||  
Db 1 FWRMXW 6

RESULT 13  
US-08-884-569A-11  
; Sequence 11, Application US/08884569A  
; Patent No. 6399326  
; GENERAL INFORMATION:  
; APPLICANT: CHIANG, MING-KO  
; APPLICANT: FLANAGAN, JOHN G.  
; TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO  
; FILE REFERENCE: HMV-020.01

; CURRENT APPLICATION NUMBER: US/08/884,569A  
; CURRENT FILING DATE: 1997-06-27  
; PRIOR APPLICATION NUMBER: 60/021,040  
; PRIOR FILING DATE: 1996-07-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)  
; OTHER INFORMATION: Ile or Val  
US-08-884-569A-11

Query Match 57.9%; Score 22; DB 3; Length 6;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
: || ||  
Db 1 FWRMXW 6

RESULT 14  
US-08-884-569A-14  
; Sequence 14, Application US/08884569A  
; Patent No. 6399326  
; GENERAL INFORMATION:  
; APPLICANT: CHIANG, MING-KO  
; APPLICANT: FLANAGAN, JOHN G.  
; TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO  
; FILE REFERENCE: HMV-020.01  
; CURRENT APPLICATION NUMBER: US/08/884,569A  
; CURRENT FILING DATE: 1997-06-27  
; PRIOR APPLICATION NUMBER: 60/021,040  
; PRIOR FILING DATE: 1996-07-02  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
; NAME/KEY: MOD\_RES  
; LOCATION: (3)  
; OTHER INFORMATION: Arg or Gln  
; NAME/KEY: MOD\_RES  
; LOCATION: (5)  
; OTHER INFORMATION: Ile or Val  
US-08-884-569A-14

Query Match 57.9%; Score 22; DB 3; Length 6;  
Best Local Similarity 66.7%; Pred. No. 3.8e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
: || ||  
Db 1 FWRMXW 6

RESULT 15  
US-09-430-626A-2  
; Sequence 2, Application US/09430626A  
; Patent No. 6482605  
; GENERAL INFORMATION:  
; APPLICANT: Aoki, Naohito  
; APPLICANT: Ullrich, Axel

;; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20  
;; AND RELATED PRODUCTS AND METHODS  
;;  
;; NUMBER OF SEQUENCES: 7  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street  
;; Suite 4700  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071-2066  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; storage  
;;  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: FastSeq for Windows 2.0  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/430,626A  
;; FILING DATE: 29-Oct-1999  
;; CLASSIFICATION: <Unknown>  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/951,260  
;; FILING DATE: October 16, 1997  
;; APPLICATION NUMBER: 60/030,860  
;; FILING DATE: No. 6482605ember 13, 1996  
;; APPLICATION NUMBER: PCT/1897/00946  
;; FILING DATE: June 17, 1997  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard J.  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 227/004  
;;  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;;  
;; INFORMATION FOR SEQ ID NO: 2:  
;;  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;;  
;; MOLECULE TYPE: peptide  
;;  
;; FEATURE:  
;;  
;; OTHER INFORMATION: "Xaa" in positions 3 and 5 stand  
;; for an unspecified amino acid.  
;;  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-430-626A-2

Query Match 57.9%; Score 22; DB 4; Length 6;  
Best Local Similarity 66.7%; Pred No. 3.8e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YWXXW 7  
: |||  
Db 1 FWXW 6

Search completed: December 29, 2004, 22:08:13  
Job time : 37 secs

**F**

## SUMMARIES

## ALIGNMENTS

```

US-10-046-922-67
; Sequence 67, Application US/10045922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGF-3 INHIBITOR MAT
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being predicted and is derived by analysis of the total score distribution.



QY 1 GYW 3  
|||  
Db 1 GYW 3

## RESULT 5

US-10-712-425-525  
; Sequence 525, Application US/10712425  
; Publication No. US20040180380A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, FRANK D.  
; APPLICANT: MENG, XUN  
; APPLICANT: LIVINGSTON, DAVID  
; TITLE OF INVENTION: PROTEOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN  
; TITLE OF INVENTION: MODIFICATION ANALYSIS  
; FILE REFERENCE: ENGR-P02-001  
; CURRENT APPLICATION NUMBER: US/10/712,425  
; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/379,626  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/393,137  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,197  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,211  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,223  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,233  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,235  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,280  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/430,948  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/433,319  
; PRIOR FILING DATE: 2002-12-13  
; Remaining prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1386  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 525  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Homo sapiens

## US-10-712-425-525

Query Match 63.2%; Score 24; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 2 GYW 4

## RESULT 6

US-10-418-943-48  
; Sequence 48, Application US/10418943  
; Publication No. US2004002441A1  
; GENERAL INFORMATION:  
; APPLICANT: Segall, Anca  
; APPLICANT: Pinilla, Clemencia  
; TITLE OF INVENTION: RECOMBINATION MODULATORS AND METHODS  
; TITLE OF INVENTION: FOR PRODUCING AND USING THE SAME  
; FILE REFERENCE: 011443 008-999  
; CURRENT APPLICATION NUMBER: US/10/418,943  
; CURRENT FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: 09/602,087  
; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 48  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-418-943-48

Query Match 63.2%; Score 24; DB 15; Length 6;  
Best Local Similarity 50.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXW 7  
|||  
Db 1 YWCYW 6

## RESULT 7

US-10-346-737A-45  
; Sequence 45, Application US/10346737A  
; Publication No. US20040142379A1  
; GENERAL INFORMATION:  
; APPLICANT: St. Hilaire, Phaedria  
; TITLE OF INVENTION: AFFINITY FISHING FOR LIGANDS AND PROTEIN RECEPTORS  
; FILE REFERENCE: 11225.16US01  
; CURRENT APPLICATION NUMBER: US/10/346,737A  
; CURRENT FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 45  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide  
US-10-346-737A-45

Query Match 63.2%; Score 24; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 4 GYW 6

## RESULT 8

US-09-884-767A-38  
; Sequence 38, Application US/09884767A  
; Publication No. US20020192789A1  
; GENERAL INFORMATION:  
; APPLICANT: DYAX Corp.  
; APPLICANT: Ley, Arthur C.  
; APPLICANT: Luneau, Christopher J.  
; APPLICANT: Ladner, Robert C.  
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES  
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT  
; CURRENT APPLICATION NUMBER: US/09/884,767A  
; CURRENT FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 09/597,321  
; PRIOR FILING DATE: 2000-06-19  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic enterokinase cleavage sequence  
US-09-884-767A-38

Query Match 63.2%; Score 24; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
|||  
Db 1 GYW 3

## RESULT 9

US-09-563-222-53  
; Sequence 53, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222-53

Query Match 63.2%; Score 24; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
|||  
Db 2 GYW 4

## RESULT 10

US-10-403-938-27  
; Sequence 27, Application US/10403938  
; Publication No. US20040025195A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,  
; FILE REFERENCE: D0227 NP  
; CURRENT APPLICATION NUMBER: US/10/403,938  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: U.S. 60/368,422  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-403-938-27

Query Match 63.2%; Score 24; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
|||  
Db 3 GYW 5

## RESULT 11

US-10-475-853-6  
; Sequence 6, Application US/10475853  
; Publication No. US20040121442A1  
; GENERAL INFORMATION:  
; APPLICANT: Chet, Ilan  
; APPLICANT: Viterbo, Ada  
; TITLE OF INVENTION: RECOMBINANT FUNGAL CHITINASES, POLYNUCLEOTIDE SEQUENCES ENCODING  
; TITLE OF INVENTION: PROMOTERS OF SAME AND USES THEREOF

; FILE REFERENCE: 27049  
; CURRENT APPLICATION NUMBER: US/10/475,853  
; CURRENT FILING DATE: 2003-11-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: peptide derived from chit36  
US-10-475-853-6

Query Match 63.2%; Score 24; DB 16; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
|||  
Db 1 GYW 3

## RESULT 12

US-10-783-950-53  
; Sequence 53, Application US/10783950  
; Publication No. US20040199945A1  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; APPLICANT: HEIN, MICH B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/10/783,950  
; CURRENT FILING DATE: 2004-02-19  
; PRIOR APPLICATION NUMBER: US/09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02  
; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 53  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-783-950-53

Query Match 63.2%; Score 24; DB 17; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
|||  
Db 2 GYW 4

## RESULT 13

US-10-858-271-10  
; Sequence 10, Application US/10858271  
; Publication No. US20040259829A1  
; GENERAL INFORMATION:  
; APPLICANT: Danks, Mary K.  
; APPLICANT: Potter, Philip M.  
; APPLICANT: Houghton, Peter J.  
; TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of  
; TITLE OF INVENTION: Tumor Cells  
; FILE REFERENCE: SJ-0005  
; CURRENT APPLICATION NUMBER: US/10/858,271  
; CURRENT FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: US/09/595,682  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: 60/075,258

;; PRIOR FILING DATE: 1998-02-19  
;; PRIOR APPLICATION NUMBER: PCT/US99/03171  
;; PRIOR FILING DATE: 1999-02-12  
;; NUMBER OF SEQ ID NOS: 30  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 10  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Oryctolagus cuniculus  
US-10-858-271-10

Query Match 60.5%; Score 23; DB 17; Length 7;  
Best Local Similarity 33.3%; Pred. No. 1.5e+06;  
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXW 7  
DB 2 FTWELW 7

RESULT 14  
US-10-243-613-84  
;; Sequence 84, Application US/10243613  
;; Publication No. US20040053823A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Smith, Jeffrey W.  
;; APPLICANT: Chen, Emily I.  
;; APPLICANT: Kridel, Steven J.  
;; TITLE OF INVENTION: Selective Substrates for Matrix  
;; TITLE OF INVENTION: Metalloproteinases  
;; FILE REFERENCE: P-LJ 5432  
;; CURRENT APPLICATION NUMBER: US/10/243,613  
;; CURRENT FILING DATE: 2002-09-13  
;; PRIOR APPLICATION NUMBER: US 09/953,592  
;; PRIOR FILING DATE: 2001-09-14  
;; NUMBER OF SEQ ID NOS: 129  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 84  
;; LENGTH: 5  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: synthetic construct  
US-10-243-613-84

Query Match 57.9%; Score 22; DB 15; Length 5;  
Best Local Similarity 40.0%; Pred. No. 1.5e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 WXXW 7  
DB 1 WTSSW 5

RESULT 15  
US-10-087-993-1  
;; Sequence 1, Application US/10087993  
;; Publication No. US20020169303A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ullrich, Axel  
;; Aoki, Naohito  
;; Kim, Yeong Woong  
;; Wang, Hong Yang  
;; Chen, Zhengjun  
;; Naylor, Oliver  
;; Kharitonov, Alexei Igorevich  
;; TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDPL, CLK,  
;; AND SIRP POLYPEPTIDES AND RELATED  
;; PRODUCTS AND METHODS  
;; NUMBER OF SEQUENCES: 38  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Lyon & Lyon  
;; STREET: 633 West Fifth Street

;; Suite 4700  
;; CITY: Los Angeles  
;; STATE: California  
;; COUNTRY: U.S.A.  
;; ZIP: 90071-2066  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
;; storage  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: IBM P.C. DOS 5.0  
;; SOFTWARE: FastSeq for Windows 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/10/087,993  
;; FILING DATE: 05-Mar-2002  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/877,150  
;; FILING DATE: June 17, 1997  
;; APPLICATION NUMBER: U.S. 60/019,629  
;; FILING DATE: June 17, 1996  
;; APPLICATION NUMBER: U.S. 60/023,485  
;; FILING DATE: August 9, 1996  
;; APPLICATION NUMBER: U.S. 60/030,860  
;; FILING DATE: No. US20020169303A1ember 13, 1996  
;; APPLICATION NUMBER: U.S. 60/034,286  
;; FILING DATE: December 19, 1996  
;; APPLICATION NUMBER: U.S. 60/030,964  
;; FILING DATE: No. US20020169303A1ember 15, 1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Warburg, Richard J.  
;; REGISTRATION NUMBER: 32,327  
;; REFERENCE/DOCKET NUMBER: 225/298  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (213) 489-1600  
;; TELEFAX: (213) 955-0440  
;; TELEX: 67-3510  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; FEATURE:  
;; OTHER INFORMATION: "Xaa" in positions 3 and 5 stands  
;; for an unspecified amino acid.  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-10-087-993-1

Query Match 57.9%; Score 22; DB 13; Length 6;  
Best Local Similarity 66.7%; Pred. No. 1.5e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YWXXW 7  
DB 1 FWXW 6

Search completed: December 29, 2004, 22:13:17  
JOB time : 142 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:57:34 ; Search time 38 Seconds  
(without alignments)  
17.724 Million cell updates/sec

Title: US-10-046-922-67

Perfect score: 38  
Sequence: 1 GYWXXXW 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216783 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	52.6	5	2 JH0253	gut pentapeptide -
2	15	39.5	6	2 PT0532	T-cell receptor be
3	14	36.8	6	2 B35640	cerebellar degener
4	14	36.8	6	2 PT0629	T-cell receptor be
5	14	36.8	7	2 S21230	dermorphin (trp-4,
6	14	36.8	7	2 PT0728	T-cell receptor be
7	14	36.8	7	2 S33567	tubulin beta-3 cha
8	13	34.2	4	2 S09478	globulin IV alpha
9	13	34.2	6	2 A61411	ameletin - rat
10	13	34.2	7	1 A61324	dermorphin - Rohde
11	13	34.2	7	2 A60139	fatty-acid synthas
12	13	34.2	7	2 S71870	glutathione transf
13	13	34.2	7	2 S36662	dermorphin (lys-7)
14	11	28.9	3	3 F37196	bradykinin-potenti
15	11	28.9	4	2 A34626	RPCH-related neuro
16	11	28.9	4	2 B53284	T-cell receptor be
17	11	28.9	4	2 PT0661	T-cell receptor be
18	11	28.9	5	2 A32516	cholecystokinin-5
19	11	28.9	5	2 A60803	neuropeptide - sea
20	11	28.9	5	2 PT0281	Ig heavy chain CRD
21	11	28.9	5	2 PT0308	Ig heavy chain CRD
22	11	28.9	5	2 PT0729	T-cell receptor be
23	11	28.9	5	2 PT0580	T-cell receptor be
24	11	28.9	5	2 G37196	bradykinin-potenti
25	11	28.9	6	2 S66195	alcohol dehydrogen
26	11	28.9	6	2 B34835	dnaA protein - Pse
27	11	28.9	6	2 A31263	dihydrofolate redu
28	11	28.9	6	2 B31263	dihydrofolate redu
29	11	28.9	6	2 PT0519	T-cell receptor be

30 11 28.9 6 2 PT0637 T-cell receptor be  
31 11 28.9 6 2 PT0641 T-cell receptor be  
32 11 28.9 6 2 PT0726 T-cell receptor be  
33 11 28.9 6 2 F41946 T-cell receptor qa  
34 11 28.9 6 2 PD0028 pev-kinin 2 - pena  
35 11 28.9 6 2 A61068 locustakinin - mlg  
36 11 28.9 6 4 I79564 hypothetical TCL3  
37 11 28.9 7 2 S09652 hypothetical prote  
38 11 28.9 7 2 PQ0727 H2 class I protein  
39 11 28.9 7 2 E48394 glycoprotein compo  
40 11 28.9 7 2 PH1602 Ig H chain V-D-J r  
41 11 28.9 7 2 PT0526 T-cell receptor be  
42 11 28.9 7 2 PT0628 T-cell receptor be  
43 11 28.9 7 2 PT0642 T-cell receptor be  
44 11 28.9 7 2 PT0722 T-cell receptor be  
45 11 28.9 7 2 PT0688 T-cell receptor be

#### ALIGNMENTS

##### RESULT 1

JH0253  
gut pentapeptide - Japanese eel  
C:Species: Anguilla japonica (Japanese eel)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C:Accession: JH0253  
R:Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A>Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
A:Reference number: JH0253; MUID:92062113; PMID:1953755  
A:Accession: JH0253  
A:Molecule type: protein  
A:Residues: 1-5 <UES>  
A:Experimental source: gut  
C:Comment: This peptide increased basal tone of the circular muscle of the esophagogastric  
, and of the circular muscle of the gastro-intestinal junction.

Query Match 52.6%; Score 20; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|:  
Db 1 GFW 3

##### RESULT 2

PT0532  
T-cell receptor beta chain V-D-J region (100-4AJ) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0532  
R:Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991

A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0532  
A>Status: translation not shown

A:Molecule type: mRNA  
A:Residues: 1-6 <FEE>  
A:Experimental source: adult thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 39.5%; Score 15; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYW 3  
|:  
Db 4 GYW 6

RESULT 3  
B35640  
cerebellar degeneration-related protein - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 24-Jun-1993  
C;Accession: B35640  
R;Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.H.  
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990  
A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal marker  
A;Reference number: A35640; MUID:90222173; PMID:2336268  
A;Accession: B35640  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-6 <CHE>

Query Match 36.8%; Score 14; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YW 3  
:|  
Db 1 FW 2

RESULT 4  
PT0629  
T-cell receptor beta chain V-D-J region (100-2AH) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0629; PT0528  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0629  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <PEE>  
A;Experimental source: newborn thymus, strain BALB/c, clone 100-2AH  
A;Accession: PT0528  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-6 <PE2>  
A;Experimental source: adult thymus, strain BALB/c, clone 100-4AB  
C;Keywords: T-cell receptor

Query Match 36.8%; Score 14; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYW 3  
:|  
Db 3 GDW 5

RESULT 5  
S21230  
dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)  
C;Species: Phyllomedusa bicolor (two-colored leaf frog)  
C;Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 18-Aug-2000  
C;Accession: S21230  
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.  
FEBS Lett. 302, 151-154, 1992  
A;Title: Identification and characterization of two dermorphins from skin extracts of the  
A;Reference number: S21152; MUID:92339502; PMID:1633846  
A;Accession: S21230  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <MIG>  
C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 36.8%; Score 14; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YW 3  
:|  
Db 3 FW 4

RESULT 6  
PT0728  
T-cell receptor beta chain V-D-J region (161-2H) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C;Accession: PT0728  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0728  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-7 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c  
C;Keywords: T-cell receptor

Query Match 36.8%; Score 14; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYW 3  
:|  
Db 3 GDW 5

RESULT 7  
S33567  
tubulin beta-3 chain - fruit fly (Drosophila melanogaster) (fragment)  
C;Species: Drosophila melanogaster  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C;Accession: S33567  
R;Hinz, U.; Wolk, A.; Renkawitz-Pohl, R.  
Development 116, 543-554, 1992  
A;Title: Ultrathorax is a regulator of beta-3 tubulin expression in the Drosophila vis  
A;Reference number: S33567; MUID:93170162; PMID:1363225  
A;Accession: S33567  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-7 <HIN>  
A;Cross-references: UNIPROT:P08841; EMBL:X68393; NID:g7669; PIDN:CAA48459.1; PID:g4377448  
C;Genetics:  
A;Gene: FlyBase:beta-Tub60D  
A;Cross-references: FlyBase:FBgn0003888  
A;Introns: 5/3

Query Match 36.8%; Score 14; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YW 3  
:|  
Db 6 FW 7

RESULT 8  
S09478  
globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)  
N;Alternate names: 11S globulin alpha subunit gamma chain  
C;Species: Cucurbita sp. (cucurbit)  
C;Date: 21-Nov-1993 #sequence\_revision 08-Nov-1996 #text\_change 08-Nov-1996  
C;Accession: S09478  
R;Ohmura, M.; Hara, I.; Matsubara, H.  
Plant Cell Physiol. 21, 157-167, 1980  
A;Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and  
A;Reference number: S09066

A:Accession: S09478  
A:Molecule type: protein  
A:Residues: 1-4 <OHM>

Query Match 34.2%; Score 13; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
||  
Db 3 GY 4

## RESULT 9

A61411  
ameletin - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 18-Aug-2000  
C:Accession: A61411  
R:Burzynski, S.R.  
Anal. Biochem. 70, 359-365, 1976  
A:Title: Sequential analysis in subnanomolar amounts of peptides. Determination of the  
A:Reference number: A61411, MUID:76182447; PMID:1267130  
A:Accession: A61411  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-6 <BUR>  
C:Superfamily: unassigned animal peptides  
C:Keywords: pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 34.2%; Score 13; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
||  
Db 3 GY 4

## RESULT 10

A61324  
dermorphin - Rohde's leaf frog  
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)  
C:Date: 17-Jul-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C:Accession: A61324  
R:Montecucchi, P.C.; De Castiglione, R.; Erspamer, V.  
Int. J. Pept. Protein Res. 17, 316-321, 1981  
A:Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Braz  
A:Reference number: A61324; MUID:82029915; PMID:7287302  
A:Accession: A61324  
A:Molecule type: protein  
A:Residues: 1-7 <MON>  
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology  
C:Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin  
F:2/Modified site: D-alanine (Ala) #status experimental  
F:6/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental  
F:7/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 34.2%; Score 13; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
||  
Db 4 GY 5

## RESULT 11

A60139  
fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 26-May-2000

C:Accession: A60139

R:Hardie, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.  
Biochim. Biophys. Acta 828, 380-382, 1985

A:Title: Amino acid sequence around the reactive serine residue of the thioesterase domain

A:Reference number: A60139; MUID:85175165; PMID:3921056

A:Accession: A60139

A:Molecule type: protein

A:Residues: 1-7 <HAR>

C:Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homol  
ydrolase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein] S-n

C:Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enzy  
F:5/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) #status experimental

Query Match 34.2%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
||  
Db 3 GY 4

## RESULT 12

S71870  
glutathione transferase (EC 2.5.1.18) class mu 9 - pig (fragment)  
N:Alternate names: glutathione S-transferase class mu 9  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 19-Mar-1998 #sequence\_revision 13-Sep-1998 #text\_change 07-May-1999  
C:Accession: S71870  
R:Aouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.  
Biochem. J. 317, 879-884, 1996  
A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospra  
A:Reference number: S71864; MUID:96332484; PMID:8760377  
A:Accession: S71870  
A:Molecule type: protein  
A:Residues: 1-7 <ROU>  
C:Comment: At least five species-independent classes of cytosolic glutathion transferase  
s mitochondrial form are known.  
C:Complex: dimer  
C:Function:  
A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a v  
A:Pathway: detoxification; xenobiotics metabolism  
A>Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism  
es of damage  
C:Superfamily: glutathione transferase  
C:Keywords: acetylated amino end; blocked amino end; dimer; transferase  
F:1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 34.2%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
||  
Db 5 GY 6

## RESULT 13

S36662  
dermorphin (Iys-7) [validated] - two-colored leaf frog  
C:Species: Phyllomedusa bicolor (two-colored leaf frog)  
C:Date: 10-Dec-1993 #sequence\_revision 13-Mar-1997 #text\_change 18-Aug-2000  
C:Accession: S36662  
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.;  
FEBS Lett. 302, 151-154, 1992  
A:Title: Identification and characterization of two dermorphins from skin extracts of the  
A:Reference number: S21152; MUID:92339502; PMID:1633846  
A:Accession: S36662  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <MIG>  
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 34.2%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2  
|  
Db 4 GY 5

## RESULT 14

F37196  
bradykinin-potentiating peptide 6 - island jararaca  
C:Species: Bothrops insularis (island jararaca)  
C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C:Accession: F37196  
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A:Title: Primary structure and biological activity of bradykinin potentiating peptides 6  
A:Reference number: A37196; MUID:90351557; PMID:2386615  
A:Accession: F37196  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-3 <CIN>  
C:Keywords: pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 28.9%; Score 11; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 W 3  
|  
Db 3 W 3

## RESULT 15

A34626  
RPCH-related neuropeptide - ferruginous spindle  
C:Species: Fusinus ferrugineus (ferruginous spindle)  
C:Date: 06-Jul-1990 #sequence\_revision 06-Jul-1990 #text\_change 31-Dec-1993  
C:Accession: A34626  
R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;  
Biochem. Biophys. Res. Commun. 167, 273-279, 1990  
A:Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.  
A:Reference number: A34626; MUID:90179762; PMID:2310394  
A:Accession: A34626  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-4 <KUR>  
C:Keywords: neuropeptide

Query Match 28.9%; Score 11; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 W 3  
|  
Db 4 W 4

Search completed: December 29, 2004, 22:08:58  
Job time : 39 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:43:03 ; Search time 188 Seconds  
(without alignments)  
21.424 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYXXXXX 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 167

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	50.0	5	1 UF01_MOUSE	P38639 mus musculus
2	16	42.1	7	2 Q9BRY4	Q9bry4 homo sapien
3	15	39.5	4	1 OCP3_OCTMI	P58649 octopus min
4	11	28.9	2	1 GWA_SEPOF	P83570 sepiia offic
5	11	28.9	5	1 BPP7_BOTIN	P30425 bothrops in
6	11	28.9	6	1 EI01_LITRU	P82096 litoria rub
7	11	28.9	6	1 LOK1_LOCFI	P41491 locusta mig
8	11	28.9	7	1 BRHP_CONIM	P58803 conus imper
9	11	28.9	7	1 TPFY_PACDA	P83455 pachymedusa
10	11	28.9	7	1 TY51_LITRU	P82065 litoria rub
11	11	28.9	7	1 WWA1_ACHFU	P35919 achatina fu
12	11	28.9	7	1 WWA2_ACHFU	P35920 achatina fu
13	11	28.9	7	1 WWA3_ACHFU	P35921 achatina fu
14	11	28.9	7	2 Q95945	Q95945 saccharomyc
15	11	28.9	7	2 Q49223	Q49223 glycine max
16	11	28.9	7	2 Q8GL00	Q8gl00 borrelia bu
17	11	28.9	7	2 Q8GL04	Q8gl04 borrelia bu
18	11	28.9	7	2 Q8KMS9	Q8kms9 enterobacte
19	11	28.9	7	2 Q8JEB1	Q8jeb1 human immun
20	10	26.3	5	1 PAP2_PARMA	P81864 pardachirus
21	10	26.3	5	1 RE32_LITRU	P82073 litoria rub
22	9	23.7	4	1 ACH1_ACHFU	P35904 achatina fu
23	9	23.7	4	1 OCP1_OCTMI	P58648 octopus min
24	8	21.1	3	1 GRWV_HUMAN	P01157 homo sapien
25	8	21.1	4	1 DCML_PSECH	P19916 pseudomonas
26	8	21.1	7	2 P82445	P82445 nicotiana t
27	7	18.4	4	1 FAR3_HIRME	P42562 hirudo medi
28	7	18.4	4	1 FAR4_HIRME	P42563 hirudo medi
29	7	18.4	4	1 FYR1_ATEL	P58706 anthopleura
30	7	18.4	4	2 Q96AT0	Q96at0 homo sapien
31	7	18.4	5	1 AL14_CARMA	P81817 carcinus ma

32	7	18.4	5	1 FARP_ARTTR	P41853 artiopesthi
33	7	18.4	5	1 PRCT_PERAM	P01373 periplaneta
34	7	18.4	5	1 PSK_DAUCA	P58261 daucus caro
35	7	18.4	6	1 ASP2_LACSN	P82655 lactobacill
36	7	18.4	6	1 OVM_LEPDE	P42985 leptinotars
37	7	18.4	7	1 ALI2_CARMA	P81805 carcinus ma
38	7	18.4	7	1 ALL3_CARMA	P81806 carcinus ma
39	7	18.4	7	1 ALL4_CARMA	P81807 carcinus ma
40	7	18.4	7	1 ALI5_CARMA	P81808 carcinus ma
41	7	18.4	7	1 ALL7_CVDPO	P82158 cydia pomon
42	7	18.4	7	1 ASCL_ALLAS	P84071 allium asca
43	7	18.4	7	1 EI05_LITRU	P82101 litoria rub
44	7	18.4	7	1 FAR2_ASCSU	P31890 ascaris suu
45	7	18.4	7	1 FAR3_HAECC	P81298 haemonchus

ALIGNMENTS

RESULT 1  
UF01\_MOUSE STANDARD; PRT; 5 AA.  
AC P38639;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Fibroblast;  
RX MEDLINE=95009907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins using  
RT preparative two-dimensional gel electrophoresis.";  
RL Electrophoresis 15:735-745(1994).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 6.6, its MW is: 19 kDa.  
KW Direct protein sequencing.  
FT NON\_TER 5  
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;  
  
Query Match 50.0%; Score 19; DB 1; Length 5;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06; Mismatches 3; Indels 0; Gaps 0;  
Matches 2; Conservative 0;  
  
QY 3 WXXXW 7  
Db 1 WIGRW 5  
  
RESULT 2  
Q9BRY4 PRELIMINARY; PRT; 7 AA.  
AC Q9BRY4;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE SQSTM1 protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=23388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzley D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blackley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC005857; AAH05857.3; -;  
 DR GO; GO:0005829; C:cytosol; ISS.  
 DR GO; GO:0019901; F:protein kinase binding; ISS.  
 DR GO; GO:0042169; F:SH2 domain binding; ISS.  
 DR GO; GO:0043130; F:ubiquitin binding; ISS.  
 DR GO; GO:0016197; F:endosome transport; ISS.  
 DR GO; GO:0007242; P:intracellular signaling cascade; ISS.  
 DR GO; GO:0045944; P:positive regulation of transcription from P. . ; ISS.  
 DR GO; GO:0008104; P:protein localization; ISS.  
 DR GO; GO:0043122; P:regulation of I-kappaB kinase/NF-kappaB cas. . ; ISS.  
 DR GO; GO:0006950; P:response to stress; ISS.  
 DR InterPro; IPR000449; UBA.  
 DR InterPro; IPR000433; Znf\_ZZ.  
 DR Pfam; PF00569; ZZ; 1.  
 DR SMART; SM00165; UBA; 1.  
 DR SMART; SM00291; ZNF\_ZZ; 1.  
 DR PROSITE; PS00030; UBA; 1.  
 DR PROSITE; PS01357; ZF\_ZZ\_1; UNKNOWN\_1.  
 DR PROSITE; PS0135; ZF\_ZZ\_2; 1.  
 SQ SEQUENCE 7 AA; 779 MW; 737728769DDDD6F0 CRC64;  
 Query Match 42.1%; Score 16; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GYW 3  
 DB 5 GLW 7  
 RESULT 3  
 OCP3\_OCTMI STANDARD; PRT; 4 AA.  
 AC PS8649;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Cardioactive peptides Ocp-3/Ocp-4.  
 OS Octopus minor (Octopus).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
 OX NCBI\_TaxID=89766;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
 RC TISSUE=Brain;  
 RX MEDLINE=20336815; PubMed=10876044;  
 RA Iwakoshi E., Hisada M., Minakata H.;  
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
 RL Octopus minor.";  
 RL Peptides 21:623-630(2000).  
 CC -!- FUNCTION: Cardioactive; has both positive chronotropic and

CC inotropic effects on the heart. Ocp-4 is a 1000 time less active  
 CC than Ocp-3.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.  
 CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.  
 KW D-amino acid; Direct protein sequencing; Hormone.  
 FT MOD\_RES 2 2 D-serine (in form Ocp-4).  
 SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;  
 Query Match 39.5%; Score 15; DB 1; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GYW 3  
 DB 1 GSW 3  
 RESULT 4  
 GWA\_SEPOF STANDARD; PRT; 2 AA.  
 ID GWA\_SEPOF STANDARD; PRT; 2 AA.  
 AC P83570;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Neuropeptide Gwa.  
 OS Sepia officinalis (Common cuttlefish).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Decapodiformes; Sepioidea; Sepiidae; Sepia.  
 OX NCBI\_TaxID=6610;  
 RN [1]  
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.  
 RC TISSUE=Optic lobe;  
 RX MEDLINE=98100358; PubMed=9437704;  
 RA Henry J., Favrel P., Boucaud-Camou E.;  
 RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related  
 RT peptide inhibiting the motility of the mature oviduct in the  
 RL cuttlefish, Sepia officinalis.";  
 RL Peptides 18:1469-1474(1997).  
 CC -!- FUNCTION: Regulatory neuropeptide with myotropic activity  
 CC targeting the distal oviduct. Inhibits the motility of the oviduct  
 CC by decreasing tonus, frequency and amplitude of contractions.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 2 2 Tryptophan amide.  
 SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;  
 Query Match 28.9%; Score 11; DB 1; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 W 3  
 DB 2 W 2  
 RESULT 5  
 BPP7\_BOTIN STANDARD; PRT; 5 AA.  
 ID BPP7\_BOTIN STANDARD; PRT; 5 AA.  
 AC P30425;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Island jararaca) (Queimada Jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Venom;  
RX MEDLINE=90351557; PubMed=2386615;  
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
RT "Primary structure and biological activity of bradykinin potentiating  
peptides from Bothrops insularis snake venom.";  
RL J. Protein Chem. 9:221-227(1990)  
CC -!- FUNCTION: This peptide both inhibits the activity of the  
angiotensin-converting enzyme and enhances the action of  
bradykinin by inhibiting the kinases that inactivate it. It acts  
as an indirect hypotensive agent.  
DR PIR: G37196; G37196.  
KW Direct protein sequencing; Hypotensive agent;  
KW Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;  
Query Match 28.9%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 W 3  
Db 3 W 3  
RESULT 6  
EI01 LITRU STANDARD; PRT; 6 AA.  
ID EI01 LITRU STANDARD; PRT; 6 AA.  
AC P82096;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Electrin 1.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylloidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
Litoria electrica. Comparison with the skin peptides from Litoria  
rubella.";  
RL Aust. J. Chem. 52:639-645(1999).  
CC -!- SUBCELLULAR LOCATION: Skin.  
CC -!- TISSUE SPECIFICITY: Skin.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing.  
FT MOD\_RES 6 6 Methionine amide.  
SQ SEQUENCE 6 AA; 792 MW; 6683704772C9A000 CRC64;  
Query Match 28.9%; Score 11; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 W 3  
Db 5 W 5  
RESULT 7  
LOK1 LOCM1 STANDARD; PRT; 6 AA.  
ID LOK1 LOCM1 STANDARD; PRT; 6 AA.  
AC P41491;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Locustakinin I.  
OS Locusta migratoria (Migratory locust).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;  
OC Acridoidea; Acrididae; Oedipodinae; Locusta.

OX NCBI\_TaxID=7004;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Corpora cardiaca;  
RX MEDLINE=92262851; PubMed=1585017;  
RA Schoofs L., Holman G.M., Proost P., van Damme J., Hayes T.K.,  
RA de Loof A.;  
RT "Locustakinin, a novel myotropic peptide from Locusta migratoria,  
isolation, primary structure and synthesis.";  
RL Regul. Pept. 37:49-57(1992).  
CC -!- FUNCTION: Myotropic peptide. May be important in the stimulation  
of ion transport and inhibition of diuretic activity in Malpighian  
tubules.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
DR PIR: A61068; A61068.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 6 6 Glycine amide.  
SQ SEQUENCE 6 AA; 654 MW; 686365A5B9CDB000 CRC64;  
Query Match 28.9%; Score 11; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 W 3  
Db 5 W 5  
RESULT 8  
BRHP CONIM STANDARD; PRT; 7 AA.  
ID BRHP CONIM STANDARD; PRT; 7 AA.  
AC P58803;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Bromheptapeptide Im.  
OS Conus imperialis (Imperial cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorboconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=35631;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC TISSUE=Venom;  
RX MEDLINE=97184108; PubMed=9030520;  
RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,  
RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,  
RA McIntosh J.M.;  
RT "A novel post-translational modification involving bromination of  
tryptophan. Identification of the residue, L-6-bromotryptophan, in  
peptides from Conus imperialis and Conus radiatus venom.";  
RL J. Biol. Chem. 272:4689-4698(1997).  
CC -!- FUNCTION: Does not elicit gross behavioral symptoms when injected  
centrally or peripherally in mice.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -!- MASS SPECTROMETRY: MW=853.19; METHOD=LSI; RANGE=1-7; NOTE=Ref.1.  
DR PIR: A58512; A58512.  
KW Amidation; Bromination; Direct protein sequencing;  
KW Pyrrolidone carboxylic acid.  
FT DISULFID 2 7  
FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
FT MOD\_RES 6 6 6'-bromotryptophan.  
FT MOD\_RES 7 7 Cysteine amide.  
SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;  
Query Match 28.9%; Score 11; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 W 3  
Db 6 W 6

## RESULT 9

TPFY\_PACDA STANDARD; PRT; 7 AA.  
 AC P83455;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Tryptophyllin-1 (pdt-1).  
 OS Pachymedusa dactylophora (Giant Mexican leaf frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;  
 OC Phyllomedusinae; Pachymedusa.  
 OX NCBI\_TaxID=75988;  
 RN [1]  
 RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF PRO-7.  
 RC TISSUE=Skin secretion;  
 RA Chen T.B., Orr D.F., Shaw C.;  
 RT "Pachymedusa dactylophora tryptophyllin-1 (pdt-1): structural characterization, pharmacological activity and cloning of precursor cDNA";  
 RT Submitted (SEP-2002) to Swiss-Prot.  
 RL -1- FUNCTION: Myoactive. Has selective relaxing activity on vascular smooth muscle.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0045986; P:negative regulation of smooth muscle contraction; NAS.  
 KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
 KW Hydroxylation.  
 FT MOD\_RES 3 3 Hydroxyproline.  
 FT MOD\_RES 7 7 Proline amide.  
 SQ SEQUENCE 7 AA; 794 MW; 777237DC7776350 CRC64;

Query Match 28.9%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3

Db 5 W 5

## RESULT 10

TY51\_LITRU STANDARD; PRT; 7 AA.  
 AC P82065;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Tryptophyllin 5.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C., Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog 'Litoria rubella'. The skin peptide profile as a probe for the study of evolutionary trends of amphibians";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -1- FUNCTION: May act as a neuromodulator or neurotransmitter.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -1- MASS SPECTROMETRY: MW=965; METHOD=FAB; RANGE=1-7; NOTE=Ref.1.  
 KW Amidation; Amphibian defense peptide; Direct protein sequencing;

KW Neuropeptide; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
 FT MOD\_RES 7 7 Arginine amide.  
 SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match 28.9%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3

Db 4 W 4

## RESULT 11

WWA1\_ACHFU STANDARD; PRT; 7 AA.  
 AC P35919;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Wwamide-1.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Ganglion;  
 RX MEDLINE=93265912; PubMed=8495720;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica";  
 RL FEBS Lett. 323:104-108(1993).  
 CC -1- FUNCTION: Exhibits modulatory effects on the peripheral nervous system. Inhibits activity on a central neuron.  
 CC PIR; S33245; S33245.  
 DR Amidation; Direct protein sequencing; Neuropeptide.  
 KW MOD\_RES 7 7 Tryptophan amide.  
 SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 28.9%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3

Db 1 W 1

## RESULT 12

WWA2\_ACHFU STANDARD; PRT; 7 AA.  
 AC P35920;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Wwamide-2.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Ganglion;  
 RX MEDLINE=93265912; PubMed=8495720;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RT "Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia of the African giant snail, Achatina fulica";  
 RL FEBS Lett. 323:104-108(1993).  
 DR PIR; S33246; S33246.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 7 7 Tryptophan amide.

SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 28.9%; Score 11; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
|  
Db 1 W 1

## RESULT 13

WHA3\_ACHFU STANDARD; PRT; 7 AA.

AC P35921;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Wamide-3.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.

RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "Wamide-1, -2 and -3; novel neuromodulatory peptides isolated from  
RT ganglia of the African giant snail, Achatina fulica.";  
RL FEBS Lett. 323:104-108 (1993).  
DR PIR; S33244; S33244.

KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 7  
7 Tryptophan amide.

SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;

Query Match 28.9%; Score 11; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
|  
Db 1 W 1

## RESULT 14

Q95945 PRELIMINARY; PRT; 7 AA.

AC Q95945;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Inside intron 5 (Fragment).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OG Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=D273-10B;  
RX MEDLINE=81069885; PubMed=6254986;  
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;  
RT "Assembly of the mitochondrial membrane system: Structure and  
RT nucleotide sequence of the gene coding for subunit 1 of yeast  
RT cytochrome oxidase.";  
RL J. Biol. Chem. 255:11927-11941 (1980).  
DR EMBL; V00694; CAA24066.1; -.  
DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.  
FT NON\_TER 1  
1  
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 28.9%; Score 11; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
|  
Db 4 W 4

## RESULT 15

O49223 PRELIMINARY; PRT; 7 AA.

AC O49223;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HMG-1-like protein (Fragment).  
OS Glycine max (Soybean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
OX NCBI\_TaxID=3847;  
RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=Roots;  
RX MEDLINE=91367679; PubMed=1891369;  
RA Laux T., Goldberg R.B.;

RT "A plant DNA binding protein shares highly conserved sequence motifs  
RT with HMG-box proteins.";  
RL Nucleic Acids Res. 19:4769-4769 (1991).  
RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Roots;  
RA Mahalingam R., Knap H.T.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF047050; AAC03556.1; -.

FT NON\_TER 1  
1

SQ SEQUENCE 7 AA; 850 MW; 6AAAAAB378637810 CRC64;

Query Match 28.9%; Score 11; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3  
|  
Db 2 W 2

Search completed: December 29, 2004, 22:07:31  
Job time : 189 secs

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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:55:07 ; Search time 48.7358 Seconds  
(without alignments)  
51.525 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYXXXXX 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	10	4	AAB99759 Rhesus D
2	34	89.5	12	4	AAB99769 Rhesus D
3	34	89.5	452	4	Aau03644 Group B S
4	34	89.5	466	6	Abu21589 Protein e
5	34	89.5	472	6	Abu38334 Protein e
6	34	89.5	474	6	Abu24881 Protein e
7	34	89.5	475	5	Abp30560 Streptoco
8	34	89.5	475	6	Abu40245 Protein e
9	34	89.5	475	6	Abu29756 Protein e
10	34	89.5	478	7	Adc97241 E. faeciu
11	34	89.5	479	5	Abp26968 Streptoco
12	34	89.5	490	5	Abb55389 Lactococc
13	34	89.5	496	5	Abb55385 Lactococc
14	34	89.5	499	7	Abu74582 Pseudomon
15	34	89.5	506	6	Abu22414 Protein e
16	34	89.5	585	7	Ada49403 Multi-epi
17	34	89.5	585	8	Ado24081 Epigene c
18	34	89.5	865	7	Abp70593 Pseudomon
19	33	86.8	10	5	Abp53931 VEGFR-3 b
20	33	86.8	10	5	Abp53932 VEGFR-3 b
21	33	86.8	69	4	AAO13595 Human pol
22	33	86.8	116	2	AAR15437 Heavy cha
23	33	86.8	116	6	ABO27261 ICAM-1 bi
24	33	86.8	116	6	ABO27269 ICAM-1 bi
25	33	86.8	116	6	ABO27263 ICAM-1 bi

26	33	86.8	116	6	ABO27259	Abc27259 ICAM-1 bi
27	33	86.8	116	6	ABO27255	Abc27255 ICAM-1 bi
28	33	86.8	116	6	ABO27277	Abc27277 Humanised
29	33	86.8	116	6	ABO27273	Abc27273 Murine 1A
30	33	86.8	116	6	ABO27257	Abc27257 ICAM-1 bi
31	33	86.8	116	6	ABO27271	Abc27271 ICAM-1 bi
32	33	86.8	116	6	ABO27267	Abc27267 ICAM-1 bi
33	33	86.8	117	6	ABO27265	Abc27265 ICAM-1 bi
34	33	86.8	118	7	ADJ95639	Adj95639 Insulin-1
35	33	86.8	119	8	ADL11890	Adl11890 CDR trans
36	33	86.8	119	8	ADL11886	Adl11886 Chimera a
37	33	86.8	120	4	AB62747	Ab62747 Human HIV
38	33	86.8	137	7	ADJ95626	Adj95626 Rat insul
39	33	86.8	138	3	AAJ77591	Aaj77591 Anti-huma
40	33	86.8	138	3	AAJ77595	Aaj77595 Anti-huma
41	33	86.8	138	4	AAJ78864	Aab78864 Anti-huma
42	33	86.8	138	4	AAJ78860	Aab78860 Anti-huma
43	33	86.8	163	7	ABM73967	Abm73967 DNA clone
44	33	86.8	227	6	ABU36339	Abu36339 Protein e
45	33	86.8	240	2	AAR15443	Aar15443 Single ch

ALIGNMENTS

RESULT 1  
AAB99759  
ID AAB99759 standard; peptide; 10 AA.  
XX  
AC AAB99759;  
XX  
DT 21-SEP-2001 (first entry)  
XX  
DE Rhesus D antibody binding peptide SEQ ID NO:4.  
XX  
KW Rhesus D antibody binding peptide; Rhesus D; RHD; identification;  
anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;  
prophylaxis; haemolytic disease of the newborn; HDN; ITP;  
idiopathic thrombocytopenic purpura; immunoglobulin.

OS Homo sapiens.  
XX  
XX EP1106625-A1.  
XX  
PD 13-JUN-2001.  
XX  
PF 17-NOV-1999; 99EP-00122858.  
XX  
PR 17-NOV-1999; 99EP-00122858.  
XX (ZLBB-) ZLB BIOPLASMA AG.  
XX  
PI Miescher S, Hofmann A, Fisch I;  
XX WPI; 2001-383568/41.  
DR  
XX Novel peptides capable of binding Rhesus D antibodies are used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. hemolytic disease of the newborn (HDN).  
PT  
XX Claim 1; Page 12; 19pp; English.  
XX  
CC The present sequence represents a peptide capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more (II) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (MI) peptides having immunologic properties of Rhesus D protein epitopes comprising subjecting an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are mimotopes which differ in their amino acid sequence from the amino acid

CC sequences of Rhesus D protein; and (6) peptides (V) with immunological  
 CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to  
 CC manufacture an agent for the diagnosis, therapy or prophylaxis of  
 CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the  
 CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the  
 CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified  
 CC or removed from body fluids or immunoglobulin preparations. Using (I) as  
 CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation  
 CC with foreign erythrocytes thereby avoiding the risk of transmission of  
 CC viral diseases like AIDS and hepatitis B

XX  
 SQ Sequence 10 AA;

Query Match 89.5%; Score 34; DB 4; Length 10;  
 Best Local Similarity 57.1%; Pred. No. 9.9;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7  
 |||||  
 Db 1 GYWSAKW 7

RESULT 2  
 ID AAB99769 standard; peptide; 12 AA.  
 XX  
 AC AAB99769;  
 XX  
 DT 21-SEP-2001 (first entry)  
 XX  
 DE Rhesus D antibody related peptide #5.  
 XX  
 KW Rhesus D antibody binding peptide; Rhesus D; RhD; identification;  
 KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;  
 KW prophylaxis; haemolytic disease of the newborn; HDN; ITP; cyclic;  
 KW idiopathic thrombocytopenic purpura; immunoglobulin; circular.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.

XX  
 Key Location/Qualifiers  
 FH Disulfide-bond 1..12  
 FT  
 XX  
 XX EPI106625-A1.  
 PN  
 XX  
 XX 13-JUN-2001.  
 PD  
 XX  
 XX 17-NOV-1999; 99EP-00122858.  
 PF  
 XX  
 XX 17-NOV-1999; 99EP-00122858.  
 PR  
 XX  
 XX (ZLBB-) ZLB BIOPLASMA AG.  
 PA  
 XX  
 XX Miescher S, Hofmann A, Fisch I;  
 PI  
 XX  
 XX WPI; 2001-383568/41.  
 DR  
 XX  
 XX Novel peptides capable of binding Rhesus D antibodies are used to  
 PT manufacture an agent for the diagnosis, therapy or prophylaxis of  
 PT diseases associated with Rhesus D antigen, e.g. hemolytic disease of the  
 PT newborn (HDN).  
 PT  
 XX  
 XX Example 1; Page 8; 19pp; English.

XX  
 CC The present invention describes peptides capable of binding Rhesus D  
 CC antibodies (I). Also described in the present invention are: (1) a  
 CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more  
 CC (II) operably linked to an expression control system; (3) a cell (IV)  
 CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)  
 CC peptides having immunologic properties of Rhesus D protein epitopes  
 CC comprising subjecting an antibody/antibody fragment recognising an  
 CC epitope of Rhesus D protein to several panning rounds with a phage  
 CC display library, and identifying immunogenic peptide sequences which are

CC mimotopes which differ in their amino acid sequence from the amino acid  
 CC sequences of Rhesus D protein; and (6) peptides (V) with immunological  
 CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to  
 CC manufacture an agent for the diagnosis, therapy or prophylaxis of  
 CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the  
 CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the  
 CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified  
 CC or removed from body fluids or immunoglobulin preparations. Using (I) as  
 CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation  
 CC with foreign erythrocytes thereby avoiding the risk of transmission of  
 CC viral diseases like AIDS and hepatitis B. The present sequence represents  
 CC an anti-Rhesus D (RhD) antibody related peptide which is used in an  
 CC example from the present invention

XX  
 SQ Sequence 12 AA;

Query Match 89.5%; Score 34; DB 4; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 12;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7  
 |||||  
 Db 2 GYWSAKW 8

RESULT 3  
 ID AAU03644 standard; protein; 452 AA.  
 XX  
 AC AAU03644;  
 XX  
 DT 12-SEP-2001 (first entry)  
 XX  
 DE Group B Streptococcus antigenic protein, ID-119.  
 XX  
 KW Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis;  
 KW meningitis; neonate; antigenic; vaccine; infection; genital tract;  
 KW capsid polysaccharide vaccination.  
 XX  
 OS Streptococcus agalactiae.  
 XX  
 XX WO200132882-A2.  
 PN  
 XX  
 XX 10-MAY-2001.  
 PD  
 XX  
 XX 07-SEP-2000; 2000WO-GB003437.  
 PF  
 XX  
 XX 07-SEP-1999; 99GB-00021125.  
 PR  
 XX  
 XX (MICR-) MICROBIAL TECHNIQS LTD.  
 PA  
 XX  
 XX Le Page RWF, Wells JM, Hanniffy SB;  
 PI  
 XX  
 XX WPI; 2001-316444/33.  
 DR  
 XX  
 XX N-PSDB; AAS07061.  
 DR  
 XX  
 XX New polypeptides derived from Streptococcus agalactiae are useful to  
 PT provide detection of, and vaccination against, Group B Streptococcus  
 PT infections, particularly to prevent infection in neonates.  
 PT  
 XX  
 XX Claim 1; Fig 1; 178pp; English.

XX  
 CC AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus  
 CC agalactiae) amino acid sequences of the invention. S. agalactiae is an  
 CC encapsulated bacterium which is a major pathogen of humans causing sepsis  
 CC and meningitis in neonates as well as adults. The S. agalactiae antigenic  
 CC polypeptides are used to vaccinate against Group B Streptococcus  
 CC infections, particularly to prevent infection in new born children  
 CC arising from the maternal genital tract. An immunogenic composition is  
 CC useful in the preparation of a medicament for the treatment or  
 CC prophylaxis of Group B Streptococcus infection. The invention does not  
 CC have the disadvantages of varied response rate associated with prior art  
 CC capsid polysaccharide vaccination against Group B Streptococcus

XX SQ Sequence 452 AA;  
 Query Match 89.5%; Score 34; DB 4; Length 452;  
 Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7  
 ||| |  
 Db 92 GYWSAW 98

RESULT 4  
 ABU21589  
 ID ABU21589 standard; protein; 466 AA.  
 XX  
 AC ABU21589;  
 XX  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Protein encoded by Prokaryotic essential gene #7116.  
 XX  
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX  
 OS Burkholderia fungorum.  
 XX  
 PN WO200277183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX  
 DR WPI; 2003-029926/02.  
 DR N-PSDB; ACA25459.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 25; SEQ ID NO 49513; 1766pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC the gene product or that has an activity against a biological pathway  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *X. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: the sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 466 AA;  
 Query Match 89.5%; Score 34; DB 6; Length 466;  
 Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7  
 ||| |  
 Db 86 GYWSAW 92

RESULT 5  
 ABU38334  
 ID ABU38334 standard; protein; 472 AA.  
 XX  
 AC ABU38334;  
 XX  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Protein encoded by Prokaryotic essential gene #23861.  
 XX  
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX  
 OS Pseudomonas aeruginosa.  
 XX  
 PN WO200277183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX  
 DR WPI; 2003-029926/02.  
 DR N-PSDB; ACA2204.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 25; SEQ ID NO 66258; 1766pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC the gene product or that has an activity against a biological pathway  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the

CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 472 AA;

Query Match 89.5%; Score 34; DB 6; Length 472;  
 Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
 |||||  
 Db 94 GYWSAW 100

## RESULT 6

ID ABU24881 standard; protein; 474 AA.

AC ABU24881;

DT 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #10408.

DE Antisense; prokaryotic essential gene; cell proliferation; drug design.

KW Clostridium botulinum.

OS WO200277183-A2.

PN 03-OCT-2002.

PD 21-MAR-2002; 2002WO-US009107.

PF 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WFI; 2003-029926/02.

DR N-PSDB; ACA28751.

XX New antisense nucleic acids, useful for identifying proteins or screening

XX for homologous nucleic acids required for cellular proliferation to

XX isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 52805; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 474 AA;

Query Match 89.5%; Score 34; DB 6; Length 474;  
 Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
 |||||  
 Db 95 GYWSAW 101

## RESULT 7

ABP30560 standard; protein; 475 AA.

XX ABP30560;

XX 02-JUL-2002 (first entry)

DE Streptococcus polypeptide SEQ ID NO 10296.

XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.

OS Streptococcus agalactiae.

XX WO200234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB004789.

XX 27-OCT-2000; 2000GB-00026333.

PR 24-NOV-2000; 2000GB-00028727.

PR 07-MAR-2001; 2001GB-00005640.

XX (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

XX Telford J, Masignani V, Margarit Y Rosi, Grandi G, Fraser C;

PI Tettelin H;



```

PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA33626.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 57680; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 475 AA;

Query Match 89.5%; Score 34; DB 6; Length 475;
Best Local Similarity 57.1%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db |||||
95 GYWLSAW 101

RESULT 10
ADC97241
XX ADC97241 standard; protein; 478 AA.
XX
AC ADC97241;
XX
XX 01-JAN-2004 (first entry)
DT
XX
DE E. faecium protein sequence SEQ ID 6868.
XX
XX Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
KW abdominal-pelvic infection.
XX
XX Enterococcus faecium.
OS

PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA33626.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 57680; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 475 AA;

Query Match 89.5%; Score 34; DB 6; Length 475;
Best Local Similarity 57.1%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db |||||
95 GYWLSAW 101

RESULT 10
ADC97241
XX ADC97241 standard; protein; 478 AA.
XX
AC ADC97241;
XX
XX 01-JAN-2004 (first entry)
DT
XX
DE E. faecium protein sequence SEQ ID 6868.
XX
XX Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
KW abdominal-pelvic infection.
XX
XX Enterococcus faecium.
OS

```

```

XX US56583275-B1.
PN
XX
XX 24-JUN-2003.
PD
XX
XX 30-JUN-1998; 98US-00107532.
PF
XX
XX 02-JUL-1997; 97US-0051571P.
PR
XX 14-MAY-1998; 98US-0085598P.
PR
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX Doucette-Stamm LA, Bush D;
XX
XX WPI; 2003-799836/75.
DR N-PSDB; ADC93587.
DR
XX
XX New isolated nucleic acid derived from Enterococcus faecium encoding an
PT Enterococcus faecium polypeptide useful for detection, prevention and
PT treatment of a pathological condition resulting from a bacterial
PT infection.
XX
XX Example 1; SEQ ID NO 6868; 243pp; English.
XX
CC The invention relates to an isolated nucleic acid derived from
CC Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC one of 10 fully defined sequences given in the (or comprising 40
CC sequential nucleotides chosen from any of the nucleic acids, its
CC complement or sequences hybridising to it). Also included are a
CC recombinant vector comprising the nucleic acid operably linked to
CC transcription regulatory element, a cell comprising the vector and a
CC single-stranded probe comprising the nucleic acid. The nucleic acids are
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC The nucleic acids is useful for diagnosing pathological conditions
CC resulting from E. faecium bacterial infection (e.g. urinary tract
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC infection) and for screening drugs such as agonists and antagonists. The
CC nucleic acid is useful for recombinant production of Candida albicans -
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating Enterococcus faecium infections. The present sequence represents
CC one if the disclosed E. faecium proteins.
XX
SQ Sequence 478 AA;

Query Match 89.5%; Score 34; DB 7; Length 478;
Best Local Similarity 57.1%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db |||||
98 GYWLSAW 104

RESULT 11
ABP26968
ID ABP26968 standard; protein; 479 AA.
XX
XX AC ABP26968;
XX
XX 02-JUL-2002 (first entry)
DT
XX
XX Streptococcus polypeptide SEQ ID NO 3112.
DE
XX
XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
XX anti-inflammatory; infection; vaccine; meningitis; gene therapy.
XX
XX Streptococcus agalactiae.
OS
XX
XX WO200234771-A2.
PN
XX 02-MAY-2002.
PD

```

XX PF 29-OCT-2001; 2001WO-GB004789.  
 XX XX  
 PR 27-OCT-2000; 2000GB-00026333.  
 PR 24-NOV-2000; 2000GB-00028727.  
 PR 07-MAR-2001; 2001GB-00005640.  
 XX XX  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 XX XX  
 PI Telford J, Massignani V, Margarit Y Rosi, Grandi G, Fraser C;  
 PI Tettelin H;  
 XX XX  
 DR WPI; 2002-352536/38.  
 DR N-PSDB; ABN67599.  
 XX XX  
 PT New Streptococcus protein for the treatment or prevention of infection or  
 PT disease caused by Streptococcus bacteria, such as meningitis, and for  
 PT detecting a compound that binds to the protein.  
 XX XX  
 PS Claim 1; Page 3464; 4525pp; English.  
 XX XX  
 CC The invention relates to a protein (ABP25413-ABP30895) from group B  
 CC Streptococcus/GBS (Streptococcus agalactiae) or group A Streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in  
 CC the specification. The proteins have antibacterial and antiinflammatory  
 CC activity. (I), nucleic acids encoding (I), ABN65044-ABN71526 and  
 CC antibodies that bind (I) are used in the manufacture of medicaments for  
 CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
 CC biological sample. (I) is used to determine whether a compound binds to  
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (I) may be used to recombinantly produce (I) and may be  
 CC used in gene therapy. Antibodies to (I) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins  
 XX XX  
 SQ Sequence 479 AA;  
 Query Match 89.5%; Score 34; DB 5; Length 479;  
 Best Local Similarity 57.1%; Pred. No. 3.9e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GYVXXXW 7  
 DB 96 GYVLSAW 102  
 RESULT 12  
 ABB55389  
 ID ABB55389 standard; protein; 490 AA.  
 XX AC ABB55389;  
 XX XX  
 DT 29-AUG-2003 (revised)  
 DT 16-MAY-2002 (first entry)  
 XX XX  
 DE Lactococcus lactis protein arcDl.  
 XX XX  
 KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.  
 XX OS Lactococcus lactis; IL1403.  
 XX XX  
 PN FR2807446-A1.  
 XX PD 12-OCT-2001.  
 XX XX  
 PF 11-APR-2000; 2000FR-00004630.  
 PR 11-APR-2000; 2000FR-00004630.  
 XX XX  
 PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
 XX XX  
 PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;  
 XX WPI; 2002-043418/06.  
 XX XX  
 OS New nucleotide sequence useful in the identification or Lactococcus  
 XX PT lactis and related species.  
 XX PS Claim 6; SEQ ID NO 2087; 2504pp; French.  
 CC The present invention is related to a Lactococcus lactis nucleotide  
 CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic  
 CC acid sequence is useful in the detection and/or amplification of nucleic  
 CC acid sequence is useful in the detection and/or amplification of nucleic

XX PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
 XX Bolotine A, Sorokine A, Renault P, Ehrlich SD;  
 XX WPI; 2002-043418/06.  
 XX New nucleotide sequence useful in the identification or Lactococcus  
 XX PT lactis and related species.  
 XX PS Claim 6; SEQ ID NO 2091; 2504pp; French.  
 XX XX  
 CC The present invention is related to a Lactococcus lactis nucleotide  
 CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic  
 CC acid sequence is useful in the detection and/or amplification of nucleic  
 CC acid sequence, particularly to identify Lactococcus lactis or related  
 CC species. The proteins of the invention are useful for the biosynthesis or  
 CC biodegradation of a composition of interest. The invention helps research  
 CC in lactic bacteria, particularly useful in the production of yogurt and  
 CC cheese. Note: The sequence data for this patent is based on equivalent  
 CC patent WO200177334 (published 18-OCT-2001) which is available in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 29-AUG-2003 to  
 CC standardise OS field)  
 XX SQ Sequence 490 AA;  
 Query Match 89.5%; Score 34; DB 5; Length 490;  
 Best Local Similarity 57.1%; Pred. No. 3.9e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GYVXXXW 7  
 DB 93 GYVLSAW 99  
 RESULT 13  
 ABB55385  
 ID ABB55385 standard; protein; 496 AA.  
 XX AC ABB55385;  
 XX XX  
 DT 29-AUG-2003 (revised)  
 DT 16-MAY-2002 (first entry)  
 XX XX  
 DE Lactococcus lactis protein arcD2.  
 XX XX  
 KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.  
 XX OS Lactococcus lactis; IL1403.  
 XX PN FR2807446-A1.  
 XX PD 12-OCT-2001.  
 XX XX  
 PF 11-APR-2000; 2000FR-00004630.  
 PR 11-APR-2000; 2000FR-00004630.  
 XX XX  
 PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.  
 XX XX  
 PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;  
 XX WPI; 2002-043418/06.  
 XX XX  
 OS New nucleotide sequence useful in the identification or Lactococcus  
 XX PT lactis and related species.  
 XX PS Claim 6; SEQ ID NO 2087; 2504pp; French.  
 CC The present invention is related to a Lactococcus lactis nucleotide  
 CC sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic  
 CC acid sequence is useful in the detection and/or amplification of nucleic

CC acid sequence, particularly to identify *Lactococcus lactis* or related  
CC species. The proteins of the invention are useful for the biosynthesis or  
CC biodegradation of a composition of interest. The invention helps research  
CC in lactic bacteria, particularly useful in the production of yogurt and  
CC cheese. Note: The sequence data for this patent is based on equivalent  
CC patent WO2001/7334 (published 18-OCT-2001) which is available in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences. (Updated on 29-AUG-2003 to  
CC standardise OS field)  
XX SQ Sequence 496 AA;  
  
Query Match 89.5%; Score 34; DB 5; Length 496;  
Best Local Similarity 57.1%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXW 7  
|||  
Db 93 GYWISAW 99  
  
RESULT 14  
ABO74582  
ID ABO74582 standard; protein; 499 AA.  
XX AC ABO74582;  
XX DT 29-JUL-2004 (first entry)  
XX XX  
XX Pseudomonas aeruginosa polypeptide #6757.  
XX DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX KW Pseudomonas aeruginosa.  
XX OS  
XX PN US651795-B1.  
XX XX  
XX PD 22-APR-2003.  
XX PF 18-FEB-1999; 99US-00252991.  
XX PR 18-FEB-1998; 98US-0074788P.  
XX PR 27-JUL-1998; 98US-0094190P.  
XX PA (GENO-) GENOME THERAPEUTICS CORP.  
XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX WPI; 2003-615309/58.  
XX DR N-PSDB; ABD08153.  
XX PS Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,  
XX useful as molecular targets for diagnostics, prophylaxis and treatment of  
XX pathological conditions resulting from bacterial infection.  
XX  
XX Disclosure; SEQ ID NO 23328; 455pp; English.  
XX  
CC The invention relates to *Pseudomonas aeruginosa* polypeptides and the  
CC polynucleotides encoding them. The sequences are useful in diagnosis and  
CC therapy of pathological conditions, as molecular targets for diagnostics,  
CC prophylaxis and treatment of pathological conditions resulting from a  
CC bacterial infection, for evaluating a compound, such as a polypeptide,  
CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of  
CC effective antibacterial targets, as targets for antibacterial drugs,  
CC including anti-*P. aeruginosa* drugs, as templates for recombinant  
CC production of *P. aeruginosa*-derived peptides or polypeptides, as target  
CC components for diagnosis and/or treatment of *P. aeruginosa*-caused  
CC infection, and in detection of *P. aeruginosa* sequences or other sequences  
CC of *Pseudomonas* species using biochip technology. Sequences ABO67826-  
CC ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification but was obtained in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html

XX SQ Sequence 499 AA;  
  
Query Match 89.5%; Score 34; DB 7; Length 499;  
Best Local Similarity 57.1%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 GYWXW 7  
|||  
Db 111 GYWISAW 117  
  
RESULT 15  
ABU22414  
ID ABU22414 standard; protein; 506 AA.  
XX AC ABU22414;  
XX DT 19-JUN-2003 (first entry)  
XX XX  
XX DE Protein encoded by Prokaryotic essential gene #7941.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Burkholderia mallei.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
XX Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX DR N-PSDB; ACA26284.  
XX PS New antisense nucleic acids, useful for identifying proteins or screening  
XX for homologous nucleic acids required for cellular proliferation to  
XX isolate candidate molecules for rational drug discovery programs.  
XX  
XX Claim 25; SEQ ID NO 50338; 1766pp; English.  
XX  
CC The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway;  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC or a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 506 AA;

Query Match 89.5%; Score 34; DB 6; Length 506;  
Best Local Similarity 57.1%; Pred. NO. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7

DB 124 GYISAW 130

Search completed: December 30, 2004, 13:07:56  
Job time : 51.7358 secs

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Query Match      89.5%; Score 34; DB 4; Length 478;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYXXXXX 7
   |||||
Db 98 GYWLAW 104

RESULT 2
US-09-252-991A-23328
; Sequence 23328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23328
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23328

Query Match      89.5%; Score 34; DB 4; Length 499;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYXXXXX 7
   |||||
Db 111 GYWLAW 117

RESULT 3
US-09-252-991A-19339
; Sequence 19339, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19339
; LENGTH: 865
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19339

Query Match      89.5%; Score 34; DB 4; Length 865;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYXXXXX 7
   |||||
Db 487 GYWLAW 493

RESULT 4
```

```
US-09-252-991A-18697
; Sequence 18697, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18697
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18697

Query Match      86.8%; Score 33; DB 4; Length 543;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYXXXXX 7
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Db 331 GYWLAW 337

RESULT 5
US-09-792-616-9
; Sequence 9, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1498
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-792-616-9

Query Match      86.8%; Score 33; DB 4; Length 1498;
Best Local Similarity 57.1%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYXXXXX 7
   |||||
Db 960 GYWLAW 966

RESULT 6
US-09-792-616-3
; Sequence 3, Application US/09792616
; Patent No. 6780587
; GENERAL INFORMATION:
; APPLICANT: PXE International, Inc.
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing
; FILE REFERENCE: PXE-001
; CURRENT APPLICATION NUMBER: US/09/792,616
; CURRENT FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-616-3

Query Match      86.8%; Score 33; DB 4; Length 1503;
Best Local Similarity 57.1%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
DB 965 GIWLSLW 971

RESULT 7
US-09-543-681A-7620
; Sequence 7620, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7620
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7620

Query Match      84.2%; Score 32; DB 4; Length 177;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
DB 43 GIWVNW 49

RESULT 8
US-09-502-653-10
; Sequence 10, Application US/09502653
; Patent No. 6331426
; GENERAL INFORMATION:
; APPLICANT: Bj rnvad, Mads Eskelund
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Schleim, Martin
; APPLICANT: Bech, Lisbeth
; APPLICANT: stergaard, Peter Rahbek
; APPLICANT: Sj holm, Carsten
; TITLE OF INVENTION: NOVEL GALACTANASES
; FILE REFERENCE: 5481.200-US
; CURRENT APPLICATION NUMBER: US/09/502,653
; CURRENT FILING DATE: 2000-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00184
; EARLIER FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00799
; EARLIER FILING DATE: 1999-06-07
; EARLIER APPLICATION NUMBER: 60/125,885
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/138,445
; EARLIER FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Bacillus circulans
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US-09-502-653-10

Query Match      84.2%; Score 32; DB 3; Length 252;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
DB 210 GYWEPAW 216

RESULT 9
US-09-610-906-12
; Sequence 12, Application US/09610906
; Patent No. 6566066
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Klingner, Tod M.
; TITLE OF INVENTION: AQUAPORIN-8 VARIANT
; FILE REFERENCE: PC-0012 CIP
; CURRENT APPLICATION NUMBER: US/09/610,906
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 09/226,994
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. 6566066: g2346968
; PUBLICATION INFORMATION:
US-09-610-906-12

Query Match      84.2%; Score 32; DB 4; Length 263;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
DB 224 GYWDPHW 230

RESULT 10
US-09-248-796A-15791
; Sequence 15791, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15791
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15791

Query Match      84.2%; Score 32; DB 4; Length 274;
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7
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Db      84 GYWPITW 90
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RESULT 11
US-09-145-828A-11
; Sequence 11, Application US/09145828A
; Patent No. 6403349
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E. Y.
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Kirchner, Stephen J.
; APPLICANT: Parker-Barnes, Jennifer M.
; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF
; FILE REFERENCE: 6407.US.01
; CURRENT APPLICATION NUMBER: US/09/145,828A
; CURRENT FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-145-828A-11

Query Match      84.2%; Score 32; DB 4; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.le+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXW 7
Db      108 GYWIPLW 114
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RESULT 12
US-09-903-456-18
; Sequence 18, Application US/09903456
; Patent No. 6677145
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda Eun-Yeong
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF
; FILE REFERENCE: 6407.US.P3
; CURRENT APPLICATION NUMBER: US/09/903,456
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 09/624,670
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: US 09/379,095
; PRIOR FILING DATE: 1999-08-23
; PRIOR APPLICATION NUMBER: US 09/145,828
; PRIOR FILING DATE: 1998-09-02
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-903-456-18

Query Match      84.2%; Score 32; DB 4; Length 278;
Best Local Similarity 57.1%; Pred. No. 2.le+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXW 7
Db      108 GYWIPLW 114
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RESULT 13
US-09-252-991A-26841
; Sequence 26841, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26841
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26841

Query Match      84.2%; Score 32; DB 4; Length 339;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXW 7
Db      261 GYGGYW 267
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RESULT 14
US-08-415-751-6
; Sequence 6, Application US/08415751
; Patent No. 5643772
; GENERAL INFORMATION:
; APPLICANT: PETERSEN, CAROLYN
; APPLICANT: LEECH, JAMES
; APPLICANT: NELSON, RICHARD, C.
; APPLICANT: GUT, JIRI
; TITLE OF INVENTION: POLYPEPTIDES BINDING ANTI-
; TITLE OF INVENTION: CRYPTOSPORIDIUM ANTIBODIES, DNA
; TITLE OF INVENTION: AND RNA ENCODING THEM, HYBRID
; TITLE OF INVENTION: VECTOR AND TRANSFORMED HOST AND
; TITLE OF INVENTION: METHODS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS AND KIT
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PHILLIPS, MOORE, LEMPPIO & FINLEY
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: California
; COUNTRY: United States of America
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
; COMPUTER: PC
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/415,751
; FILING DATE: 03-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/071,880
; FILING DATE: June 1, 1993
; APPLICATION NUMBER: 07/891,301
; FILING DATE: May 29, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hana Dolezalova
; REGISTRATION NUMBER: 30,518
; REFERENCE/DOCKET NUMBER: 480.19-2 (HHD)
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## TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-1677  
; TELEFAX: (415) 324-1678  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 362 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; ORIGINAL SOURCE:  
; ORGANISM: Cryptosporidium parvum  
; FEATURE:  
; NAME/KEY: Positions coded by nonsense codons are  
; NAME/KEY: identified as Xaa.  
US-08-415-751-6

Query Match 84.2%; Score 32; DB 1; Length 362;  
Best Local Similarity 57.1%; Pred. NO. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
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Db 216 GYWLTV 222

## RESULT 15

US-09-248-796A-15188  
; Sequence 15188, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstock et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 15188  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-15188

Query Match 84.2%; Score 32; DB 4; Length 367;  
Best Local Similarity 57.1%; Pred. NO. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
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Db 276 GYWLVDW 282

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OM protein - protein search, using sw model

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## SUMMARIES

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1	34	89.5	58	17 US-10-425-115-308836	Sequence 308836,
2	34	89.5	72	16 US-10-437-963-176036	Sequence 176036,
3	34	89.5	452	14 US-10-091-007-88	Sequence 88, Appl
4	34	89.5	466	15 US-10-282-122A-49513	Sequence 49513, A
5	34	89.5	469	14 US-10-369-493-23291	Sequence 23291, A
6	34	89.5	472	15 US-10-282-122A-66258	Sequence 66258, A
7	34	89.5	474	15 US-10-282-122A-52805	Sequence 52805, A
8	34	89.5	475	14 US-10-369-493-13733	Sequence 13733, A
9	34	89.5	475	15 US-10-282-122A-57680	Sequence 57680, A
10	34	89.5	475	15 US-10-282-122A-68169	Sequence 68169, A
11	34	89.5	506	15 US-10-282-122A-50338	Sequence 50338, A
12	34	89.5	585	9 US-09-894-018-87	Sequence 87, Appl
13	34	89.5	585	17 US-10-474-960A-87	Sequence 87, Appl

14	33	86.8	10	13	US-10-046-922-34	Sequence 34, Appl
15	33	86.8	10	13	US-10-046-922-35	Sequence 35, Appl
16	33	86.8	47	17	US-10-425-115-287762	Sequence 287762,
17	33	86.8	104	17	US-10-425-115-273234	Sequence 273234,
18	33	86.8	116	10	US-09-910-483-1	Sequence 1, Appl
19	33	86.8	116	10	US-09-910-483-5	Sequence 5, Appl
20	33	86.8	116	10	US-09-910-483-9	Sequence 9, Appl
21	33	86.8	116	10	US-09-910-483-13	Sequence 13, Appl
22	33	86.8	116	10	US-09-910-483-17	Sequence 17, Appl
23	33	86.8	116	10	US-09-910-483-21	Sequence 21, Appl
24	33	86.8	116	10	US-09-910-483-25	Sequence 25, Appl
25	33	86.8	116	10	US-09-910-483-29	Sequence 29, Appl
26	33	86.8	116	10	US-09-910-483-33	Sequence 33, Appl
27	33	86.8	116	10	US-09-910-483-37	Sequence 37, Appl
28	33	86.8	116	10	US-09-910-483-41	Sequence 41, Appl
29	33	86.8	116	10	US-09-910-483-43	Sequence 43, Appl
30	33	86.8	129	17	US-10-425-115-357518	Sequence 357518,
31	33	86.8	138	14	US-10-160-232-86	Sequence 86, Appl
32	33	86.8	138	14	US-10-160-232-90	Sequence 90, Appl
33	33	86.8	227	15	US-10-282-122A-64263	Sequence 64263, A
34	33	86.8	229	17	US-10-425-115-344695	Sequence 344695,
35	33	86.8	296	14	US-10-156-761-9632	Sequence 9632, Ap
36	33	86.8	296	14	US-10-369-493-19811	Sequence 19811, A
37	33	86.8	466	14	US-10-369-493-16537	Sequence 16537, A
38	33	86.8	467	16	US-10-437-963-199114	Sequence 199114,
39	33	86.8	516	16	US-10-450-022-7	Sequence 7, Appl
40	33	86.8	526	16	US-10-450-022-5	Sequence 5, Appl
41	33	86.8	526	17	US-10-433-747B-2	Sequence 2, Appl
42	33	86.8	526	17	US-10-433-747B-17	Sequence 17, Appl
43	33	86.8	526	17	US-10-450-185B-2	Sequence 2, Appl
44	33	86.8	526	17	US-10-450-185B-17	Sequence 17, Appl
45	33	86.8	526	17	US-10-450-185B-17	Sequence 17, Appl

## ALIGNMENTS

## RESULT 1

US-10-425-115-308836  
; Sequence 308836, Application US/10425115  
; Publication No. US2004021472A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 308836  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_44726C.1.pep  
US-10-425-115-308836

Query Match 89.5%; Score 34; DB 17; Length 58;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7  
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Db 49 GYWGASW 55

## RESULT 2

US-10-437-963-176036  
; Sequence 176036, Application US/10437963  
; Publication No. US20040123343A1

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; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 176036
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73824C.1.pep
US-10-437-963-176036

Query Match      89.5%; Score 34; DB 16; Length 72;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7
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Db 34 GYWSW 40

RESULT 3
US-10-091-007-88
; Sequence 88, Application US/10091007
; Publication No. US20030170782A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics limited
; APPLICANT: Le Page, Richard W F Wells, Jeremy M
; APPLICANT: Hanniffy, Sean B
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PWC/P21978WO
; CURRENT APPLICATION NUMBER: US/10/091,007
; CURRENT FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: GB 9921125.2
; PRIOR FILING DATE: 1999-09-07
; NUMBER OF SEQ ID NOS: 276
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 88
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Streptococcus agalactiae
US-10-091-007-88

Query Match      89.5%; Score 34; DB 14; Length 452;
Best Local Similarity 57.1%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7
   |||||
Db 92 GYWSW 98

RESULT 4
US-10-282-122A-49513
; Sequence 49513, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
```

```
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 49513
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Burkholderia fungorum
US-10-282-122A-49513

Query Match      89.5%; Score 34; DB 15; Length 466;
Best Local Similarity 57.1%; Pred. No. 5.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7
   |||||
Db 86 GYWSW 92

RESULT 5
US-10-369-493-23291
; Sequence 23291, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23291
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-10-369-493-23291
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Query Match 89.5%; Score 34; DB 14; Length 469;  
 Best Local Similarity 57.1%; Pred. No. 5.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7  
 |||||  
 Db 97 GYVVASW 103

## RESULT 6

US-10-282-122A-66258  
 ; Sequence 66258, Application US/10282122A  
 ; Publication No. US20040029129A1  
 ; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Malone, Cheryl  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Kari  
 ; APPLICANT: Zyskind, Judith  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John  
 ; APPLICANT: Carr, Grant  
 ; APPLICANT: Yamamoto, Robert  
 ; APPLICANT: Forsyth, R.  
 ; APPLICANT: Xu, H.  
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A  
 ; CURRENT APPLICATION NUMBER: US/10/282,122A  
 ; CURRENT FILING DATE: 2003-02-20  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/230,335  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/230,347  
 ; PRIOR FILING DATE: 2000-09-09  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/267,636  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 78614  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 66258  
 ; LENGTH: 472  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa

US-10-282-122A-66258  
 ; GENERAL INFORMATION:

Query Match 89.5%; Score 34; DB 15; Length 472;  
 Best Local Similarity 57.1%; Pred. No. 5.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7  
 |||||  
 Db 94 GYVVASW 100

## RESULT 7

US-10-282-122A-52805  
 ; Sequence 52805, Application US/10282122A  
 ; Publication No. US20040029129A1  
 ; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Malone, Cheryl  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Kari  
 ; APPLICANT: Zyskind, Judith  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John  
 ; APPLICANT: Carr, Grant  
 ; APPLICANT: Yamamoto, Robert  
 ; APPLICANT: Forsyth, R.  
 ; APPLICANT: Xu, H.  
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A  
 ; CURRENT APPLICATION NUMBER: US/10/282,122A  
 ; CURRENT FILING DATE: 2003-02-20  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/230,335  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/230,347  
 ; PRIOR FILING DATE: 2000-09-09  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/267,636  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 78614  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 52805  
 ; LENGTH: 474  
 ; TYPE: PRT  
 ; ORGANISM: Clostridium botulinum

US-10-282-122A-52805

Query Match 89.5%; Score 34; DB 15; Length 474;  
 Best Local Similarity 57.1%; Pred. No. 5.9e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7  
 |||||  
 Db 95 GYVLSAW 101

## RESULT 8

US-10-369-493-13733  
 ; Sequence 13733, Application US/10369493  
 ; Publication No. US20030233675A1  
 ; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Chen, Xianfeng  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 ; FILE REFERENCE: 38-10(52052)B  
 ; CURRENT APPLICATION NUMBER: US/10/369,493  
 ; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039  
 ; PRIOR FILING DATE: 2002-02-21  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO 13733

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; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-13733

Query Match      89.5%; Score 34; DB 14; Length 475;
Best Local Similarity 57.1%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      93 GYWISAW 99

RESULT 9
US-10-282-122A-57680
; Sequence 57680, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57680
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Enterococcus faecium
US-10-282-122A-57680

Query Match      89.5%; Score 34; DB 15; Length 475;
Best Local Similarity 57.1%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      95 GYWLISAW 101

US-10-282-122A-68169
; Sequence 68169, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68169
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Pseudomonas putida
US-10-282-122A-68169

Query Match      89.5%; Score 34; DB 15; Length 475;
Best Local Similarity 57.1%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXXXW 7
      |||||
Db      93 GYWISAW 99

RESULT 11
US-10-282-122A-50338
; Sequence 50338, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

```

APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 50338  
LENGTH: 506  
TYPE: PRT  
ORGANISM: Burkholderia mallei  
US-10-282-122A-50338

Query Match 89.5%; Score 34; DB 15; Length 506;  
Best Local Similarity 57.1%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
DB 124 GYISAW 130

RESULT 12  
US-09-894-018-87  
Sequence 87, Application US/09894018  
Patent No. US20020119127A1  
GENERAL INFORMATION:  
APPLICANT: EPIMMUNE, Inc.  
APPLICANT: Sette, Alessandro  
APPLICANT: Chestnut, Robert  
APPLICANT: Livingston, Brian  
APPLICANT: Baker, Denise  
APPLICANT: Newman, Mark  
APPLICANT: Brown, David  
TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING  
TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY  
FILE REFERENCE: 39963-20033.00  
CURRENT APPLICATION NUMBER: US/09/894,018  
CURRENT FILING DATE: 2001-06-27  
PRIOR APPLICATION NUMBER: PCT/US00/35568  
PRIOR FILING DATE: 2000-12-28  
PRIOR APPLICATION NUMBER: US 60/173,390  
PRIOR FILING DATE: 1999-12-28  
PRIOR APPLICATION NUMBER: US 60/284,221  
PRIOR FILING DATE: 2001-04-16  
NUMBER OF SEQ ID NOS: 368  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 87  
LENGTH: 585  
TYPE: PRT

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HIV-TC  
US-09-894-018-87

Query Match 89.5%; Score 34; DB 9; Length 585;  
Best Local Similarity 57.1%; Pred. No. 6.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
DB 22 GYQATW 28

RESULT 13  
US-10-474-960A-87  
Sequence 87, Application US/10474960A  
Publication No. US20040248113A1  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Chestnut, Robert  
APPLICANT: Livingston, Brian  
APPLICANT: Baker, Denise  
APPLICANT: Newman, Mark  
APPLICANT: Brown, David  
TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic  
TITLE OF INVENTION: Acid Constructs and Peptides Encoded Thereby  
FILE REFERENCE: 2060.0320004  
CURRENT APPLICATION NUMBER: US/10/474,960A  
CURRENT FILING DATE: 2003-10-16  
PRIOR APPLICATION NUMBER: PCT/US02/09877  
PRIOR FILING DATE: 2002-03-28  
PRIOR APPLICATION NUMBER: US 09/894,018  
PRIOR FILING DATE: 2001-06-27  
PRIOR APPLICATION NUMBER: US 60/284,221  
PRIOR FILING DATE: 2001-04-16  
NUMBER OF SEQ ID NOS: 419  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 87  
LENGTH: 585  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: HIV-TC  
US-10-474-960A-87

Query Match 89.5%; Score 34; DB 17; Length 585;  
Best Local Similarity 57.1%; Pred. No. 6.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
DB 22 GYQATW 28

RESULT 14  
US-10-046-922-34  
Sequence 34, Application US/10046922  
Publication No. US20020164667A1  
GENERAL INFORMATION:  
APPLICANT: Alitalo, Kari  
APPLICANT: Koivunen, Erkki  
APPLICANT: Kubo, Hajime  
TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
FILE REFERENCE: 28967/37084A  
CURRENT APPLICATION NUMBER: US/10/046,922  
CURRENT FILING DATE: 2002-01-15  
NUMBER OF SEQ ID NOS: 80  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 34  
LENGTH: 10  
TYPE: PRT  
ORGANISM: isolated peptide

; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1)...(1)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (10)...(10)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-34

Query Match 86.8%; Score 33; DB 13; Length 10;  
Best Local Similarity 57.1%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GYXXXXW 7  
Db 2 GYWLTIW 8

RESULT 15  
US-10-046-922-35  
; Sequence 35, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 35  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: isolated peptide  
US-10-046-922-35

Query Match 86.8%; Score 33; DB 13; Length 10;  
Best Local Similarity 57.1%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GYXXXXW 7  
Db 2 GYWLTIW 8

Search completed: December 30, 2004, 13:50:02  
Job time : 53.1698 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 12:58:17 ; Search time 8.0566 Seconds  
(without alignments)  
83.598 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYVXXXW 7  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	72	2	S12190
2	34	89.5	108	2	S12193
3	34	89.5	345	2	T37139
4	34	89.5	469	2	D70048
5	34	89.5	472	2	E83497
6	34	89.5	475	2	T46745
7	34	89.5	482	2	JH0110
8	34	89.5	490	2	C86879
9	34	89.5	497	2	G86878
10	33	86.8	142	2	C34903
11	33	86.8	227	2	S73905
12	33	86.8	250	2	A69843
13	33	86.8	289	2	G72215
14	33	86.8	360	2	AE2047
15	33	86.8	441	2	C95307
16	33	86.8	508	2	C95282
17	33	86.8	517	2	A13201
18	33	86.8	519	2	E83268
19	33	86.8	534	2	T15414
20	33	86.8	535	2	B95952
21	33	86.8	541	2	AC2392
22	33	86.8	563	2	AH2975
23	33	86.8	563	2	C98307
24	33	86.8	592	2	T15413
25	33	86.8	778	2	T31037
26	33	86.8	1502	2	T42216
27	32	84.2	71	2	S22905
28	32	84.2	83	2	E69903
29	32	84.2	187	2	G83047

30	32	84.2	218	2	S76385	hypothetical prote
31	32	84.2	218	2	D87264	hypothetical prote
32	32	84.2	257	2	E75325	probable mcfp prot
33	32	84.2	261	2	JCS806	aquaporin 8 - mous
34	32	84.2	263	2	JCS622	aquaporin 8 - rat
35	32	84.2	271	2	P83188	phosphatidate cyti
36	32	84.2	271	2	JC4832	phosphatidate cyti
37	32	84.2	282	2	H95869	probable sugar ABC
38	32	84.2	286	2	H88690	protein F4IH10.7 (
39	32	84.2	344	2	C82611	hypothetical prote
40	32	84.2	447	2	H97146	siderophore/Surfac
41	32	84.2	448	2	AB0301	conserved hypothet
42	32	84.2	466	2	T35164	probable secreted
43	32	84.2	519	2	S77572	oligopeptide trans
44	32	84.2	536	2	G95389	probable ABC trans
45	32	84.2	631	2	B86233	hypothetical prote

ALIGNMENTS

RESULT 1

T03190  
hypothetical protein 72B - rice mitochondrion  
C:Species: mitochondrion Oryza sativa (rice)  
C>Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
C:Accession: T03190  
R:Itadani, H.; Wakasugi, T.; Sugita, M.; Sugiura, M.; Nakazono, M.; Hirai, A.  
Plant Cell Physiol. 35, 1239-1244, 1994  
A:Title: Nucleotide sequence of a 28-Kbp portion of rice mitochondrial DNA: the existence  
A:Reference number: Z14841; MUID:95211382; PMID:7545979  
A:Accession: T03190  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-72 <ITA>  
A:Cross-references: UNIPROT:Q35302; EMBL:D32052; NID:g769704; PIDN:BAA06811.1; PID:g76970  
A:Experimental source: cultivar Nipponbare  
C:Genetics:  
A:Genome: mitochondrion  
C:Keywords: mitochondrion

Query Match 89.5%; Score 34; DB 2; Length 72;  
Best Local Similarity 57.1%; Pred. No. 15;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	GYVXXXW	7
Db	34	GYVSSHW	40

RESULT 2

S12193  
hypothetical protein 4 - Thiobacillus ferrooxidans plasmid pTF1  
C:Species: Thiobacillus ferrooxidans  
C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S12193  
R:Drolet, M.; Zanga, P.; Lau, P.C.K.  
Mol. Microbiol. 4, 1381-1391, 1990  
A:Title: The mobilization and origin of transfer regions of a Thiobacillus ferrooxidans  
A:Reference number: S12188; MUID:91125140; PMID:2280689  
A:Accession: S12193  
A>Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-108 <DRO>  
A:Cross-references: UNIPROT:P20088; EMBL:X52699; NID:g48158; PIDN:CAA36930.1; PID:g48164  
C:Genetics:  
A:Genome: plasmid pTF1

Query Match 89.5%; Score 34; DB 2; Length 108;  
Best Local Similarity 57.1%; Pred. No. 21;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	GYVXXXW	7
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Db      89 GYWRSSW 95
|||||
RESULT 3
T37139
hypothetical protein SCJ9A.03c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37139
R:Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A:Reference number: Z21622
A:Accession: T37139
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-345 <HAR>
A:Cross-references: UNIPROT:Q981R7; EMBL:AL109972; PIDN:CAB53264.1; GSPDB:GN00070; SCORE
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCJ9A.03c
C:Superfamily: Streptomyces coelicolor hypothetical protein SCJ9A.03c

Query Match      89.5%; Score 34; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
|||
Db 147 GYWAARW 153

RESULT 4
D70048
ABC transporter (amino acid permease) homolog yvsh - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: D70048
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berta
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koeter, P.; Koningsstein, G.; Kroch, S.; Kunano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Laubert, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Serof
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yaumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D70048
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-469 <KUN>
A:Cross-references: UNIPROT:O32204; GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15339.
A:Experimental source: strain 168
C:Genetics:
A:Gene: yvsh
C:Superfamily: L-lysine transport protein

Query Match      89.5%; Score 34; DB 2; Length 469;
Best Local Similarity 57.1%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
|||
Db 97 GYVWASW 103

RESULT 5
E83497
probable amino acid permease PA1194 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: E83497
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: E83497
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-472 <STO>
A:Cross-references: UNIPROT:Q914E4; GB:AE004549; GB:AE004091; NID:G9947110; PIDN:AAG0456;
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA1194
C:Superfamily: L-lysine transport protein

Query Match      89.5%; Score 34; DB 2; Length 472;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
|||
Db 94 GYWISAW 100

RESULT 6
T46745
arginine/ornithine antiporter [imported] - Lactobacillus sakei
C:Species: Lactobacillus sakei
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T46745
R:Zuniga, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, C
J. Bacteriol. 180, 4154-4159, 1998
A:Title: Structural and functional analysis of the gene cluster encoding the enzymes of t
A:Reference number: Z23141; MUID:98361904; PMID:9696763
A:Accession: T46745
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-475 <ZUN>
A:Cross-references: UNIPROT:O53092; EMBL:AJ001330; NID:G2764610; PIDN:CAA04686.1; PID:G2
C:Genetics:
A:Gene: arcD
C:Function:
A:Description: necessary for arginine transport; involved in ornithine-arginine exchange
A:Pathway: arginine catabolism
C:Superfamily: L-lysine transport protein

Query Match      89.5%; Score 34; DB 2; Length 475;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7
|||
Db 94 GYWSAW 100

RESULT 7
JH0110
arginine/ornithine antiporter PAS170 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: JH0110; AB2999
R:Luethi, E.; Baur, H.; Gamber, M.; Brunner, F.; Villevall, D.; Mercenier, A.; Haas, D.
Gene 87, 37-43, 1990
A:Title: The arc operon for anaerobic arginine catabolism in Pseudomonas aeruginosa cont
A:Reference number: JH0110; MUID:90236296; PMID:2158926
A:Accession: JH0110

```

A:Molecule type: DNA  
A:Residues: 1-482 <LUE>  
A:Cross-references: UNIPROT:P18275; GB:W33223; NID:g151030; PIDN:AAA25719.1; PID:g151031  
A:Experimental source: strain PA01  
A:Note: the gene encoding this protein is located upstream of the arcABC genes which encode for the production of the autoinducer.  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim, J.; Lory, S.; Olson, M.V.  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen.  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: A82999  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-482 <STO>  
A:Cross-references: GB:AE004930; GB:AE004091; NID:g9951472; PIDN:AAG08555.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: arcD; PA5170  
C:Superfamily: L-lysine transport protein  
C:Keywords: transmembrane protein

Query Match 89.5%; Score 34; DB 2; Length 482;  
Best Local Similarity 57.1%; Pred. No. 82;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
|||  
DB 94 GYWSANW 100

RESULT 8  
C86879  
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: C86879  
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich, G.  
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* subsp. *lactis*.  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: C86879  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-490 <STO>  
A:Cross-references: UNIPROT:Q8CE15; GB:AE005176; PID:g12725084; PIDN:AAK06133.1; GSPDB:G000000000  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: arcD  
C:Superfamily: L-lysine transport protein

Query Match 89.5%; Score 34; DB 2; Length 490;  
Best Local Similarity 57.1%; Pred. No. 84;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
|||  
DB 93 GYWSANW 99

RESULT 9  
C86878  
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: G86878  
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich, G.  
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* subsp. *lactis*.  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: G86878  
A>Status: preliminary  
A:Molecule type: DNA

Db 84 GYWARW 90

## RESULT 12

A69843

hypothetical protein yjba - Bacillus subtilis

C:Species: Bacillus subtilis

C&gt;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C:Accession: A69843

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteon  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A:Authors: Schleicher, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Seron  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A:Authors: Yoshikawa, H.F.; Zunstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A:Reference number: A69580; MUID:98044033; PMID:9384377

A:Accession: A69843

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-250 &lt;KUN&gt;

A:Cross-references: UNIPROT:O31597; GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB12998.

A:Experimental source: strain 168

C:Genetics:

A:Gene: yjba

C:Superfamily: Bacillus subtilis hypothetical protein yjba

Query Match 86.8%; Score 33; DB 2; Length 250;

Best Local Similarity 57.1%; Pred. No. 68;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYXXXXX 7

Db 185 GYWTW 191

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## RESULT 14

AE2047

hypothetical protein all1931 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

C&gt;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C:Accession: AE2047

R;kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AE2047

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-360 &lt;KUR&gt;

A:Cross-references: UNIPROT:Q8YVP3; GB:BA000019; PIDN:BAB73630.1; PID:g17131021; GSPDB:G

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all1931

Query Match 86.8%; Score 33; DB 2; Length 360;

Best Local Similarity 57.1%; Pred. No. 94;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYXXXXX 7

Db 127 GYWSYGV 133

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Search completed: December 30, 2004, 13:17:15

Job time : 10.2233 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 30, 2004, 12:57:52 ; Search time 64.5849 Seconds  
(without alignments)  
62.362 Million cell updates/sec

Title: US-10-046-922-67  
Perfect score: 38  
Sequence: 1 GYVXXXW 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	89.5	72	2 Q35302	Oryza sativa
2	34	89.5	108	1 YML2	THIFE
3	34	89.5	130	2 Q7U395	prochloroco
4	34	89.5	236	2 Q9WGM9	human immun
5	34	89.5	253	2 Q32816	lactococcus
6	34	89.5	234	2 Q8ET30	oceanobacill
7	34	89.5	333	2 Q6F6U4	acinetobact
8	34	89.5	345	2 Q9S1R7	streptomyce
9	34	89.5	459	2 Q9KGV3	lactococcus
10	34	89.5	464	2 Q84DL5	oenococcus
11	34	89.5	465	2 Q6HNI4	bacillus th
12	34	89.5	465	2 Q613F7	bacillus an
13	34	89.5	465	2 Q73DL5	bacillus ce
14	34	89.5	465	2 Q81HZ7	bacillus ce
15	34	89.5	465	2 A81V71	bacillus an
16	34	89.5	465	2 AAS39630	bacillus
17	34	89.5	465	2 AAT29732	bacillus
18	34	89.5	469	2 Q6TK71	streptococc
19	34	89.5	469	2 Q32204	bacillus au
20	34	89.5	469	2 AAR30325	streptoco
21	34	89.5	471	2 Q6HP27	bacillus th
22	34	89.5	471	2 Q73E85	bacillus ce
23	34	89.5	471	2 Q81IH9	bacillus ce
24	34	89.5	471	2 AAS39409	bacillus
25	34	89.5	472	2 Q914E4	pseudomonas
26	34	89.5	473	2 Q7NRJ8	chromobacte
27	34	89.5	475	1 ARCD	LACSK
28	34	89.5	475	2 Q88P50	pseudomonas
29	34	89.5	475	2 Q88P51	pseudomonas
30	34	89.5	475	2 Q8DWP9	streptococc
31	34	89.5	475	2 Q8E2J7	streptococc

32	34	89.5	478	1 ARCD_CLOPE	Q46170 clostridium
33	34	89.5	482	1 ARCD_ESEAE	P18275 pseudomonas
34	34	89.5	490	2 Q9CE15	lactococcus
35	34	89.5	497	2 Q9KGV0	lactococcus
36	34	89.5	497	2 Q9CE19	lactococcus
37	34	89.5	526	2 Q9K574	lactococcus
38	34	89.5	879	2 Q7ZJJ7	human immun
39	33	86.8	130	2 Q7VBG3	prochloroco
40	33	86.8	135	2 Q7TUV7	prochloroco
41	33	86.8	160	2 Q6NF17	corynebacte
42	33	86.8	160	2 CAE50615	Caes0615 corynebac
43	33	86.8	213	2 Q9KY37	streptomyce
44	33	86.8	224	2 Q8S486	zea mays (m
45	33	86.8	227	1 PGSA_MYCPN	P75520 mycoplasma

ALIGNMENTS

RESULT 1  
Q35302 PRELIMINARY; PRT; 72 AA.  
AC Q35302;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE ORF72B.  
OS Oryza sativa (japonica cultivar-group).  
OG Mitochondrion.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Baev A.A., Dzhumagaliev E.B., Lyubomirskaya N.V., Mizrokhi L.Y.,  
RA Il'in Y.V.;  
RT "Structure of long and short copies of the mobile dispersed gene MDG3  
of *Drosophila melanogaster*.";  
RL Dokl. Akad. Nauk SSSR 282:1483-1486(1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95308541; PubMed=7788722;  
RA Nakazono M., Itadani H., Wakasugi T., Tsutsumi N., Sugiyama M.,  
RA Hirai A.;  
RT "The rps3-rpl16-nad3-rps12 gene cluster in rice mitochondrial DNA is  
transcribed from alternative promoters.";  
RL Curr. Genet. 27:184-189(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95211382; PubMed=7545979;  
RA Itadani H., Wakasugi T., Sugita M., Sugiyama M., Nakazono M., Hirai A.;  
RT "Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA:  
the existence of many sequences that correspond to parts of  
mitochondrial genes in intergenic regions.";  
RL Plant Cell Physiol. 35:1239-1244(1994).  
DR EMBL; D32052; BAA06811.1; -;  
DR F01; T03190; T03190.  
DR Gramene; Q35302; -;  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
SQ SEQUENCE 72 AA; 8155 MW; D42D53BED28432E CRC64;

Query Match 89.5%; Score 34; DB 2; Length 72;  
Best Local Similarity 57.1%; Pred. No. 87;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYVXXXW 7

Db 34 GYVSSHW 40

RESULT 2

```
YML2_THIFE
ID YML2_THIFE STANDARD; PRT; 108 AA.
AC P20088;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DS Hypothetical 12.3 kDa protein in mobL 3' region (ORF 4).
OS Thiobacillus ferrooxidans.
OG Plasmid pTF1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
OC Acidithiobacillaceae; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33020;
RX MEDLINE=91125140; PubMed=2280689;
RA Drolet M., Zanga P., Lau P.C.K.;
RT "The mobilization and origin of transfer regions of a Thiobacillus
RT ferrooxidans plasmid: relatedness to plasmids RSF1010 and pSC101.";
RL Mol. Microbiol. 4:1381-1391(1990).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; X52699; CAA36930.1; -.
DR PIR; S12193; S12193.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 108 AA; 12335 MW; A8E67717C109A57E CRC64;

Query Match 89.5%; Score 34; DB 1; Length 108;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 89 GYWRSSW 95

RESULT 3
Q7U395 PRELIMINARY; PRT; 130 AA.
AC Q7U395;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Possible Adenoviral fiber protein (Repeat/shaf.
GN OrderedLocustNames=PMM1067;
OS Prochlorococcus marinus subsp. pastoris (strain COMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=59919;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Algren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Stiglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572092; CAE19526.1; -.
KW Complete proteome.
SQ SEQUENCE 130 AA; 14024 MW; E80F4A997FCA8CD8 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 130;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
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Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 7 GYWTAW 13

RESULT 4
Q9WGW9 PRELIMINARY; PRT; 236 AA.
AC Q9WGW9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
GN Namespol;
OS Human immunodeficiency virus 1.
OC Human immunodeficiency viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99214336; PubMed=10196293;
RA Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
RA Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
RA Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wolinsky S.M.,
RA Walker B.D.;
RT "Frequent detection of escape from cytotoxic T-lymphocyte recognition
RT in perinatal human immunodeficiency virus (HIV) type 1 transmission:
RT the ariel project for the prevention of transmission of HIV from
RT mother to infant.";
RL J. Virol. 73:3975-3985(1999).
DR EMBL; AF121641; AAD29013.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004523; F:ribonuclease H activity; IEA.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR010659; RVT connect.
DR InterPro; IPR010661; RVT thumb.
DR Pfam; PF06815; RNaseH; 1.
DR Pfam; PF06817; RVT_thumb; 1.
KW Polyprotein.
FT NON_TER 1
FT NON_TER 236
SQ SEQUENCE 236 AA; 27062 MW; 24D6BB040A80BB8 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 236;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 129 GYQATW 135

RESULT 5
Q32816 PRELIMINARY; PRT; 253 AA.
AC Q32816;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Arginine/ornithine antiporter homolog ArcD (Fragment).
GN NamesarcD;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MG1363;
RX MEDLINE=97389814; PubMed=9226255;
RA Duwat P., Cochu A., Ehrlich S.D., Gruss A.;
RT "Characterization of Lactococcus lactis UV-sensitive mutants obtained
RT by ISS1 transposition.";
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RL J. Bacteriol. 179:4473-4479 (1997).
DR EMBL; U81991; AAC45504.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0008665; F:amino acid transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
KW Transmembrane.
FT NON TER 253
SQ SEQUENCE 253 AA; 26569 MW; 1CB8FAEF6C38FBB1 CRC64;

Query Match      89.5%; Score 34; DB 2; Length 253;
Best Local Similarity 57.1%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 93 GYWLSAW 99

RESULT 6
ID Q8ET30 PRELIMINARY; PRT; 294 AA.
AC Q8ET30;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter permease.
GN OrderedLocusNames=OB0434;
OS Oceanobacillus iheyensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX NCBI_TaxID=182710;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=HTE831;
RC MEDLINE=22220767; PubMed=12235376;
RA Takami H., Takaki Y., Uchiyama I.;
RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT Ridge and its unexpected adaptive capabilities to extreme
RT environments.";
RL Nucleic Acids Res. 30:3927-3935 (2002).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -|- SIMILARITY: BELONGS TO THE ABC-3 SUBFAMILY OF INTEGRAL MEMBRANE
CC PROTEINS.
DR EMBL; AP004594; BAC12390.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001626; ABC_3.
DR Pfam; PF00950; ABC-3; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 294 AA; 31323 MW; F7550F22EA4071A CRC64;

Query Match      89.5%; Score 34; DB 2; Length 294;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 244 GYWIATW 250

RESULT 7
ID Q6F6U4 PRELIMINARY; PRT; 333 AA.
AC Q6F6U4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transporter; putative sodium/bile acid transporter family
DE protein.
GN OrderedLocusNames=ACIAD3583;
OS Acinetobacter sp. (strain ADP1).

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OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=62977;
RN [1]
RP SEQUENCE FROM N.A.
RA Barbe V., Vallienet D., Fonknechten N., Kreimeyer A., Oztas S.,
RA Labarre L., Cruveillier S., Robert C., Duprat S., Wincker P.,
RA Ornston L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
RT "Unique features revealed by the genome sequence of Acinetobacter sp.
RT ADP1, a versatile and naturally transformation competent bacterium.";
RL Nucleic Acids Res. 0:0-0 (2004).
DR EMBL; CR543861; CAG70223.1; -.
DR InterPro; IPR002657; BilAC/Na_sympor.
DR Pfam; PF01758; SBF; 1.
KW Complete proteome.
SQ SEQUENCE 333 AA; 36530 MW; 7C887F5127A40682 CRC64;

Query Match      89.5%; Score 34; DB 2; Length 333;
Best Local Similarity 57.1%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 252 GYWASRW 258

RESULT 8
ID Q9S1R7 PRELIMINARY; PRT; 345 AA.
AC Q9S1R7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein SCO0224.
GN OrderedLocusNames=SCO0224; ORFNames=SCJ9A.03c;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kießer H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kießer T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147 (2002).
DR EMBL; AL939104; CAB53264.1; -.
DR PIR; T37139; T37139.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 345 AA; 36929 MW; 23643009936285B8 CRC64;

Query Match      89.5%; Score 34; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 147 GYWAARW 153

RESULT 9
Q9KGV3 PRELIMINARY; PRT; 459 AA.
ID Q9KGV3
AC Q9KGV3;

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DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ArcD1.

GN Name=arcD1;  
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
OX NCBI\_TaxID=1360;  
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ML3;

RA Chou L., Welmer B., Xie Y.;

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=ML3;

RA Chou L.-S., Welmer B., Xie Y.;

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF282249; AAF86987.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.

DR GO; GO:0006865; P:amino acid transport; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR002293; AA/permease1.

DR InterPro; IPR004841; Permease\_region.

DR Pfam; PF00324; AA\_permease; 1.

KW Transmembrane; Transport.

SQ SEQUENCE 459 AA; 49146 MW; 9718F27B7E937242 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 459;

Best Local Similarity 57.1%; Pred. No. 4.6e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWXW 7

Db 92 GYMSAW 98

RESULT 10

Q84DL5

ID Q84DL5 PRELIMINARY;

AC Q84DL5; PRT; 464 AA.

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Arginine/ornithine antiporter ArcD2.

GN Name=arcD2;

OS Oenococcus oeni (Leuconostoc oenos).

OC Bacteria; Firmicutes; Lactobacillales; Oenococcus.

OX NCBI\_TaxID=1247;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 23279;

RX MEDLINE=22519090; PubMed=12631210;

RA Divol B., Tonon T., Morichon S., Gindreau E., Lonvaud-Funel A.;

RT "Molecular characterization of Oenococcus oeni genes encoding proteins

involved in arginine transport.";

RL J. Appl. Microbiol. 94:1738-746 (2003).

DR EMBL; AF541253; AA/O83382.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.

DR GO; GO:0006865; P:amino acid transport; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR002293; AA/permease1.

DR InterPro; IPR004841; Permease\_region.

DR Pfam; PF00324; AA\_permease; 1.

KW Transmembrane; Transport.

SQ SEQUENCE 464 AA; 50557 MW; 1C6EE79AFF9F8B84 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 464;

Best Local Similarity 57.1%; Pred. No. 4.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWXW 7

Db 92 GYMSAW 98

Qy 1 GYWXW 7

Db 94 GYWLSSW 100

RESULT 11

Q6HNI4

ID Q6HNI4 PRELIMINARY;

AC Q6HNI4; PRT; 465 AA.

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Probable arginine/ornithine antiporter protein.

GN Name=arcD; ORFNames=BT9727\_0540;

OS Bacillus thuringiensis serovar konkukian str. 97-27.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;

OC Bacillus thuringiensis serovar konkukian.

OX NCBI\_TaxID=281309;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=97-27;

RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,

RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,

RA Richardson P., Rubin E., Tice H.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AS017355; AAT62417.1; -.

DR InterPro; IPR002293; AA/permease1.

DR InterPro; IPR004841; Permease\_region.

DR Pfam; PF00324; AA\_permease; 1.

KW Transmembrane; Transport.

SQ SEQUENCE 465 AA; 50153 MW; 534F038C0A379B04 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 465;

Best Local Similarity 57.1%; Pred. No. 4.7e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7

Db 96 GYWAANW 102

RESULT 12

Q613F7

ID Q613F7 PRELIMINARY;

AC Q613F7; PRT; 465 AA.

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Amino acid permease family protein.

GN OrderedLocusNames=BAS0596;

OS Bacillus anthracis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI\_TaxID=1392;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Storne;

RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,

RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,

RA Richardson P., Rubin E., Tice H.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE017225; AAT52924.1; -.

DR InterPro; IPR002293; AA/permease1.

DR InterPro; IPR004841; Permease\_region.

DR Pfam; PF00324; AA\_permease; 1.

KW Transmembrane; Transport.

SQ SEQUENCE 465 AA; 50192 MW; 45E4E63506085DF4 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 465;

Best Local Similarity 57.1%; Pred. No. 4.7e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7

Db 96 GYWAANW 102

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Db          96 GYWAANW 102

RESULT 13
Q73DL5
ID Q73DL5 PRELIMINARY; PRT; 465 AA.
AC Q73DL5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Amino acid permease family protein.
GN OrderedLocusNames=BC0697;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Anguoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01.";
RL Nucleic Acids Res. 32:977-988(2004).
DR EMBL; AB017266; AAS39630.1; -.
DR TIGR; BCE0697; -.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 465 AA; 50193 MW; C18384E10BEC639D CRC64;

Query Match 89.5%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 96 GYWAANW 102

RESULT 14
Q91HZ7
ID Q91HZ7 PRELIMINARY; PRT; 465 AA.
AC Q91HZ7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Arginine/ornithine antiporter.
GN ORFNames=BC0629;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Greckin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91(2003).
DR EMBL; AE017000; AAP07646.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR Pfam; PF00324; AA_permease; 1.
KW Transmembrane; Transport.

SQ SEQUENCE 465 AA; 50040 MW; 9750B5D1019142F2 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 96 GYWAANW 102

RESULT 15
Q81V71
ID Q81V71 PRELIMINARY; PRT; 465 AA.
AC Q81V71; Q6KX71;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Amino acid permease family protein.
GN OrderedLocusNames=BA0629; ORFNames=GBAA0629;
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Oekstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Bean M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017026; AAP24646.1; -.
DR EMBL; AE017334; AAT29732.1; -.
DR TIGR; BA0629; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 465 AA; 50250 MW; AA04D53505386FA9 CRC64;

Query Match 89.5%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
Db 96 GYWAANW 102

Search completed: December 30, 2004, 13:16:12
Job time : 66.5849 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 22:08:20 ; Search time 148 Seconds  
(without alignments)  
19.391 Million cell updates/sec

Title: US-10-046-922-68

Perfect score: 39  
Sequence: 1 GYWXWXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 153769

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	82.1	7	5	ABP53964
2	32	82.1	8	5	ABP53965
3	31	79.5	7	3	AAy76794 Somatosta
4	31	79.5	7	5	ABP53418 Backbone
5	28	71.8	8	4	ABP24270 HIV A24 m
6	28	71.8	8	4	ABP15891 HIV A24 s
7	28	71.8	8	4	ABP15892 HIV A24 s
8	28	71.8	8	4	ABP24235 HIV A24 m
9	27	69.2	8	2	AAR32766 Lanthioni
10	27	69.2	8	6	ABU61730 Lanthioni
11	26	66.7	6	2	AAR33713 Cyclol-Ty
12	26	66.7	8	2	AAW27066 Galactana
13	26	66.7	8	2	AAy02418 Somatosta
14	25	64.1	7	3	AAy76792 Somatosta
15	25	64.1	7	5	ABP53416 Backbone
16	25	64.1	8	1	AAp61465 Cyclic oc
17	25	64.1	8	1	AAp90981 Water-ins
18	25	64.1	8	2	AAR14237 Somatosta
19	25	64.1	8	2	AAR15362 Somatosta
20	25	64.1	8	2	AAR10505 Pamoste o
21	25	64.1	8	2	AAR26369 Somatosta
22	25	64.1	8	2	AAR27185 Somatosta
23	25	64.1	8	2	AAR27187 Somatosta
24	25	64.1	8	2	AAR27197 Somatosta
25	25	64.1	8	2	AAR23952 LH-RH, so

26	25	64.1	8	2	AAR40822	Aar40822 Octapepti
27	25	64.1	8	2	AAR41502	Aar41502 Somatosta
28	25	64.1	8	2	AAR31513	Aar31513 Somatosta
29	25	64.1	8	2	AAR31511	Aar31511 Somatosta
30	25	64.1	8	2	AAR42653	Aar42653 Somatosta
31	25	64.1	8	2	AAR56781	Aar56781 Somatosta
32	25	64.1	8	2	AAR76207	Aar76207 Somatosta
33	25	64.1	8	2	AAR76205	Aar76205 Somatosta
34	25	64.1	8	2	AAR85570	Aar85570 Somatosta
35	25	64.1	8	2	AAW18454	AAW18454 Somatosta
36	25	64.1	8	2	AAW51865	AAW51865 Somatosta
37	25	64.1	8	2	AAy22844	AAy22844 Somatosta
38	25	64.1	8	2	AAy18229	AAy18229 Somatosta
39	25	64.1	8	2	AAW45740	AAW45740 Somatosta
40	25	64.1	8	2	AAW97185	AAW97185 Somatosta
41	25	64.1	8	2	ADH35407	Adh35407 Human som
42	25	64.1	8	2	ADH68008	Adh68008 Somatosta
43	25	64.1	8	2	ADK11160	Adk11160 Somatosta
44	25	64.1	8	2	ADK11282	Adk11282 Somatosta
45	25	64.1	8	2	ADK11283	Adk11283 Somatosta

ALIGNMENTS

RESULT 1  
ABP53964  
ID ABP53964 standard; peptide; 7 AA.  
AC ABP53964;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE VEGFR-3 binding peptide SEQ ID NO:67.  
XX

KW Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
KW vulnary; cell surface receptor; cancer; neovascularisation;  
KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
KW diabetes; PDGF; platelet derived growth factor.  
XX Homo sapiens.  
OS Synthetic.

EH Key Location/Qualifiers  
FT Misc-difference 4..6 /note= "X is any amino acid"  
FT

XX WO200257299-A2.  
XX 25-JUL-2002.  
XX  
PF 16-JAN-2002; 2002WO-IB0000099.  
XX

PR 17-JAN-2001; 2001US-0262476P.  
XX

PA (LUDW-) LUDWIG INST CANCER RES.  
PA (LICN) LICENTIA LTD.

XX Alitalo K, Koivunen E, Kubo H;  
PI

XX WPI; 2002-691521/74.  
XX

PT New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
such as cancer and diseases of neovascularization.

PS Claim 21; Page 81; 149pp; English.

XX The present invention describes an isolated peptide (I) that binds to and  
inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
have cytostatic, hepatotropic, antiinflammatory, hypotensive,

CC antidiabetic and vulnery activities, and can be used in gene therapy.  
 CC Compositions and methods from the present invention are useful for  
 CC diagnosing, evaluating and treating disorders mediated by the activity of  
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangionas and diabetes. The present sequence  
 CC represents a specifically claimed VEGFR-3 binding peptide from the  
 CC present invention  
 XX  
 XX  
 SQ Sequence 7 AA;

Query Match 82.1%; Score 32; DB 5; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
 |||||  
 Db 1 GYWXXXW 7

RESULT 2  
 ABP53965  
 ID ABP53965 standard; peptide; 8 AA.

AC ABP53965;

XX 09-JAN-2003 (first entry)

XX VEGFR-3 binding peptide SEQ ID NO:68.

XX Vascular endothelial growth factor receptor 3 inhibitor; VEGFR-3;  
 KW angiogenesis; lymphangiogenesis; vascular endothelial growth factor;  
 KW cytostatic; hepatotropic; antiinflammatory; hypotensive; antidiabetic;  
 KW vulnery; cell surface receptor; cancer; neovascularisation;  
 KW liver disease; hypertension; post-trauma; chronic hepatitis; haemangioma;  
 KW diabetes; PDGF; platelet derived growth factor.

XX Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Misc-difference 4..6  
 FT Misc-difference /note= "X is any amino acid"  
 FT Misc-difference 8  
 FT Misc-difference /note= "any amino acid"

XX WO200257299-A2.

XX 25-JUL-2002.

XX 16-JAN-2002; 2002WO-IB000099.

XX 17-JAN-2001; 2001US-0262476P.

XX (LUDW-) LUDWIG INST CANCER RES.  
 PA (LICN) LICENTIA LTD.

XX Alitalo K, Koivunen E, Kubo H;

XX WPI; 2002-691521/74.

XX New isolated peptide that inhibits VEGF-C and VEGF-D, useful for  
 PT diagnosing, evaluating, treating disorders mediated by VEGFR-3 activity,  
 PT such as cancer and diseases of neovascularization.

XX Claim 22; Page 81; 149pp; English.

XX The present invention describes an isolated peptide (I) that binds to and  
 CC inhibits vascular endothelial growth factor receptor 3 (VEGFR-3). (I)  
 CC have cytostatic, hepatotropic, antiinflammatory, hypotensive,

CC antidiabetic and vulnery activities, and can be used in gene therapy.  
 CC Compositions and methods from the present invention are useful for  
 CC diagnosing, evaluating and treating disorders mediated by the activity of  
 CC the cell surface receptor VEGFR-3 such as cancer, e.g. brain, lung,  
 CC liver, spleen, kidney, lymph node, small intestine, blood cells,  
 CC pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary,  
 CC skin, head and neck, oesophagus, bone, marrow or blood, and diseases of  
 CC neovascularisation, e.g. liver diseases, hypertension, post-trauma,  
 CC chronic hepatitis, haemangionas and diabetes. The present sequence  
 CC represents a specifically claimed VEGFR-3 binding peptide from the  
 CC present invention  
 XX  
 XX  
 SQ Sequence 8 AA;

Query Match 82.1%; Score 32; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
 |||||  
 Db 1 GYWXXXW 7

RESULT 3  
 AAY76794  
 ID AAY76794 standard; peptide; 7 AA.

AC AAY76794;

XX 20-APR-2000 (first entry)

XX Somatostatin analogue peptide 3181.

XX Somatostatin analogue; therapy; cyclic peptide; autoimmune disease;  
 KW endocrine disorder; cancer; diabetic-associated complication; diagnosis;  
 KW gastrointestinal disorder; inflammatory disease; pancreatitis;  
 KW atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor;  
 KW hormone-secreting tumour; hormone-dependent tumour; diarrhoea;  
 KW vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Misc-difference 3  
 FT Misc-difference /note= "D-form residue"  
 FT Modified-site 7  
 FT Modified-site /note= "Trp-NH2"

XX WO9965508-A1.

XX 23-DEC-1999.

XX 15-JUN-1999; 99WO-IL000329.

XX 19-JUN-1998; 98US-00100360.

XX 02-DEC-1998; 98US-00203389.

XX (PEPT-) PEPTOR LTD.

XX Hornik V, Afargan MM, Gellerman G;

XX WPI; 2000-136888/12.

XX Cyclized somatostatin analogs for inhibiting growth hormone secretion  
 PT from anterior pituitary and as antiproliferative agents for the treatment  
 PT of tumors.

XX Example 11; Page 61; 82pp; English.

XX This sequence represents a somatostatin analogue of the invention. The  
 CC invention relates to a backbone cyclised somatostatin analogue that has  
 CC one building unit containing a nitrogen atom of the peptide backbone  
 CC connected to a bridging group comprising an amide, thioether, thioester



XX The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
 CC be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines. An  
 CC additional advantage of an group-based vaccine approach is the ability to  
 CC combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
 XX

XX Sequence 8 AA;

Query Match 71.8%; Score 28; DB 4; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YWXXW 7  
 ||  
 2 YWQATW 7

DB

RESULT 6  
 ABP15891

ID ABP15891 standard; peptide; 8 AA.

XX

AC ABP15891;

XX

DT 11-SEP-2003 (revised)  
 DT 15-JUL-2002 (first entry)

DE HIV A24 super motif pol peptide #71.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
 KW vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus 1.

OS

XX WO200124810-A1.

PN

XX 12-APR-2001.

PD

XX 05-OCT-2000; 2000WO-US027766.

PF

XX 05-OCT-1999; 99US-00412863.

PR

XX (EPIM-) EPIMMUNE INC.

PA

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 FI WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 194; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
 CC be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines. An  
 CC additional advantage of an group-based vaccine approach is the ability to  
 CC combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
 XX

XX Sequence 8 AA;

Query Match 71.8%; Score 28; DB 4; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YWXXW 7  
 ||  
 2 YWQATW 7

DB

RESULT 7  
 ABP15892

ID ABP15892 standard; peptide; 8 AA.

XX

AC ABP15892;

XX

DT 11-SEP-2003 (revised)  
 DT 15-JUL-2002 (first entry)

DE HIV A24 super motif pol peptide #72.

XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
 KW vaccine; HIV infection; immunisation; virucide.

XX Human immunodeficiency virus 1.

OS

XX WO200124810-A1.

PN

XX 12-APR-2001.

PD

XX 05-OCT-2000; 2000WO-US027766.

PF

XX 05-OCT-1999; 99US-00412863.

PR

XX (EPIM-) EPIMMUNE INC.

PA

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;  
 PI Baker DM, Cellis E, Kubo RT, Grey HM;  
 FI WPI; 2001-354887/37.

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.

PS Claim 32; Page 194; 448pp; English.

XX The present invention describes a composition (I) comprising a prepared

CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to

CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
 CC be used for immunising subjects against HIV-1 infections. The use of  
 CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines. An  
 CC additional advantage of an group-based vaccine approach is the ability to  
 CC combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 8 AA;

Query Match 71.8%; Score 28; DB 4; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
 ||  
 DB 2 YWQATW 7

RESULT 8  
 ABP24235  
 ID ABP24235 standard; peptide; 8 AA.  
 XX  
 AC ABP24235;  
 XX  
 DT 11-SEP-2003 (revised)  
 DT 15-JUL-2002 (first entry)  
 DE  
 DE HIV A24 motif pol peptide #43.  
 XX  
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;  
 KW vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;  
 KW vaccine; HIV infection; immunisation; virucide.  
 XX  
 OS Human immunodeficiency virus 1.  
 XX  
 PN WO200124810-A1.  
 XX  
 PD 12-APR-2001.  
 XX  
 PF 05-OCT-2000; 2000WO-US027766.  
 XX  
 PR 05-OCT-1999; 99US-00412863.  
 XX  
 PA (EPIM-) EPIMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Livingston BD, Cheenut R;  
 PI Baker DW, Celis E, Kubo RT, Grey HW;  
 XX  
 DR WPI; 2001-354887/37.  
 XX  
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)  
 PT peptide groups, useful for vaccinating against HIV-1.  
 XX  
 PS Claim 32; Page 366; 448pp; English.  
 XX  
 CC The present invention describes a composition (I) comprising a prepared  
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid  
 CC sequence selected from 51 defined amino acid sequences (ABP25347 to  
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may  
 CC be used for immunising subjects against HIV-1 infections. The use of

CC group-based vaccines has several advantages over traditional vaccines,  
 CC particularly when compared to the use of whole antigens in vaccine  
 CC compositions. There is evidence that the immune response to whole  
 CC antigens is directed largely toward variable regions of the antigen,  
 CC allowing for immune escape due to mutations. The groups for inclusion in  
 CC an group-based vaccine may be selected from conserved regions of viral or  
 CC tumour-associated antigens, which therefore reduces the likelihood of  
 CC escape mutants. Furthermore, immunosuppressive groups that may be present  
 CC in whole antigens can be avoided with the use of group-based vaccines. An  
 CC additional advantage of an group-based vaccine approach is the ability to  
 CC combine selected groups (CTL and HTL), and further, to modify the  
 CC composition of the groups, achieving, for example, enhanced  
 CC immunogenicity. Accordingly, the immune response can be modulated, as  
 CC appropriate, for the target disease. Similar engineering of the response  
 CC is not possible with traditional approaches. ABP11501 to ABP25412  
 CC represent peptide sequences used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 8 AA;

Query Match 71.8%; Score 28; DB 4; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
 ||  
 DB 2 YWQATW 7

RESULT 9  
 AAR32766  
 ID AAR32766 standard; peptide; 8 AA.  
 XX  
 AC AAR32766;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 30-JUN-1993 (first entry)  
 DE  
 DE Lanthionine-peptide.  
 XX  
 KW Thioether; bond; bridge; monosulfide; monosulphide; disulfide;  
 KW disulphide.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 1 /note= "D-form residue"  
 FT Modified-site 2..7 /note= "thioether bond between A2 and A7 to form  
 FT Lanthionine"  
 FT Misc-difference 4 /note= "D-form residue"  
 FT Modified-site 8 /note= "amidated C-terminal"  
 FT  
 XX WO9303056-A1.  
 XX  
 PD 18-FEB-1993.  
 XX  
 PF 06-AUG-1992; 92WO-EP001789.  
 XX  
 PR 09-AUG-1991; 91US-00742908.  
 XX  
 PA (KOLB/) KOLBECK W.  
 XX  
 PI Goodman M, Osapay G;  
 XX  
 DR WPI; 1993-076437/09.  
 XX  
 PT New lanthionine bridged peptide deriva. - are analogues of ACTH,  
 PT angiotensin, neuro:peptide(s), bombesin, bradykinin, etc.  
 XX



RESULT 12  
AAW27066  
ID AAW27066 standard; peptide; 8 AA.  
XX AC AAW27066;  
XX AC AAW27066;  
XX 17-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 28-FEB-1998 (first entry)  
XX Galactanase peptide motif.  
XX Galactanase; fruit juice; vegetable juice; wine; pectin; depectinisation;  
KW animal feed; foodstuff.  
XX Corynascus heterochallicus; strain CBS 117.65.  
OS Humicola insolens; strain DSM 1800.  
XX WO9732014-A1.  
XX PN 04-SEP-1997.  
XX PD 28-FEB-1997; 97WO-DK000092.  
XX PF 01-MAR-1996; 96DK-00000233.  
XX PR 01-MAR-1996; 96DK-00000235.  
XX PA (NOVO ) NOVO-NORDISK AS.  
XX PI Kofod LV, Kauppinen MS, Andersen LN, Clausen IG, Muellertz A;  
PI WPI; 1997-448686/41.  
DR Fungal galactanase and related DNA - useful in animal feed industry and  
XX fruit juice depectinisation.  
XX Claim 7; Page 58; 67pp; English.  
XX This peptide comprises a motif located at amino acid residues 312-319 of  
CC the galactanase of Myceliophthora thermophila CBS 117.65 (see AAW27063)  
CC and at amino acid residues 311-318 of the galactanase of Humicola  
CC insolens DSM 1800 (see AAW27064). Another motif (see AAW27065) has also  
CC been identified. These motifs are characteristic of galactanases of fungi  
CC of the order Sordariales. PCR primers (see AAT85060-61) based on the  
CC motifs can be used to identify galactanase enzymes in Sordariales fungi.  
CC Such enzymes have an optimum pH above 5.8 and are useful in the food and  
CC feed industries, as well as in wine and juice processing. (Updated on 25-  
CC MAR-2003 to correct PI field.) (Updated on 17-OCT-2003 to standardise OS  
CC field)  
XX Sequence 8 AA;  
SQ Query Match 66.7%; Score 26; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 YWXXXW 7  
DB 2 YWEPW 7  
RESULT 13  
AAY02418  
ID AAY02418 standard; peptide; 8 AA.  
XX AC AAY02418;  
XX AC AAY02418;  
DT 12-JUL-1999 (first entry)  
XX Somatostatin analogue peptide.  
DE Somatostatin analogue peptide 3177.  
XX

KW Metallo-construct; metal ion-binding backbone; cyclic;  
KW biological function domain; conformational restriction; radiotherapeutic;  
KW combinatorial chemistry.  
XX Synthetic.  
XX Key Location/Qualifiers  
FH Misc-difference 1 /note= "D-form residue"  
FT Modified-site 3.8  
FT Misc-difference 4 /note= "linked with GGGC, GGC, GGGH or GGH"  
FT Misc-difference 7 /note= "D-form residue"  
FT Modified-site /label= Orn  
FT /note= "ornithine"  
XX WO9640293-A1.  
PN 19-DEC-1996.  
XX PD 06-JUN-1996; 96WO-US009840.  
XX PF 07-JUN-1995; 95US-00476652.  
XX PR 05-JUN-1996; 96US-00660697.  
XX (RHOM-) RHOMED INC.  
XX Sharma SD;  
XX WPI; 1997-077237/07.  
DR Metallo-constructs comprising a metal ion-binding backbone for complexing  
XX metals - and a biological function domain which may be converted from  
XX inactive to active form on binding of the construct to a metal ion.  
XX Disclosure; Page 21; 142pp; English.  
XX The specification describes a metallo-construct, which may be a peptide,  
CC comprising metal ion-binding backbone for complexing with a metal ion and  
CC a biological function domain which is conformationally constrained upon  
CC complexing the metal ion-binding backbone with a metal ion. The  
CC peptide/metal ion complexes are less susceptible to proteolysis than the  
CC uncomplexed peptide. The peptides lack conformational restriction if not  
CC complexed to a metal ion, so that the uncomplexed peptides are either  
CC inactive or low in potency. The complexed peptides may also exhibit  
CC altered biodistribution profiles, rate of clearance from the body and  
CC bioavailability. The constructs/peptides are useful as biological,  
CC therapeutic, diagnostic imaging and radiotherapeutic agents, or in  
CC combinatorial chemistry methods. The present cyclic peptide exemplifies  
CC the peptides of the invention  
XX Sequence 8 AA;  
SQ Query Match 66.7%; Score 26; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.7e+06;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 YWXXXW 7  
DB 3 YWVXW 8  
RESULT 14  
AAY76792  
ID AAY76792 standard; peptide; 7 AA.  
XX AC AAY76792;  
XX AC AAY76792;  
DT 20-APR-2000 (first entry)  
XX Somatostatin analogue peptide 3177.  
DE Somatostatin analogue peptide 3177.  
XX

KW Somatostatin analogue; therapy; cyclic peptide; autoimmune disease;  
 KW endocrine disorder; cancer; diabetic-associated complication; diagnosis;  
 KW gastrointestinal disorder; inflammatory disease; pancreatitis;  
 KW atherosclerosis; restenosis; post-surgical pain; VIP secretion inhibitor;  
 KW hormone-secreting tumour; hormone-dependent tumour; diarrhoea;  
 KW vasoactive intestinal peptide; non-insulin dependent diabetes mellitus.  
 XX Synthetic.  
 XX OS  
 XX PH Key Location/Qualifiers  
 FT Misc-difference 3 /note= "D-form residue"  
 FT Modified-site 7  
 FT /note= "Trp-NH2"  
 FT  
 PN WO9965508-A1.  
 XX  
 XX 23-DEC-1999.  
 XX  
 XX 15-JUN-1999; 99WO-IL000329.  
 XX  
 XX 19-JUN-1998; 98US-00100360.  
 PR 02-DEC-1998; 98US-00203389.  
 XX  
 XX (PEPT-) PEPTOR LTD.  
 XX  
 XX Hornik V, Afargan MM, Gellerman G;  
 XX WPI; 2000-136888/12.  
 DR  
 XX Cyclized somatostatin analogs for inhibiting growth hormone secretion  
 PT from anterior pituitary and as antiproliferative agents for the treatment  
 PT of tumors.  
 XX  
 XX Example 11; Page 61; 82pp; English.  
 PS  
 XX This sequence represents a somatostatin analogue of the invention. The  
 CC invention relates to a backbone cyclised somatostatin analogue that has  
 CC one building unit containing a nitrogen atom of the peptide backbone  
 CC connected to a bridging group comprising an amide, thioether, thioester  
 CC or disulphide. At least one building unit is connected via a bridging  
 CC group to form a cyclic structure with a moiety selected from a second  
 CC building unit, side chain of or N-terminal amino acid residue. A  
 CC composition containing the analogue may be used for preventing disorders  
 CC such as cancers, autoimmune diseases, endocrine disorders, diabetic-  
 CC associated complications, gastrointestinal disorders, inflammatory  
 CC diseases, pancreatitis, atherosclerosis, restenosis and post-surgical  
 CC pain. It may also be used for diagnosing cancer. The backbone cyclic  
 CC analogue is used for imaging the existence of metastases. Somatostatin  
 CC analogues can be used for the treatment of patients with hormone-secreting  
 CC and hormone-dependent tumours. They reduce diarrhoea through the  
 CC inhibition of vasoactive intestinal peptide (VIP) secretion and by direct  
 CC effect on intestinal secretion. Somatostatin analogues selective to type  
 CC 2 and 5 receptors may be used for treatment of non-insulin dependent  
 CC diabetes mellitus. They are useful for the prevention of atherosclerosis  
 CC and restenosis. The analogues are metabolically stable, selective in  
 CC their in-vivo activities and safe  
 XX  
 SQ Sequence 7 AA;

Query Match 64.1%; Score 25; DB 3; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YWXXXW 7  
 |||  
 Db 2 YWKVCW 7

RESULT 15  
 ABP53416  
 ID ABP53416 standard; peptide; 7 AA.  
 XX

AC ABP53416;  
 XX  
 XX 19-NOV-2002 (first entry)  
 XX  
 DE Backbone cyclised somatostatin analogue PTR 3177.  
 XX  
 KW Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;  
 KW somatostatin release inhibiting factor; somatostatin receptor subtype;  
 KW synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer;  
 KW antidiabetic; antiinflammatory; somatostatin receptor ligand; atherosclerosis;  
 KW atherosclerosis; autoimmune disease; diabetic-associated complication;  
 KW endocrine disorder; inflammation; gastrointestinal disorder; restenosis;  
 KW pancreatitis; post-surgical pain.  
 XX  
 XX Synthetic.  
 XX OS  
 XX PH Key Location/Qualifiers  
 FT Misc-difference 3 /note= "D form residue"  
 FT Modified-site 7 /note= "amidated"  
 FT  
 XX US2002052315-A1.  
 PN  
 XX 02-MAY-2002.  
 XX  
 XX 13-DEC-2000; 2000US-00734583.  
 PF  
 XX 19-JUN-1998; 98US-00100360.  
 PR 02-DEC-1998; 98US-00203389.  
 PR 15-JUN-1999; 99WO-IL000329.  
 XX  
 XX (HORN/) HORNIK V.  
 PA (AFAR/) AFARGAN M M.  
 PA (GELL/) GELLERMAN G.  
 XX  
 XX Hornik V, Afargan MM, Gellerman G;  
 XX WPI; 2002-681319/73.  
 DR  
 XX New backbone cyclised somatostatin analogs are e.g. useful in the  
 PT treatment of atherosclerosis, autoimmune diseases and cancers.  
 XX  
 XX Example 12; Page 21; 30pp; English.  
 PS  
 XX The present invention describes backbone cyclised somatostatin analogues  
 CC (I) that incorporates at least one building unit containing one nitrogen  
 CC atom of the peptide backbone connected to a bridging group (comprising an  
 CC amide, thioether, thioester or disulfide) where at least one building  
 CC unit is connected via the bridging group to form a cyclic structure with  
 CC a moiety selected from the group consisting of a second building unit,  
 CC the side chain of an amino acid residue of the sequence or the N-terminal  
 CC amino acid residue. (I) has antiarteriosclerotic, immunosuppressive,  
 CC cytostatic, antidiabetic, antiinflammatory and analgesic activities, and  
 CC can be used as a somatostatin receptor ligand. (I) are useful in the  
 CC treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-  
 CC associated complications, endocrine disorders, inflammation,  
 CC gastrointestinal disorders, pancreatitis, post-surgical pain, and  
 CC restenosis. (I) can also be used in the diagnosis of cancer, by imaging  
 CC the existence of metastases, it being labeled with a detectable probe.  
 CC The present sequence represents a backbone cyclised somatostatin analogue  
 CC from the present invention  
 XX  
 SQ Sequence 7 AA;

Query Match 64.1%; Score 25; DB 5; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+06;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YWXXXW 7  
 |||  
 Db 2 YWKVCW 7

Search completed: December 29, 2004, 22:23:57  
Job time : 150 secs

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OM protein - protein search, using sw model

Run on: December 29, 2004, 22:13:25 ; Search time 37 Seconds  
(without alignments)  
14.339 Million cell updates/sec

Title: US-10-046-922-68  
Perfect score: 39  
Sequence: 1 GYMXXWX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 73656

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Maximum DB seq length: 8

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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6: /cgn2.6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	61.5	5	1 US-08-353-400-27	Sequence 27, Appl
2	24	61.5	5	4 US-08-753-750B-38	Sequence 38, Appl
3	24	61.5	5	6 5185431-15	Patent No. 5185431
4	24	61.5	6	1 US-07-718-577-6	Sequence 6, Appl
5	24	61.5	7	1 US-07-973-235A-30	Sequence 30, Appl
6	24	61.5	7	1 US-08-443-640-16	Sequence 16, Appl
7	24	61.5	7	2 US-08-462-720-30	Sequence 30, Appl
8	24	61.5	7	4 US-09-388-788-2	Sequence 2, Appl
9	24	61.5	7	4 US-09-069-827A-94	Sequence 94, Appl
10	24	61.5	7	4 US-09-563-222C-53	Sequence 53, Appl
11	24	61.5	8	3 US-08-467-472C-5	Sequence 5, Appl
12	24	61.5	8	3 US-08-467-472C-6	Sequence 6, Appl
13	24	61.5	8	3 US-08-586-670A-17	Sequence 17, Appl
14	24	61.5	8	3 US-09-384-061-5	Sequence 5, Appl
15	24	61.5	8	3 US-09-384-061-6	Sequence 6, Appl
16	24	61.5	8	4 US-09-125-641-1	Sequence 1, Appl
17	24	61.5	8	4 US-09-125-641-2	Sequence 2, Appl
18	24	61.5	8	4 US-09-852-870A-5	Sequence 5, Appl
19	23	59.0	8	3 US-08-467-472C-7	Sequence 7, Appl
20	23	59.0	8	3 US-08-467-472C-8	Sequence 8, Appl
21	23	59.0	8	3 US-09-384-061-7	Sequence 7, Appl
22	23	59.0	8	3 US-09-384-061-8	Sequence 8, Appl
23	23	59.0	8	4 US-09-852-870A-7	Sequence 7, Appl
24	22	56.4	6	2 US-08-446-345-12	Sequence 12, Appl
25	22	56.4	6	3 US-08-951-260A-2	Sequence 2, Appl
26	22	56.4	6	3 US-08-884-569A-11	Sequence 11, Appl
27	22	56.4	6	3 US-08-884-569A-14	Sequence 14, Appl

28	22	56.4	6	4 US-09-430-626A-2	Sequence 2, Appl
29	22	56.4	6	4 US-09-361-096A-46	Sequence 46, Appl
30	22	56.4	6	4 US-09-743-492A-5	Sequence 5, Appl
31	22	56.4	6	4 US-10-243-687-2	Sequence 2, Appl
32	22	56.4	7	2 US-08-652-971-5	Sequence 5, Appl
33	22	56.4	7	2 US-08-991-258A-5	Sequence 5, Appl
34	22	56.4	7	2 US-08-769-399-5	Sequence 5, Appl
35	22	56.4	7	3 US-08-991-953A-5	Sequence 5, Appl
36	22	56.4	8	3 US-09-100-804-5	Sequence 5, Appl
37	22	56.4	8	3 US-09-081-345-5	Sequence 5, Appl
38	22	56.4	8	3 US-09-095-443-6	Sequence 6, Appl
39	22	56.4	8	4 US-09-794-529B-1	Sequence 1, Appl
40	22	56.4	8	4 US-09-794-517A-1	Sequence 1, Appl
41	22	56.4	8	4 US-09-011-645E-1	Sequence 1, Appl
42	22	56.4	8	4 US-09-794-832-1	Sequence 1, Appl
43	22	56.4	8	4 US-09-680-806A-1	Sequence 1, Appl
44	22	56.4	8	4 US-09-552-868-1	Sequence 1, Appl
45	22	56.4	8	4 US-09-636-295-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1  
US-08-353-400-27  
; Sequence 27, Application US/08353400  
; Patent No. 5665357  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 37  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION NUMBER: US/08/353,400  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9324819.3  
; FILING DATE: 03-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9411089.7  
; FILING DATE: 03-JUN-1994  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-353-400-27

Query Match 61.5%; Score 24; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
DB 1 GYW 3

RESULT 2  
US-08-753-750B-38  
; Sequence 38, Application US/08753750B  
; Patent No. 6610506  
; GENERAL INFORMATION:  
; APPLICANT: Lo, Reggie Y.C.  
; APPLICANT: Schryvers, Anthony B.  
; APPLICANT: Potter, Andrew A.  
; TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF

```
; TITLE OF INVENTION: PASTEURILLA HAEMOLYTICA AND VACCINES CONTAINING THE SAME
; FILE REFERENCE: A34762 021645.0105
; CURRENT APPLICATION NUMBER: US/08/753,750B
; CURRENT FILING DATE: 1996-11-29
; PRIOR APPLICATION NUMBER: CA 2,164,274
; PRIOR FILING DATE: 1995-12-01
; PRIOR APPLICATION NUMBER: 60/008,569
; PRIOR FILING DATE: 1995-12-01
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Pasteurella haemolytica
US-08-753-750B-38

Query Match          61.5%; Score 24; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYW 3
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Db      3 GYW 5

RESULT 3
5185431-15
; Patent No. 5185431
; APPLICANT: YOSHIMATSU, KENTARO; SHIKATA, YASUSHI; TANAKA, ISAO;
; HASEGAWA, YOSHIKAZU; SETO, TOSHIO; OSAWA, TOSHIO
; TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392,841
; FILING DATE: 11-AUG-1989
; SEQ ID NO: 15
; LENGTH: 5
5185431-15

Query Match          61.5%; Score 24; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYW 3
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Db      2 GYW 4

RESULT 4
US-07-718-577-6
; Sequence 6, Application US/07718577
; Patent No. 5432018
; GENERAL INFORMATION:
; APPLICANT: Dower, William J.
; APPLICANT: Cwirlla, Steven E.
; APPLICANT: Barrett, Ronald W.
; TITLE OF INVENTION: PEPTIDE LIBRARY AND
; SCREENING SYSTEMS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart Street
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/07/718,577
; FILING DATE: 19910620
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/541,108
; FILING DATE: 20-JUN-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-25-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-718-577-6

Query Match          61.5%; Score 24; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYW 3
        |||
Db      2 GYW 4

RESULT 5
US-07-973-235A-30
; Sequence 30, Application US/07973235A
; Patent No. 5491130
; GENERAL INFORMATION:
; APPLICANT: David D. Roberts, et al.
; TITLE OF INVENTION: Peptide Inhibitors of Fibronection and
; Related Collagen-Binding Proteins
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,235A
; FILING DATE: 19921110
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Robert L. Price
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: AMINO ACIDS
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-973-235A-30

Query Match          61.5%; Score 24; DB 1; Length 7;
Best Local Similarity 42.9%; Pred. No. 3.8e+05;
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Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
| | | | |  
Db 1 GWSKSW 7

## RESULT 6

US-08-443-640-16  
; Sequence 16, Application US/08443640  
; Patent No. 5691140  
; GENERAL INFORMATION:  
; APPLICANT: NOREN, CHRISTOPHER J.  
; APPLICANT: EVANS, PAUL D.  
; TITLE OF INVENTION: BIDIRECTIONAL IN VITRO TRANSCRIPTION  
; TITLE OF INVENTION: VECTORS UTILIZING A SINGLE RNA POLYMERASE FOR BOTH  
; TITLE OF INVENTION: DIRECTIONS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NEW ENGLAND BIOLABS, INC  
; STREET: 32 TOZER ROAD  
; CITY: BEVERLY  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 01915  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/443,640  
; FILING DATE: 18-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILLIAMS, GREGORY D.  
; REGISTRATION NUMBER: 30901  
; REFERENCE/DOCKET NUMBER: NEB-102  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508) 927-5054  
; TELEFAX: (508) 927-1705  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-443-640-16

Query Match 61.5%; Score 24; DB 1; Length 7;  
Best Local Similarity 42.9%; Pred. No. 3.8e+05; Indels 4; Mismatches 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
| | | | |  
Db 1 GWSKSW 7

## RESULT 7

US-08-462-720-30  
; Sequence 30, Application US/08462720  
; Patent No. 5849701  
; GENERAL INFORMATION:  
; APPLICANT: Roberts, David D.  
; APPLICANT: Kruttsch, Henry C.  
; APPLICANT: Sipes, John M.  
; APPLICANT: Guo, Neng-hua  
; APPLICANT: Negre, Eric  
; TITLE OF INVENTION: Peptide Inhibitors of Fibronectin and  
; TITLE OF INVENTION: Related Collagen-Binding Proteins  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/462,720  
; FILING DATE: 05-JUN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dow, Karen B.  
; REGISTRATION NUMBER: 29,684  
; REFERENCE/DOCKET NUMBER: 015280-02311100S  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-462-720-30

Query Match 61.5%; Score 24; DB 2; Length 7;  
Best Local Similarity 42.9%; Pred. No. 3.8e+05; Indels 4; Mismatches 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
| | | | |  
Db 1 GWSKSW 7

## RESULT 8

US-09-388-788-2  
; Sequence 2, Application US/09388788  
; Patent No. 6429359  
; GENERAL INFORMATION:  
; APPLICANT: LAMPPA, GAYLE  
; TITLE OF INVENTION: PRODUCTION OF CELLULOSE IN PLASTIDS OF TRANSGENIC  
; FILE REFERENCE: 21459/90301  
; CURRENT APPLICATION NUMBER: US/09/388,788  
; CURRENT FILING DATE: 1999-09-02  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fusion Protein  
; OTHER INFORMATION: Construct  
US-09-388-788-2

Query Match 61.5%; Score 24; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05; Indels 0; Mismatches 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYX 3  
| | |  
Db 5 GYX 7

## RESULT 9

US-09-069-827A-94

; Sequence 94, Application US/09069827A  
; Patent No. 6617114  
; GENERAL INFORMATION:  
; APPLICANT: FOWLKES, Dana M  
; KAY, Brian K  
; FRELINGER, Jeffrey A  
; HYDE-DERUYSCHE, Robin P  
; TITLE OF INVENTION: IDENTIFICATION OF DRUGS USING  
; COMPLEMENTARY COMBINATORIAL LIBRARIES  
; NUMBER OF SEQUENCES: 178  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 624 Ninth Street N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/069,827A  
; FILING DATE: 30-Apr-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/050,359  
; FILING DATE: 31-MAR-1998  
; APPLICATION NUMBER: PCT/US97/19638  
; FILING DATE: 31-OCT-1997  
; APPLICATION NUMBER: US 08/740,671  
; FILING DATE: 31-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: COOPER, Iver P  
; REGISTRATION NUMBER: 28,005  
; REFERENCE/DOCKET NUMBER: FOWLKES=4C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 94:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 94:  
US-09-069-827A-94

Query Match 61.5%; Score 24; DB 4; Length 7;  
Best Local Similarity 50.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
|||  
Db 1 YWPDW 6

RESULT 10  
US-09-563-222C-53  
; Sequence 53, Application US/09563222C  
; Patent No. 6696620  
; GENERAL INFORMATION:  
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.  
; APPLICANT: HIATT, ANDREW C.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS  
; FILE REFERENCE: 068904-0501  
; CURRENT APPLICATION NUMBER: US/09/563,222C  
; CURRENT FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: PCT/US01/14349  
; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: 09/563,222  
; PRIOR FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 53  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222C-53

Query Match 61.5%; Score 24; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 2 GYW 4

RESULT 11  
US-08-467-472C-5  
; Sequence 5, Application US/08467472C  
; Patent No. 6028168  
; GENERAL INFORMATION:  
; APPLICANT: GOODMAN, MURRAY  
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY  
; STREET: 99 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" FLOPPY DISC  
; COMPUTER: COMPAQ - IBM COMPATIBLE  
; OPERATING SYSTEM: MS-DOS Version 6.2  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US 07/742,908  
; FILING DATE: 9-AUGUST-1991  
; APPLICATION NUMBER: US 08/021,606  
; FILING DATE: 28-JANUARY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ROBINSON, WILLIAM R.  
; REGISTRATION NUMBER: 27,224  
; REFERENCE/DOCKET NUMBER: LKR-9122B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 697-3355  
; TELEFAX: (212) 557-5635  
; TELEX: NONE  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; DESCRIPTION: N/A  
; HYPOTHETICAL: N/A  
; ANTI-SENSE: N/A  
; FRAGMENT TYPE: INTERNAL  
; ORIGINAL SOURCE: INC.  
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE  
; POSITION IN GENOME: N/A  
; FEATURE:  
; NAME/KEY: ENANTIOMER  
; LOCATION: -4

/ IDENTIFICATION METHOD: amino acid analysis  
/ IDENTIFICATION METHOD: mass spectrometry  
/ OTHER INFORMATION: water is removed and  
/ OTHER INFORMATION: thereby  
/ OTHER INFORMATION: a -S- bridge is present between Cys and Ser  
/ PUBLICATION INFORMATION:  
/ AUTHORS: JUNG, GUNTHER

/ TITLE: PEPTIDES WITH SULFIDE BRIDGES AND  
/ JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
/ JOURNAL: PEPTIDE  
/ JOURNAL: SYMPOSIUM  
/ VOLUME: ESCOM (LEIDEN 1990)

/ ISSUE: 865 - 869

/ PAGES: 865 - 869

/ DATE: 1990

/ DOCUMENT NUMBER:

/ FILING DATE:

/ PUBLICATION DATE:  
/ RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER  
/ PUBLICATION INFORMATION:

/ AUTHORS: SHIBA, TETSUO

/ TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES

/ JOURNAL: BIOPOLYMERS

/ VOLUME: JOHN WILEY AND SONS, INC.

/ ISSUE: SUPPLEMENTARY

/ PAGES: 511 - 519

/ DATE: 1986

/ DOCUMENT NUMBER:

/ FILING DATE:

/ PUBLICATION DATE:  
/ RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER  
/ PUBLICATION INFORMATION:

/ AUTHORS: BEAN, MARK F.

/ TITLE: IDENTIFICATION OF A THIOETHER

/ BY-PRODUCT

/ TITLE: BY

/ TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE

/ TITLE: TANDEM MASS SPECTROMETRY

/ JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN

/ JOURNAL: PEPTIDE

/ JOURNAL: SYMPOSIUM

/ VOLUME: ESCOM (LEIDEN 1990)

/ ISSUE:

/ PAGES: 443 - 445

/ DATE: 1990

/ DOCUMENT NUMBER:

/ FILING DATE:

/ PUBLICATION DATE:

/ RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER  
/ RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE

US-08-467-472C-5

Query Match 61.5%; Score 24; DB 3; Length 8;  
Best Local Similarity 33.3%; Pred. No. 3.8e+05;  
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YWXXW 7

Db 3 FWKTSW 8

RESULT 12

US-08-467-472C-6

/ Sequence 6, Application US/08467472C

/ Patent No. 6028168

/ GENERAL INFORMATION:

/ APPLICANT: GOODMAN, MURRAY

/ TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES

/ NUMBER OF SEQUENCES: 24

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY

/ STREET: 99 PARK AVENUE

/ CITY: NEW YORK  
/ STATE: NY  
/ COUNTRY: USA  
/ ZIP: 10016  
/ COMPUTER READABLE FORM:  
/ MEDIUM TYPE: 3.5" FLOPPY DISC  
/ COMPUTER: COMPAQ - IBM COMPATIBLE  
/ OPERATING SYSTEM: MS-DOS Version 6.2  
/ SOFTWARE: ASCII  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/08/467,472C  
/ FILING DATE: 6-JUNE-1995  
/ CLASSIFICATION: 514  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: US 07/742,908  
/ FILING DATE: 9-AUGUST-1991  
/ APPLICATION NUMBER: US 08/021,606  
/ FILING DATE: 28-JANUARY-1993  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: ROBINSON, WILLIAM R.  
/ REGISTRATION NUMBER: 27,224  
/ REFERENCE/DOCKET NUMBER: LKR-9122B  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: (212) 697-3355  
/ TELEFAX: (212) 557-5635  
/ TELEX: NONE  
/ INFORMATION FOR SEQ ID NO: 6:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 8  
/ TYPE: AMINO ACID  
/ TOPOLOGY: LINEAR  
/ MOLECULE TYPE: PEPTIDE  
/ DESCRIPTION: N/A  
/ HYPOTHETICAL: N/A  
/ ANTI-SENSE: N/A  
/ FRAGMENT TYPE: INTERNAL  
/ ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -  
/ ORIGINAL SOURCE: INC.,  
/ IMMEDIATE SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104  
/ POSITION IN GENOME: N/A  
/ FEATURE:  
/ NAME/KEY: ENANTIOMER  
/ LOCATION: -4  
/ IDENTIFICATION METHOD: amino acid analysis  
/ IDENTIFICATION METHOD: and  
/ IDENTIFICATION METHOD: mass spectrometry  
/ OTHER INFORMATION: water is removed and  
/ OTHER INFORMATION: thereby  
/ OTHER INFORMATION: a -S- bridge is present between Cys and Ser  
/ PUBLICATION INFORMATION:  
/ AUTHORS: JUNG, GUNTHER  
/ TITLE: PEPTIDES WITH SULFIDE BRIDGES AND  
/ JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
/ JOURNAL: PEPTIDE  
/ JOURNAL: SYMPOSIUM  
/ VOLUME: ESCOM (LEIDEN 1990)  
/ ISSUE: 865 - 869  
/ PAGES: 865 - 869  
/ DATE: 1990  
/ DOCUMENT NUMBER:  
/ FILING DATE:  
/ PUBLICATION DATE:  
/ RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER  
/ PUBLICATION INFORMATION:  
/ AUTHORS: SHIBA, TETSUO  
/ TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES  
/ JOURNAL: BIOPOLYMERS  
/ VOLUME: JOHN WILEY AND SONS, INC.  
/ ISSUE: SUPPLEMENTARY  
/ PAGES: 511 - 519  
/ DATE: 1986  
/ DOCUMENT NUMBER:

; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER  
; PUBLICATION INFORMATION:  
; AUTHORS: BEAN, MARK F.  
; TITLE: IDENTIFICATION OF A THIOETHER  
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE  
; TITLE: BY  
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
; JOURNAL: PEPTIDE  
; JOURNAL: SYMPOSIUM  
; VOLUME: ESCOM (LEIDEN 1990)  
; ISSUE: 443 - 445  
; PAGES: 443 - 445  
; DATE: 1990  
; DOCUMENT NUMBER:  
; FILING DATE:  
; PUBLICATION DATE:  
; RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER  
; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE  
; US-08-467-472C-6

Query Match 61.5%; Score 24; DB 3; Length 8;  
Best Local Similarity 33.3%; Pred. No. 3.8e+05;  
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YWXXW 7  
Db 3 FWKTSW 8

RESULT 13  
US-08-586-670A-17  
; Sequence 17, Application US/08586670A  
; Patent No. 6241965  
; GENERAL INFORMATION:  
; APPLICANT: McBride, William  
; APPLICANT: Dean, Richard T.  
; TITLE OF INVENTION: Somatostatin Derivatives  
; TITLE OF INVENTION: And their Radiolabeled Products  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Banner & Witcoff, Ltd.  
; STREET: 10 South Wacker Drive, Suite 3000  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/586,670A  
; FILING DATE: 22-APR-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6241965nan, Kevin E  
; REGISTRATION NUMBER: 35,303  
; REFERENCE/DOCKET NUMBER: 92,385-DD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-715-1000  
; TELEFAX: 312-715-1234  
; TELEX: 910-221-5317  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FEATURE:

; NAME/KEY: Modified-site  
; LOCATION: 1..2  
; OTHER INFORMATION: /label= Variant residues  
; OTHER INFORMATION: /note= "Phe is in the D conformation and is  
; OTHER INFORMATION: linked to DTFA;  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 1..4  
; OTHER INFORMATION: /label= Variant residues  
; OTHER INFORMATION: /note= "The Phe is in the D conformation; Xaa  
; OTHER INFORMATION: is L-4-chlorophenylalanine; the trp is in the  
; OTHER INFORMATION: D conformation;  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 7..8  
; OTHER INFORMATION: /label= Variant residues  
; OTHER INFORMATION: /note= "The carboxyl group of the C-terminal  
; OTHER INFORMATION: Thr is reduced to an alcohol;  
; US-08-586-670A-17  
Query Match 61.5%; Score 24; DB 3; Length 8;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GYW 3  
Db 2 GYW 4  
RESULT 14  
US-09-384-061-5  
; Sequence 5, Application US/09384061  
; Patent No. 6268339  
; GENERAL INFORMATION:  
; APPLICANT: GOODMAN, MURRAY  
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY  
; STREET: 99 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" FLOPPY DISC  
; COMPUTER: COMPAQ - IBM COMPATIBLE  
; OPERATING SYSTEM: MS-DOS Version 6.2  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/384,061  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/467,472  
; FILING DATE:  
; APPLICATION NUMBER: US 08/021,606  
; FILING DATE: 28-JANUARY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ROBINSON, WILLIAM R.  
; REGISTRATION NUMBER: 27,224  
; REFERENCE/DOCKET NUMBER: LKR-9122B  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 697-3355  
; TELEFAX: (212) 557-5635  
; TELEX: NONE  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
; DESCRIPTION: PEPTIDE

;; HYPOTHETICAL: N/A  
;; ANTI-SENSE: N/A  
;; FRAGMENT TYPE: INTERNAL  
;; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -  
;; IMMEDIATE SOURCE: INC.,  
;; POSITION IN GENOME: SYNTHESIZED PEPTIDE  
;; FEATURE:  
;; NAME/KEY: ENANTIOMER  
;; LOCATION: -4  
;; IDENTIFICATION METHOD: amino acid analysis  
;; IDENTIFICATION METHOD: mass spectrometry  
;; OTHER INFORMATION: water is removed and  
;; OTHER INFORMATION: thereby  
;; OTHER INFORMATION: a -S- bridge is present between Cys and Ser  
;; PUBLICATION INFORMATION:  
;; AUTHORS: JUNG, GUNTHER  
;; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND  
;; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
;; JOURNAL: PEPTIDE  
;; JOURNAL: SYMPOSIUM  
;; VOLUME: ESCOM (LEIDEN 1990)  
;; ISSUE: 865 - 869  
;; PAGES: 865 - 869  
;; DATE: 1990  
;; DOCUMENT NUMBER:  
;; FILING DATE:  
;; PUBLICATION DATE:  
;; RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER  
;; PUBLICATION INFORMATION:  
;; AUTHORS: SHIBA, TETSUO  
;; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES  
;; JOURNAL: BIOPOLYMERS  
;; VOLUME: JOHN WILEY AND SONS, INC.  
;; ISSUE: SUPPLEMENTARY  
;; PAGES: 511 - 519  
;; DATE: 1986  
;; DOCUMENT NUMBER:  
;; FILING DATE:  
;; PUBLICATION DATE:  
;; RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER  
;; PUBLICATION INFORMATION:  
;; AUTHORS: BEAN, MARK F.  
;; TITLE: IDENTIFICATION OF A THIOETHER  
;; TITLE: BY-PRODUCT  
;; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE  
;; TITLE: BY  
;; TITLE: TANDEM MASS SPECTROMETRY  
;; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
;; JOURNAL: PEPTIDE  
;; JOURNAL: SYMPOSIUM  
;; VOLUME: ESCOM (LEIDEN 1990)  
;; ISSUE:  
;; PAGES: 443 - 445  
;; DATE: 1990  
;; DOCUMENT NUMBER:  
;; FILING DATE:  
;; PUBLICATION DATE:  
;; RELEVANT RESIDUES IN SEQ ID NO: 5: CYS-SER  
;; RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE  
US-09-384-061-5

Query Match 61.5%; Score 24; DB 3; Length 8;  
Best Local Similarity 33.3%; Prod. No. 3.8e+05;  
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXXW 7  
Db 3 FWKTSW 8

RESULT 15

US-09-384-061-6  
;; Sequence 6, Application US/09384061  
;; Patent No. 6268339  
;; GENERAL INFORMATION:  
;; APPLICANT: GOODMAN, MURRAY  
;; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES  
;; NUMBER OF SEQUENCES: 24  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: BROOKS HAIDT HOFFNER & DELAHUNTY  
;; STREET: 99 PARK AVENUE  
;; CITY: NEW YORK  
;; STATE: NY  
;; COUNTRY: USA  
;; ZIP: 10016  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 3.5" FLOPPY DISC  
;; COMPUTER: COMPAQ - IBM COMPATIBLE  
;; OPERATING SYSTEM: MS-DOS Version 6.2  
;; SOFTWARE: ASCII  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/384,061  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/467,472  
;; FILING DATE:  
;; APPLICATION NUMBER: US 08/021,606  
;; FILING DATE: 28-JANUARY-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: ROBINSON, WILLIAM R.  
;; REGISTRATION NUMBER: 27,224  
;; REFERENCE/DOCKET NUMBER: LKR-9122B  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 697-3355  
;; TELEFAX: (212) 557-5635  
;; TELEX: NONE  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 8  
;; TYPE: AMINO ACID  
;; TOPOLOGY: LINEAR  
;; MOLECULE TYPE: PEPTIDE  
;; DESCRIPTION: N/A  
;; HYPOTHETICAL: N/A  
;; ANTI-SENSE: N/A  
;; FRAGMENT TYPE: INTERNAL  
;; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -  
;; ORIGINAL SOURCE: INC.,  
;; IMMEDIATE SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104  
;; POSITION IN GENOME: SYNTHESIZED PEPTIDE  
;; FEATURE:  
;; NAME/KEY: ENANTIOMER  
;; LOCATION: -4  
;; IDENTIFICATION METHOD: amino acid analysis  
;; IDENTIFICATION METHOD: and  
;; IDENTIFICATION METHOD: mass spectrometry  
;; OTHER INFORMATION: water is removed and  
;; OTHER INFORMATION: thereby  
;; OTHER INFORMATION: a -S- bridge is present between Cys and Ser  
;; PUBLICATION INFORMATION:  
;; AUTHORS: JUNG, GUNTHER  
;; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND  
;; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
;; JOURNAL: PEPTIDE  
;; JOURNAL: SYMPOSIUM  
;; VOLUME: ESCOM (LEIDEN 1990)  
;; ISSUE:  
;; PAGES: 865 - 869  
;; DATE: 1990  
;; DOCUMENT NUMBER:  
;; FILING DATE:  
;; PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER  
PUBLICATION INFORMATION:  
AUTHORS: SHIBA, TETSUO  
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES  
JOURNAL: BIOPOLYMERS  
VOLUME: JOHN WILEY AND SONS, INC.  
ISSUE: SUPPLEMENTARY  
PAGES: 511 - 519  
DATE: 1986  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER  
PUBLICATION INFORMATION:  
AUTHORS: BEAN, MARK F.  
TITLE: IDENTIFICATION OF A THIOETHER  
TITLE: BY-PRODUCT  
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE  
TITLE: BY  
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN  
JOURNAL: PEPTIDE  
JOURNAL: SYMPOSIUM  
VOLUME: ESCOM (LEIDEN 1990)  
ISSUE:  
PAGES: 443 - 445  
DATE: 1990  
DOCUMENT NUMBER:  
FILING DATE:  
PUBLICATION DATE:  
RELEVANT RESIDUES IN SEQ ID NO: 6: CYS-SER  
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE  
US-09-384-061-6

Query Match 61.5%; Score 24; DB 3; Length 8;  
Best Local Similarity 33.3%; Pred. No. 3.8e+05;  
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 2 YWXXXW 7  
Db 3 FWKTSW 8

Search completed: December 29, 2004, 22:27:50  
Job time : 38 secs

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## OM protein - protein search, using sw model

Run on: December 29, 2004, 22:27:17 ; Search time 140 Seconds  
(without alignments)  
20.556 Million cell updates/sec

Title: US-10-046-922-68

Perfect score: 39

Sequence: 1 GYXXXXXW 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 83711

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA.\*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	82.1	7	13	US-10-046-922-67
2	32	82.1	8	13	US-10-046-922-68
3	25	64.1	8	14	US-10-190-082-586
4	24	61.5	5	15	US-10-436-549-496
5	24	61.5	5	15	US-10-436-549-525
6	24	61.5	5	16	US-10-712-425-496
7	24	61.5	5	16	US-10-712-425-525
8	24	61.5	6	15	US-10-418-943-48
9	24	61.5	6	16	US-10-346-737A-45
10	24	61.5	7	9	US-09-884-767A-38
11	24	61.5	7	10	US-09-563-222-53
12	24	61.5	7	15	US-10-403-938-27
13	24	61.5	7	16	US-10-475-853-6

14	24	61.5	7	17	US-10-783-950-53	Sequence 53, Appl
15	24	61.5	8	9	US-09-852-870A-5	Sequence 5, Appl
16	24	61.5	8	14	US-10-050-902-179	Sequence 179, App
17	24	61.5	8	14	US-10-050-902-180	Sequence 180, App
18	24	61.5	8	14	US-10-050-998-179	Sequence 179, App
19	24	61.5	8	14	US-10-050-998-180	Sequence 180, App
20	24	61.5	8	14	US-10-082-014-279	Sequence 279, App
21	24	61.5	8	14	US-10-372-076-133	Sequence 133, App
22	24	61.5	8	15	US-10-367-580-267	Sequence 267, App
23	24	61.5	8	15	US-10-367-593-267	Sequence 267, App
24	24	61.5	8	15	US-10-367-594-267	Sequence 267, App
25	24	61.5	8	15	US-10-367-654-267	Sequence 267, App
26	24	61.5	8	15	US-10-367-658-267	Sequence 267, App
27	24	61.5	8	15	US-10-367-668-267	Sequence 267, App
28	24	61.5	8	15	US-10-617-876-31	Sequence 31, Appl
29	24	61.5	8	15	US-10-617-876-32	Sequence 32, Appl
30	24	61.5	8	16	US-10-367-674-267	Sequence 267, App
31	24	61.5	8	16	US-10-677-074-133	Sequence 133, App
32	23	59.0	7	17	US-10-858-271-10	Sequence 10, Appl
33	23	59.0	8	9	US-09-852-870A-7	Sequence 7, Appl
34	22	56.4	5	15	US-10-243-613-84	Sequence 84, Appl
35	22	56.4	6	13	US-10-087-993-1	Sequence 1, Appl
36	22	56.4	6	14	US-10-243-687-2	Sequence 2, Appl
37	22	56.4	6	14	US-10-314-232-46	Sequence 46, Appl
38	22	56.4	7	14	US-10-190-082-55	Sequence 65, Appl
39	22	56.4	7	14	US-10-190-082-76	Sequence 76, Appl
40	22	56.4	8	9	US-09-822-295-5	Sequence 5, Appl
41	22	56.4	8	10	US-09-794-517-1	Sequence 1, Appl
42	22	56.4	8	10	US-09-794-529-1	Sequence 1, Appl
43	22	56.4	8	10	US-09-794-832-1	Sequence 1, Appl
44	22	56.4	8	10	US-09-095-478-12	Sequence 12, Appl
45	22	56.4	8	14	US-10-020-215-6	Sequence 6, Appl

## ALIGNMENTS

## RESULT 1

US-10-046-922-67  
; Sequence 67, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 67  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (4)..(6)  
; OTHER INFORMATION: X at position 4-6 is any amino acid  
US-10-046-922-67

Query Match 82.1%; Score 32; DB 13; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7

Db 1 GYXXXXXW 7

## RESULT 2

US-10-046-922-68  
; Sequence 68, Application US/10046922

; Publication No. US2002016467A1

; GENERAL INFORMATION:  
; APPLICANT: Altalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 68  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: peptide  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (4)..(6)  
; OTHER INFORMATION: X is any amino acid  
; NAME/KEY: SITE  
; LOCATION: (8)..(8)  
; OTHER INFORMATION: X is any amino acid  
US-10-046-922-68

Query Match 82.1%; Score 32; DB 13; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYXXXXW 7  
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Db 1 GYXXXXW 7

## RESULT 3

US-10-190-082-586  
; Sequence 586, Application US/10190082  
; Publication No. US20030148264A1  
; GENERAL INFORMATION:  
; APPLICANT: Lasky, Lawrence A.  
; APPLICANT: Sidhu, Sachdev S.  
; APPLICANT: Held, Heike A.  
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS  
; FILE REFERENCE: P1905R1  
; CURRENT APPLICATION NUMBER: US/10/190,082  
; CURRENT FILING DATE: 2002-07-03  
; PRIOR APPLICATION NUMBER: US 60/303,634  
; PRIOR FILING DATE: 2001-07-06  
; NUMBER OF SEQ ID NOS: 683  
; SEQ ID NO 586  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-190-082-586

Query Match 64.1%; Score 25; DB 14; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YWXXXW 7  
|||  
Db 3 YWYXW 8

## RESULT 4

US-10-436-549-496  
; Sequence 496, Application US/10436549  
; Publication No. US20040038307A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank D.  
; APPLICANT: Meng, Dr. Xun  
; APPLICANT: Chan, John W.

; APPLICANT: Zhang, Shengsheng  
; APPLICANT: Benkovic, Stephen J.  
; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN  
; TITLE OF INVENTION: PROTEIN ANALYSIS  
; FILE REFERENCE: ENGE-P01-001  
; CURRENT APPLICATION NUMBER: US/10/436,549  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: 60/379,626  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/393,233  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,235  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,211  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,280  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,197  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,223  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/430,948  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/433,319  
; PRIOR FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: 60/393,137  
; PRIOR FILING DATE: 2002-07-01  
; NUMBER OF SEQ ID NOS: 614  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 496  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Human  
US-10-436-549-496

Query Match 61.5%; Score 24; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
|||  
Db 1 GYW 3

## RESULT 5

US-10-436-549-525  
; Sequence 525, Application US/10436549  
; Publication No. US20040038307A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank D.  
; APPLICANT: Meng, Dr. Xun  
; APPLICANT: Chan, John W.  
; APPLICANT: Zhang, Shengsheng  
; APPLICANT: Benkovic, Stephen J.  
; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN  
; TITLE OF INVENTION: PROTEIN ANALYSIS  
; FILE REFERENCE: ENGE-P01-001  
; CURRENT APPLICATION NUMBER: US/10/436,549  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: 60/379,626  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/393,233  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,235  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,211  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,280  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,197  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,223  
; PRIOR FILING DATE: 2002-07-01

; PRIOR APPLICATION NUMBER: 60/430,948  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/433,319  
; PRIOR FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: 60/393,137  
; PRIOR FILING DATE: 2002-07-01  
; NUMBER OF SEQ ID NOS: 614  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 525  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Human  
US-10-436-549-525

Query Match 61.5%; Score 24; DB 15; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 2 GYW 4

## RESULT 6

US-10-712-425-496  
; Sequence 496, Application US/10712425  
; Publication No. US20040180380A1  
; GENERAL INFORMATION:

; APPLICANT: LEE, FRANK D.  
; APPLICANT: MENG, XUN

; TITLE OF INVENTION: PROTEOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN  
; MODIFICATION ANALYSIS

; FILE REFERENCE: ENGE-P02-001  
; CURRENT APPLICATION NUMBER: US/10/712,425

; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/379,626

; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/393,137

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,197

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,211

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,223

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,233

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,235

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,280

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/430,948

; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/433,319

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1386  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 496  
; LENGTH: 5

; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-712-425-496

Query Match 61.5%; Score 24; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 1 GYW 3

## RESULT 7

US-10-712-425-525  
; Sequence 525, Application US/10712425

; Publication No. US20040180380A1  
; GENERAL INFORMATION:

; APPLICANT: LEE, FRANK D.  
; APPLICANT: MENG, XUN

; TITLE OF INVENTION: PROTEOME EPITOPE TAGS AND METHODS OF USE THEREOF IN PROTEIN  
; MODIFICATION ANALYSIS

; FILE REFERENCE: ENGE-P02-001  
; CURRENT APPLICATION NUMBER: US/10/712,425

; CURRENT FILING DATE: 2003-11-13  
; PRIOR APPLICATION NUMBER: 60/379,626

; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/393,137

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,197

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,211

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,223

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,233

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,235

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,280

; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/430,948

; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/433,319

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 1386  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 525  
; LENGTH: 5

; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-712-425-525

Query Match 61.5%; Score 24; DB 16; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|||  
Db 2 GYW 4

## RESULT 8

US-10-418-943-48  
; Sequence 48, Application US/10418943

; Publication No. US2004000241A1  
; GENERAL INFORMATION:

; APPLICANT: Segall, Anca  
; APPLICANT: Pinilla, Clemencia

; TITLE OF INVENTION: RECOMBINATION MODULATORS AND METHODS  
; FOR PRODUCING AND USING THE SAME

; FILE REFERENCE: 011443 008-999  
; CURRENT APPLICATION NUMBER: US/10/418,943

; CURRENT FILING DATE: 2003-04-17  
; PRIOR APPLICATION NUMBER: 09/602,087

; PRIOR FILING DATE: 2000-06-22  
; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48

; LENGTH: 6  
; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-418-943-48

Query Match 61.5%; Score 24; DB 15; Length 6;  
Best Local Similarity 50.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 YWXXW 7  
|||  
Db 1 YWCYWW 6

RESULT 9  
US-10-346-737A-45  
; Sequence 45, Application US/10346737A  
; Publication No. US20040142379A1  
; GENERAL INFORMATION:  
; APPLICANT: St. Hilaire, Phaedria  
; TITLE OF INVENTION: AFFINITY FISHING FOR LIGANDS AND PROTEIN RECEPTORS  
; FILE REFERENCE: 11225.16US01  
; CURRENT APPLICATION NUMBER: US/10/346,737A  
; CURRENT FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 45  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide  
US-10-346-737A-45

Query Match 61.5%; Score 24; DB 16; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
|||  
Db 4 GYW 6

RESULT 10  
US-09-884-767A-38  
; Sequence 38, Application US/09884767A  
; Publication No. US20020192789A1  
; GENERAL INFORMATION:  
; APPLICANT: DYAX Corp.  
; APPLICANT: Ley, Arthur C.  
; APPLICANT: Luneau, Christopher J.  
; APPLICANT: Ladner, Robert C  
; TITLE OF INVENTION: NOVEL ENTEROKINASE CLEAVAGE SEQUENCES  
; FILE REFERENCE: DYX-012.1 US, DYX-012.1 PCT  
; CURRENT APPLICATION NUMBER: US/09/884,767A  
; CURRENT FILING DATE: 2001-06-19  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR FILING DATE: 2000-06-19  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 38  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic enterokinase cleavage sequence  
US-09-884-767A-38

Query Match 61.5%; Score 24; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
|||  
Db 1 GYW 3

RESULT 11  
US-09-563-222-53  
; Sequence 53, Application US/09563222  
; Publication No. US20030079253A1  
; GENERAL INFORMATION:  
; APPLICANT: Hiatt, Andrew  
; APPLICANT: Hein, Mich B.  
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN  
; TITLE OF INVENTION: EUKARYOTIC CELLS  
; FILE REFERENCE: 310098.406  
; CURRENT APPLICATION NUMBER: US/09/563,222  
; CURRENT FILING DATE: 2000-05-02  
; NUMBER OF SEQ ID NOS: 197  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-563-222-53

Query Match 61.5%; Score 24; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
|||  
Db 2 GYW 4

RESULT 12  
US-10-403-938-27  
; Sequence 27, Application US/10403938  
; Publication No. US20040025195A1  
; GENERAL INFORMATION:  
; APPLICANT: Bristol-Myers Squibb Company  
; TITLE OF INVENTION: NOVEL HUMAN CELL SURFACE PROTEIN WITH IMMUNOGLOBULIN FOLDS,  
; TITLE OF INVENTION: BGS-19  
; FILE REFERENCE: D0227 NP  
; CURRENT APPLICATION NUMBER: US/10/403,938  
; CURRENT FILING DATE: 2003-03-28  
; PRIOR APPLICATION NUMBER: U.S. 60/368,422  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 27  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-403-938-27

Query Match 61.5%; Score 24; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.5e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3  
|||  
Db 3 GYW 5

RESULT 13  
US-10-475-853-6  
; Sequence 6, Application US/10475853  
; Publication No. US20040121442A1  
; GENERAL INFORMATION:  
; APPLICANT: Chet, Ilan  
; APPLICANT: Viterbo, Ada  
; TITLE OF INVENTION: RECOMBINANT FUNGAL CHITINASES, POLYNUCLEOTIDE SEQUENCES ENCODING  
; TITLE OF INVENTION: PROMOTERS OF SAME AND USES THEREOF  
; FILE REFERENCE: 27049  
; CURRENT APPLICATION NUMBER: US/10/475,853  
; CURRENT FILING DATE: 2003-11-03  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: peptide derived from chit36
US-10-475-853-6

Query Match      61.5%; Score 24; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3
Db |||
1 GYW 3

RESULT 14
US-10-783-950-53
; Sequence 53, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/10/783,950
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-783-950-53

Query Match      61.5%; Score 24; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3
Db |||
2 GYW 4

RESULT 15
US-09-852-870A-5
; Sequence 5, Application US/09852870A
; Patent No. US20020165132A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Geapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge

US-09-852-870A-5
Query Match      61.5%; Score 24; DB 9; Length 8;
Best Local Similarity 33.3%; Pred. No. 1.5e+06;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 YWXXW 7
Db :|||
3 FWKTSW 8

Search completed: December 29, 2004, 22:39:08
Job time : 141 secs
```

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 22:13:51 ; Search time 38 Seconds  
(without alignments)  
20.256 Million cell updates/sec

Title: US-10-046-922-68

Perfect score: 39

Sequence: 1 GYXXXXWX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 606

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	51.3	5	JH0253	gut pentapeptide -
2	15	38.5	6	PT0532	T-cell receptor be
3	14	35.9	6	B35640	cerebellar degener
4	14	35.9	6	PT0629	T-cell receptor be
5	14	35.9	7	S21230	dermorphin (irp-4,
6	14	35.9	7	PT0728	T-cell receptor be
7	14	35.9	7	S33567	tubulin beta-3 cha
8	13	33.3	4	S09478	globulin IV alpha
9	13	33.3	6	A61411	ameletin - rat
10	13	33.3	7	A61324	dermorphin - Rohde
11	13	33.3	7	A60139	fatty-acid synthas
12	13	33.3	7	S71870	glutathione transf
13	13	33.3	7	S36662	dermorphin (Lys-7)
14	13	33.3	8	PH1618	Ig H chain V-D-J r
15	12	30.8	8	JS0315	leucokinin V - Mad
16	11	28.2	3	F37196	bradykinin-potenti
17	11	28.2	4	A34626	RPCH-related neuro
18	11	28.2	4	B53284	T-cell receptor be
19	11	28.2	4	PT0661	T-cell receptor be
20	11	28.2	5	A32516	cholecystokinin-5
21	11	28.2	5	A60803	neuropeptide - sea
22	11	28.2	5	PT0281	Ig heavy chain CRD
23	11	28.2	5	PT0308	Ig heavy chain CRD
24	11	28.2	5	PT0729	T-cell receptor be
25	11	28.2	5	PT0580	bradykinin-potenti
26	11	28.2	5	G37196	alcohol dehydrogen
27	11	28.2	6	S66195	dnaA protein - Pse
28	11	28.2	6	B34835	dihydrofolate redu
29	11	28.2	6	A31263	

30	11	28.2	6	2	B31263	dihydrofolate redu
31	11	28.2	6	2	PT0519	T-cell receptor be
32	11	28.2	6	2	PT0637	T-cell receptor be
33	11	28.2	6	2	PT0641	T-cell receptor be
34	11	28.2	6	2	PT0726	T-cell receptor be
35	11	28.2	6	2	F41946	T-cell receptor ga
36	11	28.2	6	2	PD0028	pev-kinin 2 - pena
37	11	28.2	6	2	A61068	locustakinin - mig
38	11	28.2	6	4	I79564	hypothetical TCL3
39	11	28.2	7	2	S09652	hypothetical prote
40	11	28.2	7	2	PQ0727	H2 class I protein
41	11	28.2	7	2	E48394	glycoprotein compo
42	11	28.2	7	2	PH1602	Ig H chain V-D-J r
43	11	28.2	7	2	PT0526	T-cell receptor be
44	11	28.2	7	2	PT0628	T-cell receptor be
45	11	28.2	7	2	PT0642	T-cell receptor be

ALIGNMENTS

RESULT 1

JH0253  
gut pentapeptide - Japanese eel  
C:Species: Anguilla japonica (Japanese eel)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C:Accession: JH0253  
R:Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A:Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
A:Reference number: JH0253; MUID:92062113; PMID:1953755  
A:Accession: JH0253  
A:Molecule type: protein  
A:Residues: 1-5 <UES>  
A:Experimental source: Gut  
C:Comment: This peptide increased basal tone of the circular muscle of the esophagogastric  
, and of the circular muscle of the gastro-intestinal junction.

Query Match 51.3%; Score 20; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3  
|:|  
Db 1 GFW 3

RESULT 2

PT0532  
T-cell receptor beta chain V-D-J region (100-4AJ) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
C:Accession: PT0532  
R:Feeney, A.J. Med. 174, 115-124, 1991  
J. Exp. Med. 174, 115-124, 1991  
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A:Reference number: PT0509; MUID:91277601; PMID:1711558  
A:Accession: PT0532  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-6 <FEE>  
A:Experimental source: adult thymus, strain BALB/c  
C:Keywords: T-cell receptor

Query Match 38.5%; Score 15; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYW 3  
|:|  
Db 4 GFW 6

```
RESULT 3
B35640
cerebellar degeneration-related protein - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
C/Accession: B35640
R/Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.H.
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990
A/Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal marker
A/Reference number: A35640; MUID:90222173; PMID:2326268
A/Accession: B35640
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-6 <CHE>

Query Match      35.9%; Score 14; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YW 3
      :||
Db      1 FW 2

RESULT 4
PT0629
T-cell receptor beta chain V-D-J region (100-2AH) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PT0629; PT0528
R/Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509; MUID:91277601; PMID:1711558
A/Accession: PT0629
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-6 <PEE>
A/Experimental source: newborn thymus, strain BALB/c, clone 100-2AH
A/Accession: PT0528
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-6 <PE2>
A/Experimental source: adult thymus, strain BALB/c, clone 100-4AB
C/Keywords: T-cell receptor

Query Match      35.9%; Score 14; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GYW 3
      :||
Db      3 GDW 5

RESULT 5
S21230
dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
C/Species: Phyllomedusa bicolor (two-colored leaf frog)
C/Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
C/Accession: S21230
R/Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erespamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A/Title: Identification and characterization of two dermorphins from skin extracts of the
A/Reference number: S21152; MUID:92339502; PMID:1633846
A/Accession: S21230
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-7 <MIG>
C/Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match      35.9%; Score 14; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GYW 3
      :||
Db      3 GDW 5

RESULT 6
S21230
dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
C/Species: Phyllomedusa bicolor (two-colored leaf frog)
C/Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
C/Accession: S21230
R/Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erespamer, G.; Kreil, G.
FEBS Lett. 302, 151-154, 1992
A/Title: Identification and characterization of two dermorphins from skin extracts of the
A/Reference number: S21152; MUID:92339502; PMID:1633846
A/Accession: S21230
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-7 <MIG>
C/Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match      35.9%; Score 14; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GYW 3
      :||
Db      3 GDW 5
```

```
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YW 3
      :||
Db      3 FW 4

RESULT 6
PT0728
T-cell receptor beta chain V-D-J region (161-2H) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PT0728
R/Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509; MUID:91277601; PMID:1711558
A/Accession: PT0728
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-7 <FEE>
A/Experimental source: newborn thymus, strain BALB/c
C/Keywords: T-cell receptor

Query Match      35.9%; Score 14; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 GYW 3
      :||
Db      3 GDW 5

RESULT 7
S33567
tubulin beta-3 chain - fruit fly (Drosophila melanogaster) (fragment)
C/Species: Drosophila melanogaster
C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C/Accession: S33567
R/Hinz, U.; Wolk, A.; Renkawitz-Pohl, R.
Development 116, 543-554, 1992
A/Title: Ultrathorax is a regulator of beta-3 tubulin expression in the Drosophila viscer
A/Reference number: S33567; MUID:93170162; PMID:1363225
A/Accession: S33567
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-7 <HIN>
A/Cross-references: UNIPROT:P08841; EMBL:X68393; NID:g7669; PIDN:CAA48459.1; PID:g4377448
C/Genetics:
A/Gene: FlyBase:beta-Tub60D
A/Cross-references: FlyBase:FBgn0003888
A/Introns: 5/3

Query Match      35.9%; Score 14; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YW 3
      :||
Db      6 FW 7

RESULT 8
S09478
globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
N/Alternate names: IIS globulin alpha subunit gamma chain
C/Species: Cucurbita sp. (cucurbit)
C/Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
C/Accession: S09478
R/Ohmiya, M.; Hara, I.; Matsubara, H.
Plant Cell Physiol. 21, 157-167, 1980
A/Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and
A/Reference number: S09066
```

A:Accession: S09478  
A:Molecule type: protein  
A:Residues: 1-4 <OHM>

Query Match 33.3%; Score 13; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
||  
DB 3 GY 4

## RESULT 9

A61411  
ameletin - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 18-Aug-2000  
C:Accession: A61411  
R:Burzynski, S.R.  
Anal. Biochem. 70, 359-365, 1976  
A:Title: Sequential analysis in subnanomolar amounts of peptides. Determination of the  
A:Reference number: A61411; MUID:76182447; PMID:1267130  
A:Accession: A61411  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-6 <BUR>  
C:Superfamily: unassigned animal peptides  
C:Keywords: pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 33.3%; Score 13; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
||  
DB 3 GY 4

## RESULT 10

A61324  
dermorphin - Rohde's leaf frog  
C:Species: Phyllomedusa rohdei (Rohde's leaf frog)  
C:Date: 17-Jul-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
C:Accession: A61324  
R:Montecucchi, P.C.; De Castiglione, R.; Erspamer, V.  
Int. J. Pept. Protein Res. 17, 316-321, 1981  
A:Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Braz  
A:Reference number: A61324; MUID:82029915; PMID:7287302  
A:Accession: A61324  
A:Molecule type: protein  
A:Residues: 1-7 <MON>  
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology  
C:Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin  
F:2/Modified site: D-alanine (Ala) #status experimental  
F:6/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental  
F:7/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 33.3%; Score 13; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
||  
DB 4 GY 5

## RESULT 11

A60139  
fatty-acid synthase (EC 2.3.1.85) - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 26-May-2000

C:Accession: A60139  
R:Hardie, D.G.; Dewart, K.B.; Aitken, A.; McCarthy, A.D.  
Biochim. Biophys. Acta 828, 380-382, 1985  
A:Title: Amino acid sequence around the reactive serine residue of the thioesterase domain  
A:Reference number: A60139; MUID:85175165; PMID:3921056  
A:Accession: A60139  
A:Molecule type: protein  
A:Residues: 1-7 <HAR>

C:Superfamily: rat fatty-acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homol  
ydrolase homology; short-chain alcohol dehydrogenase homology; [acyl-carrier-protein] S-n  
C:Keywords: acyltransferase; carrier protein; coenzyme A; homodimer; multifunctional enzy  
F:5/Active site: Ser (of oleoyl-[acyl-carrier-protein] hydrolase) #status experimental

Query Match 33.3%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
||  
DB 3 GY 4

## RESULT 12

S71870  
glutathione transferase (EC 2.5.1.18) class mu 9 - pig (fragment)  
A:Alternate names: glutathione S-transferase class mu 9  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 19-Mar-1998 #sequence\_revision 13-Sep-1998 #text\_change 07-May-1999  
C:Accession: S71870  
R:Rouimi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.  
Biochem. J. 317, 879-884, 1996  
A:Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospra  
A:Reference number: S71864; MUID:96332484; PMID:8760377  
A:Accession: S71870  
A:Molecule type: protein  
A:Residues: 1-7 <ROU>  
C:Comment: At least five species-independent classes of cytosolic glutathion transferases  
s mitochondrial form are known.  
C:Complex: dimer  
C:Function:  
A:Description: catalyzes the nucleophilic conjugation of intracellular glutathione to a v  
A:Pathway: detoxification; xenobiotics metabolism  
A>Note: increased hydrophilicity of GSH-conjugates facilitates their further metabolism  
es of damage  
C:Superfamily: glutathione transferase  
C:Keywords: acetylated amino end; blocked amino end; dimer; transferase  
F:1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 33.3%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
||  
DB 5 GY 6

## RESULT 13

S36662  
dermorphin (lys-7) [validated] - two-colored leaf frog  
C:Species: Phyllomedusa bicolor (two-colored leaf frog)  
C:Date: 10-Dec-1993 #sequence\_revision 13-Mar-1997 #text\_change 18-Aug-2000  
C:Accession: S36662  
R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.;  
FEBS Lett. 302, 151-154, 1992  
A:Title: Identification and characterization of two dermorphins from skin extracts of the  
A:Reference number: S21152; MUID:92339502; PMID:1633846  
A:Accession: S36662  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <MIG>  
C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 33.3%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2  
|  
Db 4 GY 5

RESULT 14  
PH1618  
Ig H chain V-D-J region (clone B-less 33) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C;Accession: PH1618  
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A;Reference number: PH1580; MUID:93301609; PMID:8315387  
A;Accession: PH1618  
A;Molecule type: DNA  
A;Residues: 1-8 <LEV>  
A;Experimental source: bone marrow pre-B lymphocyte  
C;Keywords: immunoglobulin

Query Match 33.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GY 2  
|  
Db 5 GY 6

RESULT 15  
JS0315  
Leucokinin V - Madeira cockroach  
C;Species: Leucophaea maderae (Madeira cockroach)  
C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C;Accession: JS0315  
R;Holman, G.M.; Cook, B.J.; Nachman, R.J.  
Comp. Biochem. Physiol. C 88, 27-30, 1987  
A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic  
A;Reference number: JS0315  
A;Accession: JS0315  
A;Molecule type: protein  
A;Residues: 1-8 <HOL>  
A;Cross-references: UNIPROT:P19987  
C;Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile ac  
C;Keywords: amidated carboxyl end; cephalomyotropic peptide  
F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 30.8%; Score 12; DB 2; Length 8;  
Best Local Similarity 28.6%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GYXXXW 7  
|  
Db 1 GSGFSSW 7

Search completed: December 29, 2004, 22:28:34  
Job time : 39 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 22:09:06 ; Search time 185 Seconds  
(without alignments)  
24.881 Million cell updates/sec

Title: US-10-046-922-68  
Perfect score: 39  
Sequence: 1 GYXXXXWX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 835

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_02: \*  
1: uniprot\_spot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	51.3	8	Q62721	Q62721 rattus norv
2	20	51.3	8	AAB33374	Aab33374 homo sapi
3	19	48.7	5	UF01_MOUSE	P38639 mus musculus
4	16	41.0	7	Q9BRV4	Q9brv4 homo sapien
5	15	38.5	4	OC33_OCTMI	P58649 octopus min
6	15	38.5	8	Q64971	Q64971 alfalfa mos
7	13	33.3	8	ALL5_CYPDO	P82156 cydia pomon
8	13	33.3	8	O02831	O02831 oryctolagus
9	13	33.3	8	Q95213	Q95213 oryctolagus
10	13	33.3	8	Q70Y57	Q70y57 fuerstia af
11	13	33.3	8	Q70Y84	Q70y84 plectranthu
12	13	33.3	8	Q6LDP8	Q6ldp8 pseudomonas
13	13	33.3	8	Q9R5R2	Q9r5r2 shigella dy
14	13	33.3	8	CAD45500	Cad45500 plectrant
15	13	33.3	8	CAD45547	Cad45547 fuerstia
16	13	33.3	8	AA26011	Aaa26011 pseudomon
17	13	33.3	8	AA26012	Aaa26012 pseudomon
18	12	30.8	8	LCX5_LEUMA	P19987 leucophaea
19	12	30.8	8	PK4_PERAM	P82688 periplaneta
20	11	28.2	2	GWA_SEPOF	P33070 sepiia offic
21	11	28.2	5	BPPT_BOTIN	P30425 bothrops in
22	11	28.2	6	E101_LITRU	P82096 litoria rub
23	11	28.2	6	LOK1_LOCFI	P41491 locusta mig
24	11	28.2	7	BRHP_CONIM	P58803 conus imper
25	11	28.2	7	TPFY_PACDA	P83455 pachymedusa
26	11	28.2	7	TY51_LITRU	P82065 litoria rub
27	11	28.2	7	WMA1_ACHFU	P35919 achatina fu
28	11	28.2	7	WMA2_ACHFU	P35920 achatina fu
29	11	28.2	7	WMA3_ACHFU	P35921 achatina fu
30	11	28.2	7	Q95945	Q95945 saccharomyc
31	11	28.2	7	O49223	O49223 glycine max

32	11	28.2	7	2	Q8GL00	Q8gl00 borrellia bu
33	11	28.2	7	2	Q8GL04	Q8gl04 borrellia bu
34	11	28.2	7	2	Q8KMS9	Q8kms9 enterobacte
35	11	28.2	7	2	Q8JEB1	Q8je81 human immun
36	11	28.2	8	1	ACI_THUAL	P18691 thunnus alb
37	11	28.2	8	1	AKHG_CRYBI	P14086 gryllus bim
38	11	28.2	8	1	AKH_LIBAU	P25418 libellula a
39	11	28.2	8	1	AKH_MELML	P25423 melolontha
40	11	28.2	8	1	AKH_PROTE	P61856 protophormi
41	11	28.2	8	1	AKH_TABAT	P14595 tabanus atr
42	11	28.2	8	1	C125_CYPDO	P83661 cyphononyx
43	11	28.2	8	1	CCEN_MACEU	P30369 macropus eu
44	11	28.2	8	1	COM2_CONFU	P58785 conus purpu
45	11	28.2	8	1	HTF1_PERAM	P04548 periplaneta

## ALIGNMENTS

RESULT 1  
Q62721 PRELIMINARY; PRT; 8 AA.  
AC Q62721;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DE 01-NOV-1998 (TRENBLrel. 08, Last annotation update)  
DE Prohibitin (Fragment)  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Fishier;  
RX MEDLINE=9331633; PubMed=7607556;  
RA Altus M.S., Wood C.M., Stewart D.A., Roekams A.I., Friedman V.,  
RA Henderson T., Owens G.A., Danner D.B., Jupe E.R., Dell'Orco R.T.,  
RA McClung J.K.;  
RT "Regions of evolutionary conservation between the rat and human  
RT prohibitin-encoding genes."  
RL Gene 158:291-294 (1995).  
DR EMBL; U17178; AAA86692.1; -.  
FT NON\_TER  
SQ SEQUENCE 8 AA; 1150 MW; EFD3237B05A41376 CRC64;  
Query Match 51.3%; Score 20; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 3 WXXXW 7  
Db 2 WRSEW 6

RESULT 2  
AAB33374 PRELIMINARY; PRT; 8 AA.  
AC AAB33374;  
DT 02-MAR-2004 (TRENBLrel. 27, Created)  
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)  
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)  
DE Collagen alpha 5(IV) chain (Fragment).  
GN COL4A5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95156893; PubMed=7853788;  
RA Nakazato H., Hattori S., Ushijima T., Matsuura T., Koitabashi Y.,  
RA Takada T., Yoshioka K., Endo F., Matsuda I.;  
RT "Mutations in the COL4A5 gene in Alport syndrome: a possible mutation

RT in primordial germ cells.";  
 RL Kidney Int. 46:1307-1314(1994).  
 DR ENBL, S75903; AAB33374.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 933 MW; 7370437735BAB378 CRC64;  
 Query Match 51.3%; Score 20; DB 2; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 WXXXW 7  
 | | |  
 Db 2 WDSLW 6  
 RESULT 3  
 UF01\_MOUSE STANDARD; PRT; 5 AA.  
 AC P38639;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 03-JUL-2004 (Rel. 44, Last annotation update)  
 DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Fibroblast;  
 RX MEDLINE=9500907; PubMed=7523108;  
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Sellkirk J.K.;  
 RT "Separation and sequencing of familial and novel murine proteins using  
 RT preparative two-dimensional gel electrophoresis.";  
 RL Electrophoresis 15:735-745(1994).  
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 6.6, its MW is: 19 kDa.  
 KW Direct protein sequencing.  
 FT NON\_TER 5 5  
 SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;  
 Query Match 48.7%; Score 19; DB 1; Length 5;  
 Best Local Similarity 40.0%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 WXXXW 7  
 | | |  
 Db 1 WIGRW 5  
 RESULT 4  
 Q9BRY4 PRELIMINARY; PRT; 7 AA.  
 AC Q9BRY4;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE SOSTMI protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ovary;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Ovary;  
 RA Strausberg R.;  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC005829; AA05857.3; -.  
 DR GO: GO:0005829; C:cytosol; ISS.  
 DR GO: GO:0019901; F:protein kinase binding; ISS.  
 DR GO: GO:0042169; F:SH2 domain binding; ISS.  
 DR GO: GO:0043130; F:ubiquitin binding; ISS.  
 DR GO: GO:0016197; P:endosome transport; ISS.  
 DR GO: GO:0007242; P:intracellular signaling cascade; ISS.  
 DR GO: GO:0045944; P:positive regulation of transcription from P. .; ISS.  
 DR GO: GO:0008104; P:protein localization; ISS.  
 DR GO: GO:0043122; P:regulation of I-kappaB kinase/NF-kappaB cas. .; ISS.  
 DR GO: GO:0006950; P:response to stress; ISS.  
 DR InterPro; IPR000449; UBA.  
 DR InterPro; IPR000433; Znf\_ZZ.  
 DR Pfam; PF00569; ZF\_1.  
 DR SMART; SM00165; UBA; 1.  
 DR SMART; SM00291; ZNF\_ZZ; 1.  
 DR PROSITE; PS00303; UBA; 1.  
 DR PROSITE; PS01357; ZF\_ZZ\_1; UNKNOWN\_1.  
 DR PROSITE; PS0135; ZF\_ZZ\_2; 1.  
 SQ SEQUENCE 7 AA; 779 MW; 73728769DDDD6F0 CRC64;  
 Query Match 41.0%; Score 16; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GYW 3  
 | | |  
 Db 5 GLW 7  
 RESULT 5  
 OCP3\_OCTMI STANDARD; PRT; 4 AA.  
 AC P58649;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Cardioactive peptides Ocp-3/Ocp-4.  
 OS Octopus minor (Octopus).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
 OX NCBI\_TaxID=89766;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
 RC TISSUE=Brain;  
 RX MEDLINE=20336815; PubMed=10876044;  
 RA Iwakoshi E., Hisada M., Minakata H.;  
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
 RT Octopus minor.";  
 RL Peptides 21:623-630(2000).  
 CC -1- FUNCTION: Cardioactive; has both positive chronotropic and  
 CC inotropic effects on the heart. Ocp-4 is a 1000 time less active  
 CC than Ocp-3.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: Ocp-4 has D-Ser instead of L-Ser.

CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=WALDI; RANGE=1-4; NOTE=Ref.1.  
 KW D-amino acid; Direct protein sequencing; Hormone.  
 FT MOD\_RES 2 D-serine (in form Ocp-4).  
 SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 38.5%; Score 15; DB 1; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYW 3  
 DB 1 GSW 3

RESULT 6  
 Q64971 PRELIMINARY; PRT; 8 AA.

DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Putative ORF (Fragment).  
 OS Alfalfa mosaic virus  
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;  
 OC Alfamovirus.  
 OX NCBI\_TaxID=12321;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=81124289; PubMed=6927843;  
 RA Koper-Zwarthoff E.C., Brederode F.T.M., Veeneman G., van Boom J.H.,  
 RA Bol J.F.;  
 RT "Nucleotide sequences at the 5'-termini of the alfalfa mosaic virus  
 RT RNAs and the intercistronic junction in RNA 3.";  
 RL Nucleic Acids Res. 8:5635-5647(1980).  
 DR EMBL; V00047; CAA23416.1; -.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 917 MW; 69D40B0775A365B8 CRC64;

Query Match 38.5%; Score 15; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GYW 3  
 DB 1 GSW 3

RESULT 7  
 ALL5\_CYDPO STANDARD; PRT; 8 AA.

DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Cydiaastatin 5.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 8 Leucine amide.  
 SQ SEQUENCE 8 AA; 898 MW; 922879CABB58640D CRC64;

Query Match 33.3%; Score 13; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
 DB 3 GY 4

RESULT 8  
 O02831 PRELIMINARY; PRT; 8 AA.

DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Pro alpha 1 type III collagen protein (Fragment).  
 GN Name=pro alpha 1 type III collagen;  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96377339; PubMed=8783186;  
 RA Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,  
 RA Vuorio E.;  
 RT "Evidence for insufficient chondrocytic differentiation during repair  
 RT of full-thickness defects of articular cartilage.";  
 RL Matrix Biol. 15:39-47(1996).  
 DR EMBL; S83371; AAD14433.1; -.  
 KW Collagen.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 1028 MW; B859C7272EA77371 CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YW 3  
 DB 1 HW 2

RESULT 9  
 Q95213 PRELIMINARY; PRT; 8 AA.

DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Df (Fragment).  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=F-1/rmg;  
 RX MEDLINE=97315886; PubMed=9171891;  
 RA Chen H.T., Alexander C.B., Chen F.F., Mage R.G.;  
 RT "Rabbit DQ52 and DH gene expression in early B-cell development.";  
 RL Mol. Immunol. 33:1313-1321(1996).  
 DR EMBL; U62585; AAB18735.1; -.  
 FT NON\_TER 1  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 845 MW; 5CA861B5AB58677B CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2

Db 3 GY 4 ||

Query Match 33.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
Db 2 GY 3

RESULT 10

Q70Y57 PRELIMINARY; PRT; 8 AA.

AC Q70Y57; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Ribosomal protein (Fragment).

GN Name=rp16;

OS Fierstia africana.

OS Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Puerstia.

OX NCBI\_TaxID=204226;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=15019625;

RA Paton A., Springate D.A., Sudde S., Ottieno D., Grayer R., Harley M.M., Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;

RA "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)

RT based on three plastid DNA regions.";

RL Mol. Phylogenet. Evol. 31:277-299(2004).

DR EMBL; AJ505427; CAD4547.1; -.

KW Ribosomal protein.

FT NON TER 1 8

SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
Db 5 GY 6

RESULT 11

Q70Y84 PRELIMINARY; PRT; 8 AA.

AC Q70Y84; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Ribosomal protein (Fragment).

GN Name=rp16;

OS Plectranthus buchananii.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.

OX NCBI\_TaxID=204181;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=15019625;

RA Paton A., Springate D.A., Sudde S., Ottieno D., Grayer R., Harley M.M., Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;

RA "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)

RT based on three plastid DNA regions.";

RL Mol. Phylogenet. Evol. 31:277-299(2004).

DR EMBL; AJ505379; CAD45500.1; -.

KW Ribosomal protein.

FT NON TER 1 8

SQ SEQUENCE 8 AA; 945 MW; 6EA415A5B8AB5863 CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
Db 5 GY 6

RESULT 12

Q6LDP8 PRELIMINARY; PRT; 8 AA.

AC Q6LDP8; 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE toxA gene encoding exotoxin A, 5' end ((strain PA103)

DE toxA gene encoding exotoxin A, 5' end (Fragment).

OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI\_TaxID=287;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=90202723; PubMed=2156808;

RA Pritchard A.E., Vasil M.L.;

RA "Possible insertion sequences in a mosaic genome organization upstream

RT of the exotoxin A gene in Pseudomonas aeruginosa.";

RL J. Bacteriol. 172:2020-2028(1990).

DR EMBL; M27186; AAA26011.1; -.

KW NON TER 8 8

SQ SEQUENCE 8 AA; 1046 MW; P94371F7605721E6 CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YW 3  
Db 6 HW 7

RESULT 13

Q9R5R2 PRELIMINARY; PRT; 8 AA.

AC Q9R5R2; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE 31,000 DA product of ORF6 (Fragment).

OS Shigella dysenteriae.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Shigella.

OX NCBI\_TaxID=622;

RN [1]

RP SEQUENCE.

RX MSDLINE=92085268; PubMed=1660923;

RA Polard P., Prere M.F., Chandler M., Fayet O.;

RT "Programmed translational frameshifting and initiation at an AUU codon

RT in gene expression of bacterial insertion sequence IS911.";

RL J. Mol. Biol. 222:465-477(1991).

FT NON TER 8 8

SQ SEQUENCE 8 AA; 902 MW; PE2DCAF5B586AE336 CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
Db 4 GY 5

QY 1 GY 2  
Db 5 GY 6

## RESULT 14

CAD45500 PRELIMINARY; PRT; 8 AA.  
AC CAD45500;  
DT 14-MAR-2004 (TrEMBLrel. 27, Created)  
DT 14-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Ribosomal protein (Fragment).  
GN RPS16.  
OS Plectranthus buchananii.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.  
OX NCBI\_TaxID=204181;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,  
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.,  
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)  
RT based on three plastid DNA regions.";  
RL Mol. Phylogenet. Evol. 31:277-299(2004).  
DR EMBL; AJ505379; CAD45500.1; -;  
KW Chloroplast; Ribosomal protein.  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 945 MW; 6EA415A5BEAB5863 CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2  
Db 2 GY 3

## RESULT 15

CAD45547 PRELIMINARY; PRT; 8 AA.  
AC CAD45547;  
DT 14-MAR-2004 (TrEMBLrel. 27, Created)  
DT 14-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
DT 14-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
DE Ribosomal protein (Fragment).  
GN RPS16.  
OS Fierstia africana.  
OG Chloroplast.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Fierstia.  
OX NCBI\_TaxID=204226;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,  
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.,  
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)  
RT based on three plastid DNA regions.";  
RL Mol. Phylogenet. Evol. 31:277-299(2004).  
DR EMBL; AJ505427; CAD45547.1; -;  
KW Chloroplast; Ribosomal protein.  
FT NON\_TER 1 1  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 916 MW; DABEAB58637041B5 CRC64;

Query Match 33.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: December 29, 2004, 22:27:08  
Job time : 186 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:55:07 ; Search time 55.6981 Seconds  
(without alignments)  
51.525 Million cell updates/sec

Title: US-10-046-922-68

Perfect score: 39

Sequence: 1 GYVXXWX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	87.2	10	4	Aab99759 Rhesus D
2	34	87.2	12	4	Aab99769 Rhesus D
3	34	87.2	452	4	Aau03644 Group B S
4	34	87.2	466	6	Abu21589 Protein e
5	34	87.2	472	6	Abu38334 Protein e
6	34	87.2	474	6	Abu24881 Protein e
7	34	87.2	475	5	Abp30560 Streptoco
8	34	87.2	475	6	Abu40245 Protein e
9	34	87.2	475	6	Abu29756 Protein e
10	34	87.2	478	7	Adc97241 E. faeciu
11	34	87.2	479	5	Abp26968 Streptoco
12	34	87.2	490	5	Abb55389 Lactococc
13	34	87.2	496	5	Abb55385 Lactococc
14	34	87.2	499	7	Abu74582 Pseudomon
15	34	87.2	506	6	Abu22414 Protein e
16	34	87.2	585	7	Ada49403 Multi-epi
17	34	87.2	585	8	Ado24081 Epigene c
18	34	87.2	865	7	Abu70593 Pseudomon
19	33	84.6	10	5	Abp53931 VEGFR-3 b
20	33	84.6	10	5	Abp53932 VEGFR-3 b
21	33	84.6	69	4	Aao13595 Human pol
22	33	84.6	116	2	Aar15437 Heavy cha
23	33	84.6	116	6	Abu27261 ICAM-1 bi
24	33	84.6	116	6	Abu27269 ICAM-1 bi
25	33	84.6	116	6	Abu27263 ICAM-1 bi

26	33	84.6	116	6	ABO27259	Abu27259 ICAM-1 bi
27	33	84.6	116	6	ABO27255	Abu27255 ICAM-1 bi
28	33	84.6	116	6	ABO27277	Humanised
29	33	84.6	116	6	ABO27273	Murine 1A
30	33	84.6	116	6	ABO27257	Abu27257 ICAM-1 bi
31	33	84.6	116	6	ABO27271	Abu27271 ICAM-1 bi
32	33	84.6	116	6	ABO27267	Abu27267 ICAM-1 bi
33	33	84.6	117	6	ABO27265	Abu27265 ICAM-1 bi
34	33	84.6	118	7	ADJ95639	Adj95639 Insulin-1
35	33	84.6	119	8	ADL11890	Adl11890 CDR trans
36	33	84.6	119	8	ADL11886	Adl11886 Chimera a
37	33	84.6	120	4	AB62747	Ab62747 Human HIV
38	33	84.6	137	7	ADJ95626	Adj95626 Rat insul
39	33	84.6	138	3	AAy77591	Aay77591 Anti-huma
40	33	84.6	138	3	AAy77595	Aay77595 Anti-huma
41	33	84.6	138	4	AAb78864	Aab78864 Anti-huma
42	33	84.6	138	4	AAb78860	Aab78860 Anti-huma
43	33	84.6	163	7	ABM73967	Abm73967 DNA clone
44	33	84.6	227	6	ABU36339	Abu36339 Protein e
45	33	84.6	240	2	AAR15443	Aar15443 Single ch

ALIGNMENTS

RESULT 1  
AAB99759  
ID AAB99759 standard; peptide; 10 AA.  
XX  
AC AAB99759;  
XX  
DT 21-SEP-2001 (first entry)  
XX  
DE Rhesus D antibody binding peptide SEQ ID NO:4.  
XX  
KW Rhesus D antibody binding peptide; Rhesus D; Rhd; identification;  
KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;  
KW prophylaxis; haemolytic disease of the newborn; HDN; rTP;  
KW idiopathic thrombocytopenic purpura; immunoglobulin.  
XX  
OS Homo sapiens.  
XX  
PN EP1106625-A1.  
XX  
PD 13-JUN-2001.  
XX  
PF 17-NOV-1999; 99EP-00122858.  
XX  
PR 17-NOV-1999; 99EP-00122858.  
XX  
(ZLBB-) ZLB BIOPLASMA AG.  
XX  
PI Miescher S, Hofmann A, Fisch I;  
XX  
WPI; 2001-383568/41.

Novel peptides capable of binding Rhesus D antibodies are used to manufacture an agent for the diagnosis, therapy or prophylaxis of diseases associated with Rhesus D antigen, e.g. hemolytic disease of the newborn (HDN).  
Claim 1; Page 12; 19pp; English.  
The present sequence represents a peptide capable of binding Rhesus D antibodies (I). Also described in the present invention are: (1) a nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more (II) operably linked to an expression control system; (3) a cell (IV) comprising (II) or (III); (4) preparing (I); (5) identifying (M1) peptides having immunologic properties of Rhesus D protein epitopes comprising subjecting an antibody/antibody fragment recognising an epitope of Rhesus D protein to several panning rounds with a phage display library, and identifying immunogenic peptide sequences which are mimotopes which differ in their amino acid sequence from the amino acid

CC sequences of Rhesus D protein; and (6) peptides (V) with immunological  
 CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to  
 CC manufacture an agent for the diagnosis, therapy or prophylaxis of  
 CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the  
 CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the  
 CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified  
 CC or removed from body fluids or immunoglobulin preparations. Using (I) as  
 CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation  
 CC with foreign erythrocytes thereby avoiding the risk of transmission of  
 CC viral diseases like AIDS and hepatitis B

XX SQ Sequence 10 AA;

Query Match 87.2%; Score 34; DB 4; Length 10;  
 Best Local Similarity 57.1%; Pred. No. 9.9; Mismatches 3; Indels 0; Gaps 0;  
 Matches 4; Conservative 0;

Qy 1 GYWXXXW 7  
 |||||  
 Db 1 GYWSAKW 7

RESULT 2

ID AAB99769 standard; peptide; 12 AA.

XX AC AAB99769;

XX DT 21-SEP-2001 (first entry)

XX DE Rhesus D antibody related peptide #5.

XX KW Rhesus D antibody binding peptide; Rhesus D; RhD; identification;  
 KW anti-Rhesus D antibody; immunogen; epitope; diagnosis; therapy;  
 KW prophylaxis; haemolytic disease of the newborn; HDN; ITP; cyclic;  
 KW idiopathic thrombocytopenic purpura; immunoglobulin; circular.

XX OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1..12

XX EP1106625-A1.

XX PD 13-JUN-2001.

XX PF 17-NOV-1999; 99EP-00122858.

XX PR 17-NOV-1999; 99EP-00122858.

XX PA (ZLBB-) ZLB BIOPLASMA AG.

XX PI Miescher S, Hofmann A, Fisch I;

XX WPI; 2001-383568/41.

XX Novel peptides capable of binding Rhesus D antibodies are used to  
 PT manufacture an agent for the diagnosis, therapy or prophylaxis of  
 PT diseases associated with Rhesus D antigen, e.g. haemolytic disease of the  
 PT newborn (HDN).

XX Example 1; Page 8; 19pp; English.

CC The present invention describes peptides capable of binding Rhesus D  
 CC antibodies (I). Also described in the present invention are: (1) a  
 CC nucleic acid (II) encoding (I); (2) a vector (III) comprising one or more  
 CC (II) operably linked to an expression control system; (3) a cell (IV)  
 CC comprising (II) or (III); (4) preparing (I); (5) identifying (M1)  
 CC peptides having immunologic properties of Rhesus D protein epitopes  
 CC comprising subjecting an antibody/antibody fragment recognising an  
 CC epitope of Rhesus D protein to several panning rounds with a phage  
 CC display library, and identifying immunogenic peptide sequences which are

CC mimotopes which differ in their amino acid sequence from the amino acid  
 CC sequences of Rhesus D protein; and (6) peptides (V) with immunological  
 CC properties of Rhesus D protein epitopes obtained by (M1). (I) is used to  
 CC manufacture an agent for the diagnosis, therapy or prophylaxis of  
 CC diseases associated with Rhesus D antigen, e.g. haemolytic disease of the  
 CC newborn (HDN) or idiopathic thrombocytopenic purpura (ITP), for the  
 CC manufacture of an affinity reagent for anti-Rhesus D antibodies purified  
 CC or removed from body fluids or immunoglobulin preparations. Using (I) as  
 CC an immunogen to raise anti-Rhesus D antibodies avoids using immunisation  
 CC with foreign erythrocytes thereby avoiding the risk of transmission of  
 CC viral diseases like AIDS and hepatitis B. The present sequence represents  
 CC an anti-Rhesus D (RhD) antibody related peptide which is used in an  
 CC example from the present invention

XX SQ Sequence 12 AA;

Query Match 87.2%; Score 34; DB 4; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 12;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7  
 |||||  
 Db 2 GYWSAKW 8

RESULT 3

ID AAU03644 standard; protein; 452 AA.

XX AC AAU03644;

XX DT 12-SEP-2001 (first entry)

XX DE Group B Streptococcus antigenic protein, ID-119.

XX KW Group B Streptococcus; encapsulated bacterium; therapeutic; sepsis;  
 KW meningitis; neonate; antigenic; vaccine; infection; genital tract;  
 KW capsid polysaccharide vaccination.

XX OS Streptococcus agalactiae.

XX WO200132882-A2.

XX PD 10-MAY-2001.

XX PF 07-SEP-2000; 2000WO-GB003437.

XX PR 07-SEP-1999; 99GB-00021125.

XX PA (MICR-) MICROBIAL TECHNIQS LTD.

XX PI Le Page RWF, Wells JM, Hanniffy SB;

XX WPI; 2001-316444/33.

XX N-PSDB; AAS07061.

XX New polypeptides derived from Streptococcus agalactiae are useful to  
 PT provide detection of, and vaccination against, Group B Streptococcus  
 PT infections, particularly to prevent infection in neonates.

XX Claim 1; Fig 1; 178pp; English.

XX AAU03601-AAU03722 represent Group B Streptococcus (Streptococcus  
 CC agalactiae) amino acid sequences of the invention. S. agalactiae is an  
 CC encapsulated bacterium which is a major pathogen of humans causing sepsis  
 CC and meningitis in neonates as well as adults. The S. agalactiae antigenic  
 CC polypeptides are used to vaccinate against Group B Streptococcus  
 CC infections, particularly to prevent infection in new born children  
 CC arising from the maternal genital tract. An immunogenic composition is  
 CC useful in the preparation of a medicament for the treatment or  
 CC prophylaxis of Group B Streptococcus infection. The invention does not  
 CC have the disadvantages of varied response rate associated with prior art  
 CC capsid polysaccharide vaccination against Group B Streptococcus

XX SQ Sequence 452 AA;  
Query Match 87.2%; Score 34; DB 4; Length 452;  
Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GYWXW 7  
DB 92 GYWSAW 98  
RESULT 4  
ABU21589  
ID ABU21589 standard; protein; 466 AA.  
XX AC ABU21589;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #7116.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Burkholderia fungorum.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX N-PSDB; ACA25459.  
XX PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 49513; 1766pp; English.  
XX PS The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
XX of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX (1) a vector comprising a promoter operably linked to the nucleic acid  
XX encoding a polypeptide whose expression is inhibited by the antisense  
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX polypeptide or its fragment whose expression is inhibited by the  
XX antisense nucleic acid; (4) an antibody capable of specifically binding  
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX proliferation or the activity of a gene in an operon required for  
XX the gene product or that has an activity against a biological pathway  
XX required for proliferation, or that inhibits cellular proliferation; (8)  
XX identifying a gene required for cellular proliferation or the biological  
XX pathway in which a proliferation-required gene or its gene product lies  
XX or a gene on which the test compound that inhibits proliferation of an  
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a  
XX compound's activity; (11) a culture comprising strains in which the gene  
XX product is overexpressed or underexpressed; (12) determining the extent  
XX to which each of the strains is present in a culture or collection of  
XX strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX SQ Sequence 466 AA;  
Query Match 87.2%; Score 34; DB 6; Length 466;  
Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GYWXW 7  
DB 86 GYWSAW 92  
RESULT 5  
ABU38334  
ID ABU38334 standard; protein; 472 AA.  
XX AC ABU38334;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #23861.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Pseudomonas aeruginosa.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX N-PSDB; ACA2204.  
XX PT New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 66258; 1766pp; English.  
XX PS The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
XX of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX (1) a vector comprising a promoter operably linked to the nucleic acid  
XX encoding a polypeptide whose expression is inhibited by the antisense  
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX polypeptide or its fragment whose expression is inhibited by the  
XX antisense nucleic acid; (4) an antibody capable of specifically binding  
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX proliferation or the activity of a gene in an operon required for  
XX proliferation; (7) identifying a compound that influences the activity of

CC the gene product or that has an activity against a biological pathway  
 CC identified for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 472 AA;

Query Match 87.2%; Score 34; DB 6; Length 472;  
 Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
 |||||  
 Db 94 GYWISAW 100

RESULT 6  
 ID ABU24881 87.2%; Score 34; DB 6; Length 472;  
 XX ABU24881 standard; protein; 474 AA.

AC ABU24881;  
 DT 19-JUN-2003 (first entry)

XX Protein encoded by Prokaryotic essential gene #10408.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Clostridium botulinum.

XX WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA28751.

XX New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 52805; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 474 AA;

Query Match 87.2%; Score 34; DB 6; Length 474;  
 Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
 |||||  
 Db 95 GYWLSAW 101

RESULT 7

ID ABP30560 standard; protein; 475 AA.

XX ABP30560;

XX 02-JUL-2002 (first entry)

XX Streptococcus polypeptide SEQ ID NO 10296.

XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;  
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;  
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.

XX Streptococcus agalactiae.

XX WO200234771-A2.

XX 02-MAY-2002.

XX 29-OCT-2001; 2001WO-GB004789.

XX 27-OCT-2000; 2000GB-00026333.

XX 24-NOV-2000; 2000GB-00028727.

XX 07-MAR-2001; 2001GB-00005640.

XX (CHIR-) CHIRON SPA.

XX (GENO-) INST GENOMIC RES.

XX Telford J, Maignani V, Margarit Y Rosi, Grandi G, Frazer C;

XX Tettelin H;

XX WPI; 2002-352536/38.  
 DR N-PSDB; ABN71191.  
 XX  
 PT New Streptococcus protein for the treatment or prevention of infection or  
 PT disease caused by Streptococcus bacteria, such as meningitis, and for  
 PT detecting a compound that binds to the protein.  
 XX  
 PS Claim 1; Page 4161; 4525pp; English.  
 XX  
 CC The invention relates to a protein (ABP25413-ABP30895) from group B  
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS  
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in  
 CC the specification. The proteins have antibacterial and antiinflammatory  
 CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and  
 CC antibodies that bind (I) are used in the manufacture of medicaments for  
 CC the treatment or prevention of infection or disease caused by  
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.  
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a  
 CC biological sample. (I) is used to determine whether a compound binds to  
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be  
 CC used as a vaccine or diagnostic composition. The disease caused by  
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic  
 CC acid encoding (I) may be used to recombinantly produce (I) and may be  
 CC used in gene therapy. Antibodies to (I) are used for affinity  
 CC chromatography, immunoassays, and distinguishing/identifying  
 CC Streptococcus proteins  
 XX  
 SQ Sequence 475 AA;  
 Query Match 87.2%; Score 34; DB 5; Length 475;  
 Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GYXXXXXW 7  
 DB 92 GYWSAW 98  
 |||||  
 RESULT 8  
 ABU40245  
 ID ABU40245 standard; protein; 475 AA.  
 XX  
 AC ABU40245;  
 XX  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Protein encoded by Prokaryotic essential gene #25772.  
 XX  
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX  
 OS Pseudomonas putida.  
 XX  
 PN WO20027183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US0009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PR (ELIT-) ELITRA PHARM INC.  
 PA  
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 PI  
 DR WPI; 2003-029926/02.  
 DR N-PSDB; ACA44115.  
 XX

PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 25; SEQ ID NO 68169; 1766pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than S. aureus, S. typhimurium,  
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 475 AA;  
 Query Match 87.2%; Score 34; DB 6; Length 475;  
 Best Local Similarity 57.1%; Pred. No. 3.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GYXXXXXW 7  
 DB 93 GYWSAW 99  
 |||||  
 RESULT 9  
 ABU29756  
 ID ABU29756 standard; protein; 475 AA.  
 XX  
 AC ABU29756;  
 XX  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Protein encoded by Prokaryotic essential gene #15283.  
 XX  
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX  
 OS Enterococcus faecium.  
 XX  
 PN WO20027183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US0009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 XX

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PR 06-MAR-2002; 2002US-0362699P.
XX (ELIT-) ELITRA PHARM INC.
PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX WPI: 2003-029926/02.
DR N-PSDB; ACA33626.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 57680; 1766pp; English.
PS The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 475 AA;

Query Match 87.2%; Score 34; DB 6; Length 475;
Best Local Similarity 57.1%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 95 GYWLSAW 101

RESULT 10
ADC97241
ID ADC97241 standard; protein; 478 AA.
XX
XX ADC97241;
AC
XX 01-JAN-2004 (first entry)
DT
XX
XX E. faecium protein sequence SEQ ID 6868.
DE
XX Vaccine; urinary tract infection; bacteraemia; endocarditis; wound;
KW abdominal-pelvic infection.
XX Enterococcus faecium.
OS

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XX US6583275-B1.
PN
XX 24-JUN-2003.
PD
XX 30-JUN-1998; 98US-00107532.
PF
XX 02-JUL-1997; 97US-0051571P.
PR 14-MAY-1998; 98US-0085598P.
XX (GENO-) GENOME THERAPEUTICS CORP.
PA Doucette-Stamm LA, Bush D;
XX WPI: 2003-799836/75.
PI N-PSDB; ADC33587.
DR New isolated nucleic acid derived from Enterococcus faecium encoding an
XX Enterococcus faecium polypeptide useful for detection, prevention and
PT treatment of a pathological condition resulting from a bacterial
PT infection.
XX Example 1; SEQ ID NO 6868; 243pp; English.
PS The invention relates to an isolated nucleic acid derived from
XX Enterococcus faecium encoding an Enterococcus faecium polypeptide having
CC one of 10 fully defined sequences given in the (or comprising 40
CC sequential nucleotides chosen from any of the nucleic acids, its
CC complement or sequences hybridising to it). Also included are a
CC recombinant vector comprising the nucleic acid operably linked to
CC transcription regulatory element, a cell comprising the vector and a
CC single-stranded probe comprising the nucleic acid. The nucleic acids are
CC chosen from 3654 disclosed sequences encoding 3654 disclosed proteins.
CC The nucleic acids are useful for diagnosing pathological conditions
CC resulting from E. faecium bacterial infection (e.g. urinary tract
CC infection, bacteraemia, endocarditis, wounds and abdominal-pelvic
CC infection) and for screening drugs such as agonists and antagonists. The
CC nucleic acid is useful for recombinant production of Candida albicans -
CC derived peptides or antisense polypeptides. Pharmaceutical compositions
CC and vaccines containing the nucleic acid are useful for preventing or
CC treating Enterococcus faecium infections. The present sequence represents
XX one if the disclosed E. faecium proteins.
SQ Sequence 478 AA;

Query Match 87.2%; Score 34; DB 7; Length 478;
Best Local Similarity 57.1%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 98 GYWLSAW 104

RESULT 11
ABP26968
ID ABP26968 standard; protein; 479 AA.
XX
XX ABP26968;
AC
XX 02-JUL-2002 (first entry)
DT
XX Streptococcus polypeptide SEQ ID NO 3112.
DE
XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
KW group A streptococcus; Streptococcus pyogenes; antibacterial;
XX antiinflammatory; infection; vaccine; meningitis; gene therapy.
XX Streptococcus agalactiae.
OS
XX WO200234771-A2.
PN
XX 02-MAY-2002.
PD

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XX PF 29-OCT-2001; 2001WO-GB004789.
XX PR 27-OCT-2000; 2000GB-00026333.
XX PR 24-NOV-2000; 2000GB-00028727.
XX PR 07-MAR-2001; 2001GB-00005640.
XX PA (CHIR-) CHIRON SPA.
XX PA (GENO-) INST GENOMIC RES.
XX PI Telford J, Masignani V, Margarit Y RosI, Grandi G, Fraser C;
XX PI Tettelin H;
XX PR WPI; 2002-352536/38.
XX DR N-PSDB; ABN67599.
XX PR New Streptococcus protein for the treatment or prevention of infection or
XX PT disease caused by Streptococcus bacteria, such as meningitis, and for
XX PT detecting a compound that binds to the protein.
XX PS Claim 1; Page 3464; 4525pp; English.
XX CC The invention relates to a protein (ABP25413-ABP30895) from group B
XX CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
XX CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
XX CC the specification. The proteins have antibacterial and antiinflammatory
XX CC activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and
XX CC antibodies that bind (I) are used in the manufacture of medicaments for
XX CC the treatment or prevention of infection or disease caused by
XX CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
XX CC Nucleic acids encoding (I) are used to detect Streptococcus in a
XX CC biological sample. (I) is used to determine whether a compound binds to
XX CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
XX CC used as a vaccine or diagnostic composition. The disease caused by
XX CC Streptococcus that is prevented or treated may be meningitis. Nucleic
XX CC acid encoding (I) may be used to recombinantly produce (I) and may be
XX CC used in gene therapy. Antibodies to (I) are used for affinity
XX CC chromatography, immunoassays, and distinguishing/identifying
XX CC Streptococcus proteins
XX SQ Sequence 479 AA;

Query Match 87.2%; Score 34; DB 5; Length 479;
Best Local Similarity 57.1%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 96 GYWLSAW 102
||| |

RESULT 12
ABB55389
ID ABB55389 standard; protein; 490 AA.
XX AC ABB55389;
XX DT 29-AUG-2003 (revised)
XX DT 16-MAY-2002 (first entry)
XX DE Lactococcus lactis protein arcD1.
XX KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
XX OS Lactococcus lactis; IL1403.
XX PN FR2807446-A1.
XX PD 12-OCT-2001.
XX PF 11-APR-2000; 2000FR-00004630.
XX PR 11-APR-2000; 2000FR-00004630.
XX PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
XX PI WPI; 2002-043418/06.
XX PR New nucleotide sequence useful in the identification or Lactococcus
XX PT lactis and related species.
XX PS Claim 6; SEQ ID NO 2087; 2504pp; French.

Query Match 87.2%; Score 34; DB 5; Length 490;
Best Local Similarity 57.1%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXW 7
DB 93 GYWLSAW 99
||| |

RESULT 13
ABB55385
ID ABB55385 standard; protein; 496 AA.
XX AC ABB55385;
XX DT 29-AUG-2003 (revised)
XX DT 16-MAY-2002 (first entry)
XX DE Lactococcus lactis protein arcD2.
XX KW Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
XX OS Lactococcus lactis; IL1403.
XX PN FR2807446-A1.
XX PD 12-OCT-2001.
XX PF 11-APR-2000; 2000FR-00004630.
XX PR 11-APR-2000; 2000FR-00004630.
XX PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX PI Bolotine A, Sorokine A, Renault P, Ehrlich SD;
XX PI WPI; 2002-043418/06.
XX PR New nucleotide sequence useful in the identification or Lactococcus
XX PT lactis and related species.
XX PS Claim 6; SEQ ID NO 2087; 2504pp; French.

The present invention is related to a Lactococcus lactis nucleotide
sequence (ABA90521) and related proteins (ABB53300-ABB55621). The nucleic
acid sequence is useful in the detection and/or amplification of nucleic
acid sequence, particularly to identify Lactococcus lactis or related
species. The proteins of the invention are useful for the biosynthesis or
biodegradation of a composition of interest. The invention helps research
in lactic bacteria, particularly useful in the production of yogurt and
cheese. Note: The sequence data for this patent is based on equivalent
patent WO200177334 (published 18-OCT-2001) which is available in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to
standardise OS field)
Sequence 490 AA;

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CC acid sequence, particularly to identify *Lactococcus lactis* or related  
CC species. The proteins of the invention are useful for the biosynthesis or  
CC biodegradation of a composition of interest. The invention helps research  
CC in lactic bacteria, particularly useful in the production of yogurt and  
CC cheese. Note: The sequence data for this patent is based on equivalent  
CC patent WO2001/7334 (published 18-OCT-2001) which is available in  
CC electronic format directly from WIPO at  
CC [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences). (Updated on 29-AUG-2003 to  
CC standardise OS field)  
XX SQ Sequence 496 AA;

Query Match 87.2%; Score 34; DB 5; Length 496;  
Best Local Similarity 57.1%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GYXXXXXW 7  
|||  
Db 93 GYWISAW 99

RESULT 14  
ABO74582  
ID ABO74582 standard; protein; 499 AA.  
XX AC ABO74582;  
XX DT 29-JUL-2004 (first entry)  
XX XX Pseudomonas aeruginosa polypeptide #6757.  
XX DE Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX KW Pseudomonas aeruginosa.  
XX OS US6551795-B1.  
XX PN 22-APR-2003.  
XX PD 18-FEB-1999; 99US-00252991.  
XX PF 18-FEB-1998; 98US-0074788P.  
XX PR 27-JUL-1998; 98US-0094190P.  
XX XX (GENO-) GENOME THERAPEUTICS CORP.

PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
XX WPI; 2003-615309/58.  
XX DR N-PSDB; ABD08153.  
XX PS Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,  
XX useful as molecular targets for diagnostics, prophylaxis and treatment of  
XX pathological conditions resulting from bacterial infection.  
XX Disclosure; SEQ ID NO 23328; 455pp; English.

XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the  
XX polynucleotides encoding them. The sequences are useful in diagnosis and  
XX therapy of pathological conditions, as molecular targets for diagnostics,  
XX prophylaxis and treatment of pathological conditions resulting from a  
XX bacterial infection, for evaluating a compound, such as a polypeptide,  
XX for the ability to bind a *P. aeruginosa* nucleic acid, as components of  
XX effective antibacterial targets, as targets for antibacterial drugs,  
XX including anti-*P. aeruginosa* drugs, as templates for recombinant  
XX production of *P. aeruginosa*-derived peptides or polypeptides, as target  
XX components for diagnosis and/or treatment of *P. aeruginosa*-caused  
XX infection, and in detection of *P. aeruginosa* sequences or other sequences  
XX of *Pseudomonas* species using biotech technology. Sequences ABO67826-  
XX ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The  
XX sequence data for this patent did not form part of the printed  
XX specification but was obtained in electronic format from USPTO at  
XX [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)

XX SQ Sequence 499 AA;  
Query Match 87.2%; Score 34; DB 7; Length 499;  
Best Local Similarity 57.1%; Pred. No. 4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 GYXXXXXW 7  
|||  
Db 111 GYWISAW 117

RESULT 15  
ABU22414  
ID ABU22414 standard; protein; 506 AA.  
XX AC ABU22414;  
XX DT 19-JUN-2003 (first entry)  
XX XX Protein encoded by Prokaryotic essential gene #7941.  
XX DE Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX KW Burkholderia mallei.  
XX OS WO200277183-A2.  
XX PN 03-OCT-2002.  
XX PD 21-MAR-2002; 2002WO-US009107.  
XX PF 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362699P.  
XX XX (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Hasebeck R, Ohlsen KL, Zyskind JW;  
XX PI Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX DR N-PSDB; ACA26284.  
XX XX New antisense nucleic acids, useful for identifying proteins or screening  
XX for homologous nucleic acids required for cellular proliferation to  
XX isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 50338; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of  
XX the 6213 antisense sequences given in the specification where expression  
XX of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX (1) a vector comprising a promoter operably linked to the nucleic acid  
XX encoding a polypeptide whose expression is inhibited by the antisense  
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX polypeptide or its fragment whose expression is inhibited by the  
XX antisense nucleic acid; (4) an antibody capable of specifically binding  
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX proliferation or the activity of a gene in an operon required for  
XX proliferation; (7) identifying a compound that influences the activity of  
XX the gene product or that has an activity against a biological pathway  
XX required for proliferation, or that inhibits cellular proliferation; (8)  
XX identifying a gene required for cellular proliferation or the biological  
XX pathway in which a proliferation-required gene or its gene product lies  
XX or a gene on which the test compound that inhibits proliferation of an  
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a  
XX compound's activity; (11) a culture comprising strains in which the gene  
XX product is overexpressed or underexpressed; (12) determining the extent  
XX to which each of the strains is present in a culture or collection of  
XX strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX

SQ Sequence 506 AA;

Query Match 87.2%; Score 34; DB 6; Length 506;

Best Local Similarity 57.1%; Pred. No. 4.1e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7

||| |

DB 124 GYWISAW 130

Search completed: December 30, 2004, 13:07:56

Job time : 55.6961 secs

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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:59:07 ; Search time 19.4151 Seconds  
(without alignments)  
28.810 Million cell updates/sec

Title: US-10-046-922-68  
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Scoring table: BLOSUM62  
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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	34	87.2	478	US-09-107-532A-6868	Sequence 6868, Ap
2	34	87.2	499	US-09-252-991A-23328	Sequence 23328, A
3	34	87.2	865	US-09-252-991A-19339	Sequence 19339, A
4	33	84.6	543	US-09-252-991A-18697	Sequence 18697, A
5	33	84.6	1498	US-09-792-616-9	Sequence 9, Appli
6	33	84.6	1503	US-09-792-616-3	Sequence 3, Appli
7	32	82.1	177	US-09-543-681A-7620	Sequence 7620, Ap
8	32	82.1	252	US-09-502-653-10	Sequence 10, Appl
9	32	82.1	263	US-09-610-906-12	Sequence 12, Appl
10	32	82.1	274	US-09-248-796A-15791	Sequence 15791, A
11	32	82.1	278	US-09-145-828A-11	Sequence 11, Appl
12	32	82.1	278	US-09-503-456-18	Sequence 18, Appl
13	32	82.1	339	US-09-252-991A-26841	Sequence 26841, A
14	32	82.1	362	US-08-415-751-6	Sequence 6, Appli
15	32	82.1	367	US-09-248-796A-15188	Sequence 15188, A
16	32	82.1	492	US-09-107-532A-6945	Sequence 6945, Ap
17	32	82.1	500	US-09-252-991A-21214	Sequence 21214, A
18	31	79.5	342	US-09-252-991A-32031	Sequence 32031, A
19	30	76.9	11	US-09-069-827A-87	Sequence 87, Appl
20	30	76.9	16	US-09-620-091-81	Sequence 81, Appl
21	30	76.9	519	US-09-198-452A-479	Sequence 479, App
22	30	76.9	654	US-09-252-991A-18441	Sequence 18441, A
23	29	74.4	34	US-09-270-767-60715	Sequence 60715, A
24	29	74.4	35	US-09-082-279B-1191	Sequence 1191, Ap
25	29	74.4	35	US-09-315-304B-1191	Sequence 1191, Ap
26	29	74.4	35	US-09-834-784-1191	Sequence 1191, Ap
27	29	74.4	35	US-09-515-965A-1191	Sequence 1191, Ap

28	29	74.4	35	4	US-09-350-641C-1191	Sequence 1191, Ap
29	29	74.4	35	4	US-09-350-841A-1191	Sequence 1191, Ap
30	29	74.4	55	4	US-09-621-976-7633	Sequence 7633, Ap
31	29	74.4	69	4	US-09-621-976-7239	Sequence 7239, Ap
32	29	74.4	139	4	US-09-252-991A-19685	Sequence 19685, A
33	29	74.4	142	4	US-09-252-991A-22994	Sequence 22994, A
34	29	74.4	197	4	US-09-543-681A-5312	Sequence 5312, Ap
35	29	74.4	227	4	US-09-489-039A-8752	Sequence 8752, Ap
36	29	74.4	255	4	US-09-270-767-45223	Sequence 45223, A
37	29	74.4	625	4	US-09-252-991A-28537	Sequence 28537, A
38	29	74.4	930	4	US-09-198-452A-470	Sequence 470, App
39	28	71.8	19	4	US-09-794-529B-8	Sequence 8, Appli
40	28	71.8	19	4	US-09-794-517A-8	Sequence 8, Appli
41	28	71.8	19	4	US-09-011-645B-8	Sequence 8, Appli
42	28	71.8	19	4	US-09-794-832-8	Sequence 8, Appli
43	28	71.8	19	4	US-09-680-806A-8	Sequence 8, Appli
44	28	71.8	19	4	US-09-552-868-8	Sequence 8, Appli
45	28	71.8	19	4	US-09-636-295-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-09-107-532A-6868  
; Sequence 6868, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD/ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arinello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 6868:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 478 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEetical: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...478  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6868:  
US-09-107-532A-6868

Query Match 87.2%; Score 34; DB 4; Length 478;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
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Db 98 GYWSAW 104

RESULT 2  
US-09-252-991A-23328  
; Sequence 23328, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23328  
; LENGTH: 499  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23328

Query Match 87.2%; Score 34; DB 4; Length 499;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
||| |  
Db 111 GYWSAW 117

RESULT 3  
US-09-252-991A-19339  
; Sequence 19339, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 19339  
; LENGTH: 865  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-19339

Query Match 87.2%; Score 34; DB 4; Length 865;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
||| |  
Db 487 GYWSAW 493

RESULT 4

US-09-252-991A-18697  
; Sequence 18697, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18697  
; LENGTH: 543  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18697

Query Match 84.6%; Score 33; DB 4; Length 543;  
Best Local Similarity 57.1%; Pred. No. 2.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
||| |  
Db 331 GYWSW 337

RESULT 5  
US-09-792-616-9  
; Sequence 9, Application US/09792616  
; Patent No. 6780587  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; FILE REFERENCE: PXE-001  
; CURRENT APPLICATION NUMBER: US/09/792,616  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 1498  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-792-616-9

Query Match 84.6%; Score 33; DB 4; Length 1498;  
Best Local Similarity 57.1%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
||| |  
Db 960 GYWSLW 966

RESULT 6  
US-09-792-616-3  
; Sequence 3, Application US/09792616  
; Patent No. 6780587  
; GENERAL INFORMATION:  
; APPLICANT: PXE International, Inc.  
; TITLE OF INVENTION: Mutations in a gene encoding an ABC transporter (MRP6) causing  
; FILE REFERENCE: PXE-001  
; CURRENT APPLICATION NUMBER: US/09/792,616  
; CURRENT FILING DATE: 2001-02-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 3
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-792-616-3

Query Match      84.6%; Score 33; DB 4; Length 1503;
Best Local Similarity 57.1%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 965 GYWLSLW 971

RESULT 7
US-09-543-681A-7620
; Sequence 7620, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7620
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7620

Query Match      82.1%; Score 32; DB 4; Length 177;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 43 GYWINW 49

RESULT 8
US-09-502-653-10
; Sequence 10, Application US/09502653
; Patent No. 6331426
; GENERAL INFORMATION:
; APPLICANT: Bj rnvad, Mads Eskelund
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Schlein, Martin
; APPLICANT: Bech, Lisbeth
; APPLICANT: stergaard, Peter Rahbek
; APPLICANT: Sj holm, Carsten
; TITLE OF INVENTION: NOVEL GALACTANASES
; FILE REFERENCE: 5481.200-US
; CURRENT APPLICATION NUMBER: US/09/502,653
; CURRENT FILING DATE: 2000-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00184
; EARLIER FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: PA 1999 00799
; EARLIER FILING DATE: 1999-06-07
; EARLIER APPLICATION NUMBER: 60/125,885
; EARLIER FILING DATE: 1999-03-24
; EARLIER APPLICATION NUMBER: 60/138,445
; EARLIER FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Bacillus circulans
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US-09-502-653-10

Query Match      82.1%; Score 32; DB 3; Length 252;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 210 GYWEPW 216

RESULT 9
US-09-610-906-12
; Sequence 12, Application US/09610906
; Patent No. 6566066
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Klinger, Tod W.
; TITLE OF INVENTION: AQUAPORIN-8 VARIANT
; FILE REFERENCE: PC-0012 CIP
; CURRENT APPLICATION NUMBER: US/09/610,906
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: 09/226,994
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 12
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. 6566066; g2346968
; PUBLICATION INFORMATION:
US-09-610-906-12

Query Match      82.1%; Score 32; DB 4; Length 263;
Best Local Similarity 57.1%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
DB 224 GYWDPHW 230

RESULT 10
US-09-248-796A-15791
; Sequence 15791, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15791
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15791

Query Match      82.1%; Score 32; DB 4; Length 274;
Best Local Similarity 57.1%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7
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Db 84 GYWPITW 90  
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## RESULT 11

US-09-145-828A-11

; Sequence 11, Application US/09145828A

; Patent No. 6403349

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Mukerji, Pradip

; APPLICANT: Leonard, Amanda E. Y.

; APPLICANT: Huang, Yung-Sheng

; APPLICANT: Thurmond, Jennifer

; APPLICANT: Kirchner, Stephen J.

; APPLICANT: Parker-Barnes, Jennifer M.

; TITLE OF INVENTION: THE ELONGASE GENE AND USES THEREOF

; FILE REFERENCE: 6407.US.01

; CURRENT FILING DATE: 1998-09-02

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 278

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-09-145-828A-11

Query Match

Best Local Similarity 82.1%; Score 32; DB 4; Length 278;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7

Db 108 GYWIFLW 114

## RESULT 12

US-09-903-456-18

; Sequence 18, Application US/09903456

; Patent No. 6677145

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Mukerji, Pradip

; APPLICANT: Leonard, Amanda Eun-Yeong

; APPLICANT: Huang, Yung-Sheng

; APPLICANT: Pereira, Suzette L.

; TITLE OF INVENTION: ELONGASE GENES AND USES THEREOF

; FILE REFERENCE: 6407.US.P3

; CURRENT APPLICATION NUMBER: US/09/903,456

; PRIOR FILING DATE: 2001-07-11

; PRIOR APPLICATION NUMBER: US 09/624,670

; PRIOR FILING DATE: 2000-07-24

; PRIOR APPLICATION NUMBER: US 09/379,095

; PRIOR FILING DATE: 1999-08-23

; PRIOR APPLICATION NUMBER: US 09/145,828

; PRIOR FILING DATE: 1998-09-02

; NUMBER OF SEQ ID NOS: 116

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 18

; LENGTH: 278

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-09-903-456-18

Query Match

Best Local Similarity 82.1%; Score 32; DB 4; Length 278;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7

Db 108 GYWIFLW 114

## RESULT 13

US-09-252-991A-26841

; Sequence 26841, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 26841

; LENGTH: 339

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-26841

Query Match

Best Local Similarity 82.1%; Score 32; DB 4; Length 339;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7

Db 261 GYGGY 267

## RESULT 14

US-08-415-751-6

; Sequence 6, Application US/08415751

; Patent No. 5643772

; GENERAL INFORMATION:

; APPLICANT: PETERSEN, CAROLYN

; APPLICANT: LEECH, JAMES

; APPLICANT: NELSON, RICHARD, C.

; APPLICANT: GUT, JIRI

; TITLE OF INVENTION: POLYPEPTIDES BINDING ANTI-

; TITLE OF INVENTION: CRYPTOSPORIDIUM ANTIBODIES, DNA

; TITLE OF INVENTION: AND RNA ENCODING THEM, HYBRID

; TITLE OF INVENTION: VECTOR AND TRANSFORMED HOST AND

; TITLE OF INVENTION: METHODS FOR IMMUNOTHERAPY AND

; TITLE OF INVENTION: DIAGNOSIS AND KIT

; NUMBER OF SEQUENCES: 50

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PHILLIPS, MOORE, LEMPION &amp; FINLEY

; STREET: 385 Sherman Avenue, Suite 6

; CITY: Palo Alto

; STATE: California

; COUNTRY: United States of America

; ZIP: 94306-1840

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage

; COMPUTER: PC

; OPERATING SYSTEM: DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/415,751

; FILING DATE: 03-APR-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/071,880

; FILING DATE: June 1, 1993

; APPLICATION NUMBER: 07/891,301

; FILING DATE: May 29, 1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Hana Dolezalova

; REGISTRATION NUMBER: 30,518

; REFERENCE/DOCKET NUMBER: 480.19-2 (HHD)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-1677  
TELEFAX: (415) 324-1678  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 362 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Cryptosporidium parvum  
FEATURE:  
NAME/KEY: Positions coded by nonsense codons are  
NAME/KEY: identified as Xaa.  
US-08-415-751-6

Query Match 82.1%; Score 32; DB 1; Length 362;  
Best Local Similarity 57.1%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
Db 216 GYWLVTW 222

RESULT 15  
US-09-248-796A-15188  
Sequence 15188, Application US/09248796A  
Patent No. 6747137  
GENERAL INFORMATION:  
APPLICANT: Keith Weinstock et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
CURRENT FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 15188  
LENGTH: 367  
TYPE: PRT  
ORGANISM: Candida albicans  
US-09-248-796A-15188

Query Match 82.1%; Score 32; DB 4; Length 367;  
Best Local Similarity 57.1%; Pred. No. 2.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYWXXXW 7  
Db 276 GYWLVDW 282

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 13:08:04 ; Search time 59.6226 Seconds  
(without alignments)  
48.267 Million cell updates/sec

Title: US-10-046-922-68

Perfect score: 39

Sequence: 1 GYXXXXXW 8

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Maximum Match 100%

Listing first 45 summaries

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Published Applications AA.\*

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#### SUMMARIES

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2	34	87.2	72	16	US-10-437-963-176036
3	34	87.2	452	14	US-10-091-007-88
4	34	87.2	466	15	US-10-282-122A-49513
5	34	87.2	469	14	US-10-369-493-23291
6	34	87.2	472	15	US-10-282-122A-66258
7	34	87.2	474	15	US-10-282-122A-52805
8	34	87.2	475	14	US-10-369-493-13733
9	34	87.2	475	15	US-10-282-122A-57680
10	34	87.2	475	15	US-10-282-122A-68169
11	34	87.2	506	15	US-10-282-122A-50338
12	34	87.2	585	9	US-09-894-018-87
13	34	87.2	585	17	US-10-474-960A-87

14	33	84.6	10	13	US-10-046-922-34	Sequence 34, Appl
15	33	84.6	10	13	US-10-046-922-35	Sequence 35, Appl
16	33	84.6	47	17	US-10-425-115-287762	Sequence 287762,
17	33	84.6	104	17	US-10-425-115-273234	Sequence 273234,
18	33	84.6	116	10	US-09-910-483-1	Sequence 1, Appli
19	33	84.6	116	10	US-09-910-483-5	Sequence 5, Appli
20	33	84.6	116	10	US-09-910-483-9	Sequence 9, Appli
21	33	84.6	116	10	US-09-910-483-13	Sequence 13, Appl
22	33	84.6	116	10	US-09-910-483-17	Sequence 17, Appl
23	33	84.6	116	10	US-09-910-483-21	Sequence 21, Appl
24	33	84.6	116	10	US-09-910-483-25	Sequence 25, Appl
25	33	84.6	116	10	US-09-910-483-29	Sequence 29, Appl
26	33	84.6	116	10	US-09-910-483-33	Sequence 33, Appl
27	33	84.6	116	10	US-09-910-483-37	Sequence 37, Appl
28	33	84.6	116	10	US-09-910-483-41	Sequence 41, Appl
29	33	84.6	116	10	US-09-910-483-45	Sequence 45, Appl
30	33	84.6	129	17	US-10-425-115-357518	Sequence 357518,
31	33	84.6	138	14	US-10-160-232-86	Sequence 86, Appl
32	33	84.6	138	14	US-10-160-232-90	Sequence 90, Appl
33	33	84.6	227	15	US-10-282-122A-64263	Sequence 64263, A
34	33	84.6	229	17	US-10-425-115-344695	Sequence 344695,
35	33	84.6	296	14	US-10-156-761-96332	Sequence 96332, Ap
36	33	84.6	296	14	US-10-369-493-19811	Sequence 19811, A
37	33	84.6	466	14	US-10-369-493-16537	Sequence 16537, A
38	33	84.6	467	16	US-10-437-963-199114	Sequence 199114,
39	33	84.6	516	16	US-10-450-022-7	Sequence 7, Appli
40	33	84.6	516	16	US-10-450-022-4	Sequence 4, Appli
41	33	84.6	526	16	US-10-450-022-5	Sequence 5, Appli
42	33	84.6	526	17	US-10-433-747B-2	Sequence 2, Appli
43	33	84.6	526	17	US-10-433-747B-17	Sequence 17, Appl
44	33	84.6	526	17	US-10-450-185B-2	Sequence 2, Appli
45	33	84.6	526	17	US-10-450-185B-17	Sequence 17, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-425-115-308836  
; Sequence 308836, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE OF INVENTION: Plantes  
; TITLE OF INVENTION: Plantes  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 308836  
; LENGTH: 58  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_44726C.1.pep  
US-10-425-115-308836

Query Match 87.2%; Score 34; DB 17; Length 58;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7

DB 49 GYWGASW 55

##### RESULT 2

US-10-437-963-176036  
; Sequence 176036, Application US/10437963  
; Publication No. US20040123343A1

## ; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 176036

; LENGTH: 72

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_73824C.1.pep

US-10-437-963-176036

Query Match 87.2%; Score 34; DB 16; Length 72;

Best Local Similarity 57.1%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7

||| |

Db 34 GYWSHW 40

## RESULT 3

US-10-091-007-88

; Sequence 88, Application US/10091007

; Publication No. US20030170782A1

; GENERAL INFORMATION:

; APPLICANT: Microbial Technics limited

; APPLICANT: Le Page, Richard W F Wells, Jeremy M

; APPLICANT: Hanniffy, Sean B

; TITLE OF INVENTION: Proteins

; FILE REFERENCE: PWC/P21978WO

; CURRENT APPLICATION NUMBER: US/10/091,007

; CURRENT FILING DATE: 2002-03-06

; PRIOR APPLICATION NUMBER: GB 9921125.2

; PRIOR FILING DATE: 1999-09-07

; NUMBER OF SEQ ID NOS: 276

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 88

; LENGTH: 452

; TYPE: PRT

; ORGANISM: Streptococcus agalactiae

US-10-091-007-88

Query Match 87.2%; Score 34; DB 14; Length 452;

Best Local Similarity 57.1%; Pred. No. 5.6e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7

||| |

Db 92 GYWSAW 98

## RESULT 4

US-10-282-122A-49513

; Sequence 49513, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA 034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 49513

; LENGTH: 466

; TYPE: PRT

; ORGANISM: Burkholderia fungorum

US-10-282-122A-49513

Query Match 87.2%; Score 34; DB 15; Length 466;

Best Local Similarity 57.1%; Pred. No. 5.8e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXXXW 7

||| |

Db 86 GYWSAW 92

## RESULT 5

US-10-369-493-23291

; Sequence 23291, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 23291

; LENGTH: 469

; TYPE: PRT

; ORGANISM: Bacillus subtilis

US-10-369-493-23291

Query Match 87.2%; Score 34; DB 14; Length 469;  
Best Local Similarity 57.1%; Pred. No. 5.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
Db 97 GYVWASW 103

## RESULT 6

US-10-282-122A-66258  
; Sequence 66258, Application US/10282122A  
; Publication No. US20040029129A1

## ; GENERAL INFORMATION:

; APPLICANT: Wang, Liangou  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 66258

; LENGTH: 472

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-10-282-122A-66258

Query Match 87.2%; Score 34; DB 15; Length 472;  
Best Local Similarity 57.1%; Pred. No. 5.8e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
Db 94 GYVWASW 100

## RESULT 7

US-10-282-122A-52805  
; Sequence 52805, Application US/10282122A  
; Publication No. US20040029129A1

## ; GENERAL INFORMATION:

; APPLICANT: Wang, Liangou  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 52805

; LENGTH: 474

; TYPE: PRT

; ORGANISM: Clostridium botulinum

US-10-282-122A-52805

Query Match 87.2%; Score 34; DB 15; Length 474;

Best Local Similarity 57.1%; Pred. No. 5.9e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
Db 95 GYVLSAW 101

## RESULT 8

US-10-369-493-13733

; Sequence 13733, Application US/10369493

; Publication No. US20030233675A1

## ; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 13733

; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Pseudomonas fluorescens  
US-10-369-493-13733

Query Match 87.2%; Score 34; DB 14; Length 475;  
Best Local Similarity 57.1%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
||| |  
Db 93 GYWISAW 99

RESULT 9  
US-10-282-122A-57680  
; Sequence 57680, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 57680  
; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Enterococcus faecium

US-10-282-122A-57680

Query Match 87.2%; Score 34; DB 15; Length 475;  
Best Local Similarity 57.1%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
||| |  
Db 95 GYWLAW 101

## RESULT 10

US-10-282-122A-68169  
; Sequence 68169, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 68169  
; LENGTH: 475  
; TYPE: PRT  
; ORGANISM: Pseudomonas putida

US-10-282-122A-68169

Query Match 87.2%; Score 34; DB 15; Length 475;  
Best Local Similarity 57.1%; Pred. No. 5.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
||| |  
Db 93 GYWISAW 99

## RESULT 11

US-10-282-122A-50338  
; Sequence 50338, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 50338  
; LENGTH: 506  
; TYPE: PRT  
; ORGANISM: Burkholderia mallei  
US-10-282-122A-50338

Query Match 87.2%; Score 34; DB 15; Length 506;  
Best Local Similarity 57.1%; Pred. No. 6.2e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7  
DB 124 GYISAW 130

RESULT 12  
US-09-894-018-87  
; Sequence 87, Application US/09894018  
; Patent No. US20020119127A1  
; GENERAL INFORMATION:  
; APPLICANT: EPIMUNE, Inc.  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Chestnut, Robert  
; APPLICANT: Livingston, Brian  
; APPLICANT: Baker, Denise  
; APPLICANT: Newman, Mark  
; APPLICANT: Brown, David  
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING  
; FILE REFERENCE: 39963-20033.00  
; CURRENT APPLICATION NUMBER: US/09/894,018  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: PCT/US00/35568  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/173,390  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 60/284,221  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 368  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 87  
; LENGTH: 585  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV-TC  
US-09-894-018-87

Query Match 87.2%; Score 34; DB 9; Length 585;  
Best Local Similarity 57.1%; Pred. No. 6.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7  
DB 22 GYQATW 28

RESULT 13  
US-10-474-960A-87  
; Sequence 87, Application US/10474960A  
; Publication No. US20040248113A1  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Chestnut, Robert  
; APPLICANT: Livingston, Brian  
; APPLICANT: Baker, Denise  
; APPLICANT: Newman, Mark  
; APPLICANT: Brown, David  
; TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic  
; FILE REFERENCE: 2060.0320004  
; CURRENT APPLICATION NUMBER: US/10/474,960A  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: PCT/US02/09877  
; PRIOR FILING DATE: 2002-03-28  
; PRIOR APPLICATION NUMBER: US 09/894,018  
; PRIOR FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: US 60/284,221  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 87  
; LENGTH: 585  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: HIV-TC  
US-10-474-960A-87

Query Match 87.2%; Score 34; DB 17; Length 585;  
Best Local Similarity 57.1%; Pred. No. 6.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXXW 7  
DB 22 GYQATW 28

RESULT 14  
US-10-046-922-34  
; Sequence 34, Application US/10046922  
; Publication No. US20020164667A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo, Kari  
; APPLICANT: Koivunen, Erkki  
; APPLICANT: Kubo, Hajime  
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS  
; FILE REFERENCE: 28967/37084A  
; CURRENT APPLICATION NUMBER: US/10/046,922  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 80  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 34  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: isolated peptide

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; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(1)
; OTHER INFORMATION: X is any amino acid
; NAME/KEY: SITE
; LOCATION: (10)...(10)
; OTHER INFORMATION: X is any amino acid
US-10-046-922-34

Query Match      84.6%; Score 33; DB 13; Length 10;
Best Local Similarity 57.1%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYXXW 7
Db 2 GYWTIW 8

RESULT 15
US-10-046-922-35
; Sequence 35, Application US/10046922
; Publication No. US20020164667A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo, Kari
; APPLICANT: Koivunen, Erkki
; APPLICANT: Kubo, Hajime
; TITLE OF INVENTION: VEGFR-3 INHIBITOR MATERIALS AND METHODS
; FILE REFERENCE: 28967/37084A
; CURRENT APPLICATION NUMBER: US/10/046,922
; CURRENT FILING DATE: 2002-01-15
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 35
; LENGTH: 10
; TYPE: PRT
; ORGANISM: isolated peptide
US-10-046-922-35

Query Match      84.6%; Score 33; DB 13; Length 10;
Best Local Similarity 57.1%; Pred. No. 42;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYXXW 7
Db 2 GYWTIW 8

Search completed: December 30, 2004, 13:50:03
Job time : 60.6226 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:58:17 ; Search time 9.20755 Seconds  
(without alignments)  
83.598 Million cell updates/sec

Title: US-10-046-922-68

Perfect score: 39

Sequence: 1 GYVXXXW 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	87.2	72	T03190	hypothetical prote
2	34	87.2	108	S12193	hypothetical prote
3	34	87.2	345	T37139	hypothetical prote
4	34	87.2	469	D70048	ABC transporter (a
5	34	87.2	472	E83497	probable amino aci
6	34	87.2	475	T46745	arginine/ornithine
7	34	87.2	482	JH0110	arginine/ornithine
8	34	87.2	490	C86879	arginine/ornithine
9	34	87.2	497	G86878	arginine/ornithine
10	33	84.6	142	C34903	Ig heavy chain pre
11	33	84.6	227	S73905	CDPdiacylglycerol-
12	33	84.6	250	A63843	hypothetical prote
13	33	84.6	289	G72215	oligopeptide ABC t
14	33	84.6	360	A2047	hypothetical prote
15	33	84.6	441	C95307	probable transport
16	33	84.6	508	C95282	probable ABC trans
17	33	84.6	517	A13201	hypothetical prote
18	33	84.6	519	E83268	probable carboxydr
19	33	84.6	534	T15414	hypothetical prote
20	33	84.6	535	B95952	probable dipeptide
21	33	84.6	541	AC2392	hypothetical prote
22	33	84.6	563	AH2975	hypothetical prote
23	33	84.6	563	C98307	opha protein limpo
24	33	84.6	592	T15413	hypothetical prote
25	33	84.6	778	T31037	hypothetical prote
26	33	84.6	1502	T42216	multidrug resistan
27	32	82.1	71	S22905	lysis protein S -
28	32	82.1	83	E69903	hypothetical prote
29	32	82.1	187	G83047	hypothetical prote

30	32	82.1	218	2	S76385	hypothetical prote
31	32	82.1	218	2	D87264	hypothetical prote
32	32	82.1	257	2	E75325	probable mcfp prot
33	32	82.1	261	2	JCS806	aquaporin 8 - mous
34	32	82.1	263	2	JCS622	aquaporin 8 - rat
35	32	82.1	271	2	F83188	phosphatidate cyti
36	32	82.1	271	2	JC4832	phosphatidate cyti
37	32	82.1	282	2	H95869	probable sugar ABC
38	32	82.1	286	2	E88690	protein F41H10.7 [
39	32	82.1	344	2	C82611	hypothetical prote
40	32	82.1	447	2	H97146	siderophore/Surfac
41	32	82.1	448	2	AB0301	conserved hypothet
42	32	82.1	466	2	T35164	probable secreted
43	32	82.1	519	2	S77572	oligopeptide trans
44	32	82.1	536	2	G95389	probable ABC trans
45	32	82.1	631	2	B86233	hypothetical prote

ALIGNMENTS

RESULT 1

T03190

hypothetical protein 72B - rice mitochondrion

C:Species: mitochondrion Oryza sativa (rice)

C>Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004

C:Accession: T03190

R:Itadani, H.; Wakasugi, T.; Sugita, M.; Sugiyura, M.; Nakazono, M.; Hirai, A.

Plant Cell Physiol. 35, 1239-1244, 1994

A:Title: Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA: the existence

A:Reference number: Z14841; MUID:95211382; PMID:7545979

A:Accession: T03190

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-72 <ITA>

A:Cross-references: UNIPROT:Q35302; EMBL:D32052; NID:g769704; PIDN:BAA06811.1; PID:g76970

A:Experimental source: cultivar Nipponbare

C:Genetics:

A:Genome: mitochondrion

C:Keywords: mitochondrion

Query Match 87.2%; Score 34; DB 2; Length 72;

Best Local Similarity 57.1%; Pred. No. 15;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYVXXXW 7

DB 34 GYVSSHW 40

RESULT 2

S12193

hypothetical protein 4 - Thiobacillus ferrooxidans plasmid pTF1

C:Species: Thiobacillus ferrooxidans

C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C:Accession: S12193

R:Drolet, M.; Zanga, P.; Lau, P.C.K.

Mol. Microbiol. 4, 1381-1391, 1990

A:Title: The mobilization and origin of transfer regions of a Thiobacillus ferrooxidans

A:Reference number: S12180; MUID:91125140; PMID:2280689

A:Accession: S12193

A>Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-108 <DRO>

A:Cross-references: UNIPROT:P20088; EMBL:X52699; NID:g48158; PIDN:CAA36930.1; PID:g48164

C:Genetics:

A:Genome: plasmid pTF1

Query Match 87.2%; Score 34; DB 2; Length 108;

Best Local Similarity 57.1%; Pred. No. 21;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYVXXXW 7

```

Db      89 GYWRSSW 95
|||||
RESULT 3
T37139
hypothetical protein SCJ9A.03c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37139
R;Harris, D.; Bentley, S.D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21622
A;Accession: T37139
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-345 <HAR>
A;Cross-references: UNIPROT:Q981R7; EMBL:AL109972; PIDN:CAB53264.1; GSPDB:GN00070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOE8B:SCJ9A.03c
C;Superfamily: Streptomyces coelicolor hypothetical protein SCJ9A.03c

Query Match      87.2%; Score 34; DB 2; Length 345;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7
|||||
Db 147 GYWAARW 153

RESULT 4
D70048
ABC transporter (amino acid permease) homolog yvzH - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: D70048
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berta
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yanamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: D70048
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-469 <KUN>
A;Cross-references: UNIPROT:Q32204; GB:Z99121; GB:AL009126; NID:g2635827; PIDN:CAB15339.
A;Experimental source: strain 168
C;Genetics:
A;Gene: yvzH
C;Superfamily: L-lysine transport protein

Query Match      87.2%; Score 34; DB 2; Length 469;
Best Local Similarity 57.1%; Pred. No. 80;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7
|||||
Db 97 GYVAVSW 103

RESULT 5
E83497
probable amino acid permease PA1194 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83497
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Bja
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83497
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-472 <STO>
A;Cross-references: UNIPROT:Q914E4; GB:AE004549; GB:AE004091; NID:99947110; PIDN:AAG0458;
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1194
C;Superfamily: L-lysine transport protein

Query Match      87.2%; Score 34; DB 2; Length 472;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7
|||||
Db 94 GYWISAW 100

RESULT 6
T46745
arginine/ornithine antiporter [imported] - Lactobacillus sakei
C;Species: Lactobacillus sakei
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T46745
R;Zunica, M.; Champomier-Verges, M.C.; Perez-Martinez, G.; Zagorec, M.; Perez-Martinez, C.
J. Bacteriol. 180, 4154-4159, 1998
A;Title: Structural and functional analysis of the gene cluster encoding the enzymes of
A;Reference number: Z23141; MUID:98361904; PMID:9696763
A;Accession: T46745
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-475 <ZUN>
A;Cross-references: UNIPROT:O53092; EMBL:AJ001330; NID:g2764610; PIDN:CAA04686.1; PID:92
C;Genetics:
A;Gene: arcD
C;Function:
A;Description: necessary for arginine transport; involved in ornithine-arginine exchange
A;Pathway: arginine catabolism
C;Superfamily: L-lysine transport protein

Query Match      87.2%; Score 34; DB 2; Length 475;
Best Local Similarity 57.1%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7
|||||
Db 94 GYWLAW 100

RESULT 7
JH0110
arginine/ornithine antiporter PA5170 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: JH0110; A82999
R;Luethi, E.; Baur, H.; Ganper, M.; Brunner, F.; Villevall, D.; Mercenier, A.; Haas, D.
Gene 87, 37-43, 1990
A;Title: The arc operon for anaerobic arginine catabolism in Pseudomonas aeruginosa cont
A;Reference number: JH0110; MUID:90236296; PMID:2158926
A;Accession: JH0110

```

A:Molecule type: DNA  
A:Residues: 1-482 <LUE>  
A:Cross-references: UNIPROT:P18275; GB:M33223; NID:g151030; PIDN:AAA25719.1; PID:g151031  
A:Experimental source: strain PA01  
A>Note: the gene encoding this protein is located upstream of the arcABC genes which encode the L-lysine transport protein  
R:Stover, C.K.; Phan, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Brachman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: A82999  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-482 <STO>  
A:Cross-references: GB:AE004930; GB:AE004091; NID:g9951472; PIDN:AAG08555.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: arcD; PA5170  
C:Superfamily: L-lysine transport protein  
C:Keywords: transmembrane protein

Query Match 87.2%; Score 34; DB 2; Length 482;  
Best Local Similarity 57.1%; Pred. No. 82;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
|||  
Db 94 GYWISAW 100

RESULT 8  
C86879  
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: C86879  
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich, G.  
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* subsp. *lactis* strain IL140  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: C86879  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-490 <STO>  
A:Cross-references: UNIPROT:Q9CE15; GB:AE005176; PID:g12725084; PIDN:AAK06133.1; GSPDB:GN001  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: arcD1  
C:Superfamily: L-lysine transport protein

Query Match 87.2%; Score 34; DB 2; Length 490;  
Best Local Similarity 57.1%; Pred. No. 84;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
|||  
Db 93 GYWISAW 99

RESULT 9  
G86878  
arginine/ornithine antiporter [imported] - Lactococcus lactis subsp. lactis (strain IL140)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: G86878  
R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich, G.  
A:Title: The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* subsp. *lactis* strain IL140  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: G86878  
A>Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-497 <STO>  
A:Cross-references: UNIPROT:Q9CE19; GB:AE005176; PID:g12725079; PIDN:AAK06129.1; GSPDB:GN001  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: arcD2  
C:Superfamily: L-lysine transport protein

Query Match 87.2%; Score 34; DB 2; Length 497;  
Best Local Similarity 57.1%; Pred. No. 85;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
|||  
Db 93 GYWISAW 99

RESULT 10  
C34903  
Ig heavy chain precursor V region (5-27) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 27-Jul-1990 #sequence\_revision 27-Jul-1990 #text\_change 16-Aug-1996  
C:Accession: C34903  
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.  
J. Biol. Chem. 265, 133-138, 1990  
A:Title: Active site structure and antigen binding properties of idiotypically cross-reactive antibodies  
A:Reference number: A34903; MUID:90094387; PMID:2104617  
A:Accession: C34903  
A>Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-142 <BED>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-119/Domain: immunoglobulin homology <IMM>

Query Match 84.6%; Score 33; DB 2; Length 142;  
Best Local Similarity 57.1%; Pred. No. 40;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
|||  
Db 126 GYWFAYW 132

RESULT 11  
S73905  
CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) pgsA - Mycobacterium tuberculosis  
N:Alternate names: hypothetical protein A65\_orf227  
C:Species: Mycobacterium tuberculosis  
A:Variety: ATCC 29342  
C:Date: 27-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C:Accession: S73905  
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkel, E.; Li, B.C.; Herrmann, R.  
Nucleic Acids Res. 24, 4420-4449, 1996  
A:Title: Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumoniae* strain M129  
A:Reference number: S73327; MUID:97105885; PMID:8948633  
A:Accession: S73905  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-227 <HIM>  
A:Cross-references: UNIPROT:P75520; EMBL:AE000057; GB:U00089; NID:g1674279; PIDN:AAB9622  
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C:Genetics:  
A:Gene: pgsA  
C:Superfamily: CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase  
C:Keywords: transferase

Query Match 84.6%; Score 33; DB 2; Length 227;  
Best Local Similarity 57.1%; Pred. No. 62;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GYXXXXX 7  
|||  
Db 126 GYWFAYW 132

Db 84 GYWARW 90

RESULT 12

hypothetical protein yjba - Bacillus subtilis

C/Species: Bacillus subtilis

C/Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004

C/Accession: A69843

R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berten  
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galled  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y, M.; Ogawa, K.; Ogiwara, C.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, M.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon  
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K  
A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: A69843

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-250 <KUN>

A/Cross-references: UNIPROT:O31597; GB:Z99110; GB:AL009126; NID:g2633472; PIDN:CAB12998.

A/Experimental source: strain 168

C/Genetics:

A/Gene: yjba

C/Superfamily: Bacillus subtilis hypothetical protein yjba

Query Match 84.6%; Score 33; DB 2; Length 250;  
Best Local Similarity 57.1%; Pred. No. 68;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
|||  
Db 185 GYWTW 191

RESULT 13

G72215

oligopeptide ABC transporter, permease protein - Thermotoga maritima (strain MSB8)

C/Species: Thermotoga maritima

C/Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C/Accession: G72215

R/Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;  
C.W.

Nature 399, 323-329, 1999

A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
A/Reference number: A72200; MUID:99287316; PMID:10360571

A/Accession: G72215

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-289 <ARN>

A/Cross-references: UNIPROT:Q9X270; GB:AE001813; GB:AE000512; NID:g4982321; PIDN:AAD3681

C/Genetics:

A/Gene: TM1748

C/Superfamily: oligopeptide permease protein oppB

Query Match 84.6%; Score 33; DB 2; Length 289;  
Best Local Similarity 57.1%; Pred. No. 77;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
|||  
Db 11 GYWKAF 17

RESULT 14

AE2047

hypothetical protein all1931 [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp. PCC 7120

A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004

C/Accession: AE2047

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A/Reference number: AB1807; MUID:21595285; PMID:11759840

A/Accession: AE2047

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-360 &lt;KUR&gt;

A/Cross-references: UNIPROT:Q8YVP3; GB:BA000019; PIDN:BA073630.1; PID:gl7131021; GSPDB:G

A/Experimental source: strain PCC 7120

C/Genetics:

A/Gene: all1931

Query Match 84.6%; Score 33; DB 2; Length 360;  
Best Local Similarity 57.1%; Pred. No. 94;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;Qy 1 GYWXW 7  
|||  
Db 127 GYWSYG 133

RESULT 15

C95307

probable transport protein SMA0684 [imported] - Sinorhizobium meliloti (strain 1021) meg

C/Species: Sinorhizobium meliloti

C/Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004

C/Accession: C95307

R/Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse

; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.

Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001

A/Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti

A/Reference number: A95262; MUID:21396509; PMID:11481432

A/Accession: C95307

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-441 &lt;KUR&gt;

A/Cross-references: UNIPROT:Q92ZT6; GB:AE006469; PIDN:AAK65021.1; PID:gl4523451; GSPDB:G

A/Experimental source: strain 1021, megaplasmid pSymA

R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,

hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.C.

A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A/Reference number: A96039; MUID:21368234; PMID:11474104

A/Contents: annotation

C/Genetics:

A/Gene: SMA0684

A/Genome: plasmid

C/Superfamily: L-lysine transport protein

Query Match 84.6%; Score 33; DB 2; Length 441;  
Best Local Similarity 57.1%; Pred. No. 1.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;Qy 1 GYWXW 7  
|||  
Db 92 GYWISW 98

Search completed: December 30, 2004, 13:17:15

Job time : 9.37421 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:57:52 ; Search time 73.8113 Seconds  
(without alignments)  
62.362 Million cell updates/sec

Title: US-10-046-922-68  
Perfect score: 39  
Sequence: 1 GYWXXXWX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	87.2	72	Q35302	Q35302 oryza sativ
2	34	87.2	108	1 YML2 THIFE	P20088 thioabacillu
3	34	87.2	130	Q7U395	Q7U395 prochloroco
4	34	87.2	236	Q9KGM9	Q9KGM9 human immun
5	34	87.2	253	Q32816	Q32816 lactococcus
6	34	87.2	294	Q8ET30	Q8ET30 oceanobactil
7	34	87.2	333	Q6F6U4	Q6F6U4 acinetobact
8	34	87.2	345	Q9S1R7	Q9S1R7 streptomyc
9	34	87.2	459	Q9KGV3	Q9KGV3 lactococcus
10	34	87.2	464	Q84DL5	Q84DL5 oenococcus
11	34	87.2	465	Q6HNI4	Q6HNI4 bacillus th
12	34	87.2	465	Q6I3F7	Q6I3F7 bacillus an
13	34	87.2	465	Q73DL5	Q73DL5 bacillus ce
14	34	87.2	465	Q81HZ7	Q81HZ7 bacillus ce
15	34	87.2	465	Q81V71	Q81V71 bacillus an
16	34	87.2	465	2 AAS39630	Aas39630 bacillus
17	34	87.2	465	2 AAT29732	Aat29732 bacillus
18	34	87.2	469	2 Q6TK71	Q6TK71 streptococ
19	34	87.2	469	2 Q32204	Q32204 bacillus su
20	34	87.2	469	2 AAR30325	Aar30325 streptoco
21	34	87.2	471	2 Q6HP27	Q6HP27 bacillus th
22	34	87.2	471	2 Q71E85	Q71E85 bacillus ce
23	34	87.2	471	2 Q81IH9	Q81IH9 bacillus ce
24	34	87.2	471	2 AAS39409	Aas39409 bacillus
25	34	87.2	472	2 Q914E4	Q914E4 pseudomonas
26	34	87.2	473	2 Q7NRJ8	Q7NRJ8 chromobacte
27	34	87.2	475	1 ARCD LACSK	O53092 lactobacill
28	34	87.2	475	2 Q8BP50	Q8BP50 pseudomonas
29	34	87.2	475	2 Q8BP51	Q8BP51 pseudomonas
30	34	87.2	475	2 Q8DWP9	Q8DWP9 streptococ
31	34	87.2	475	2 Q8E2J7	Q8E2J7 streptococ

32 34 87.2 478 1 ARCD\_CLOPE Q46170 clostridium  
33 34 87.2 482 1 ARCD\_PSEAE P18275 pseudomonas  
34 34 87.2 490 2 Q9CEI5 Q9CEI5 lactococcus  
35 34 87.2 497 2 Q9KGV0 Q9KGV0 lactococcus  
36 34 87.2 497 2 Q9CEI9 Q9CEI9 lactococcus  
37 34 87.2 526 2 Q9K574 Q9K574 lactococcus  
38 34 87.2 879 2 Q7ZJ77 Q7ZJ77 human immun  
39 33 84.6 130 2 Q7VBG3 Q7VBG3 prochloroco  
40 33 84.6 135 2 Q7TUV7 Q7TUV7 prochloroco  
41 33 84.6 160 2 Q6NF17 Q6NF17 corynebacte  
42 33 84.6 160 2 CAE50615 CAE50615 corynebac  
43 33 84.6 213 2 Q9KY37 Q9KY37 streptomyc  
44 33 84.6 224 2 Q8S486 Q8S486 zea mays (m  
45 33 84.6 227 1 PGSA\_MYCPN P75520 mycoplasma

#### ALIGNMENTS

RESULT 1  
Q35302 PRELIMINARY; PRT; 72 AA.  
AC Q35302;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE ORF72B.  
OS Oryza sativa (japonica cultivar-group).  
OG Mitochondrion.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzoideae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Baev A.A., Dzhumagaliev E.B., Lyubomirskaya N.V., Mizrokhi L.Y.,  
RA Il'in Y.V.;  
RT "Structure of long and short copies of the mobile dispersed gene MDG3  
of *Drosophila melanogaster*.";  
RL Dokl. Akad. Nauk SSSR 282:1483-1486(1985).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95308541; PubMed=7788722;  
RA Nakazono M., Itadani H., Wakasugi T., Tsutsumi N., Sugiyura M.,  
RA Hirai A.;  
RT "The rps3-rpl16-nad3-rps12 gene cluster in rice mitochondrial DNA is  
transcribed from alternative promoters.";  
RL Curr. Genet. 27:184-189(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95211382; PubMed=7545979;  
RA Itadani H., Wakasugi T., Sugita M., Sugiyura M., Nakazono M., Hirai A.;  
RT "Nucleotide sequence of a 28-kbp portion of rice mitochondrial DNA:  
the existence of many sequences that correspond to parts of  
mitochondrial genes in intergenic regions.";  
RL Plant Cell Physiol. 35:1239-1244(1994).  
DR EMBL; D32052; BAA06811.1;  
DR PIR; T03190; T03190.  
DR Gramene; Q35302;  
DR GO; GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
SQ SEQUENCE 72 AA; 8155 MW; D42DE53BED28432E CRC64;

Query Match 87.2%; Score 34; DB 2; Length 72;

Best Local Similarity 57.1%; Pred. No. 87; Mismatches 3; Indels 0; Gaps 0;

Matches 4; Conservative 0;

QY 1 GYWXXXW 7

Db 34 GYWSSHW 40

RESULT 2

```
YML2_THIFE
ID _YML2_THIFE STANDARD; PRT; 108 AA.
AC P20088;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 12.3 kDa protein in mobL 3' region (ORF 4).
DS Thiobacillus ferrooxidans.
OS Plasmid pF1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillales;
OC Acidithiobacillaceae; Acidithiobacillus.
OX NCBI_TaxID=920;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33020;
RX MEDLINE=91125140; PubMed=2280689;
RA Drolet M., Zanga P., Lau P.C.K.;
RT "The mobilization and origin of transfer regions of a Thiobacillus
RT ferrooxidans plasmid: relatedness to plasmids RSF1010 and pSC101.";
RL Mol. Microbiol. 4:1381-1391(1990).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC -----
DR EMBL; X52699; CAA36930.1; -.
DR PIR; S12193; S12193.
DR Hypothetical protein; Plasmid.
SQ SEQUENCE 108 AA; 12335 MW; ABE67717C109A57E CRC64;

Query Match 87.2%; Score 34; DB 1; Length 108;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7
Db 89 GYWRSSW 95

RESULT 3
Q7U395 PRELIMINARY; PRT; 130 AA.
AC Q7U395;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Possible Adenoviral fiber protein (Repeat/shaf.
DE OrderedLocNames=PM1067;
GN Prochlorococcus marinus subsp. pastoris (strain COMP 1378 / MED4).
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=59919;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA Algren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA Webb E.A., Zinser E.R., Chisholm S.W.;
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT niche differentiation.";
RL Nature 424:1042-1047(2003).
DR EMBL; BX572092; CAE19526.1; -.
KW Complete proteome.
SQ SEQUENCE 130 AA; 14024 MW; E80F4A997FCA8CD8 CRC64;

Query Match 87.2%; Score 34; DB 2; Length 130;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
```

```
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7
Db 7 GYWTW 13

RESULT 4
Q9WCW9 PRELIMINARY; PRT; 236 AA.
AC Q9WCW9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polyprotein (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9214336; PubMed=10196293;
RA Wilson C.C., Brown R.C., Korber B.T., Wilkes B.M., Ruhl D.J.,
RA Sakamoto D., Kunstman K., Luzuriaga K., Hanson I.C., Widmayer S.M.,
RA Wiznia A., Clapp S., Ammann A.J., Koup R.A., Wollinsky S.M.,
RA Walker B.D.;
RT "Frequent detection of escape from cytotoxic T-lymphocyte recognition
RT in perinatal human immunodeficiency virus (HIV) type 1 transmission:
RT the ariel project for the prevention of transmission of HIV from
RT mother to infant.";
RL J. Virol. 73:3975-3985(1999).
DR EMBL; AF121641; AAD29013.1; -.
DR GO; GO:0003676; P:nucleic acid binding; IEA.
DR GO; GO:0004523; P:ribonuclease H activity; IEA.
DR InterPro; IPR002156; RNaseH.
DR InterPro; IPR010659; RVT_thumb.
DR InterPro; IPR010661; RVT_thumb.
DR Pfam; PF00075; RNaseH; 1_
DR Pfam; PF06815; RVT_connect; 1.
DR Pfam; PF06817; RVT_thumb; 1.
KW Polyprotein.
FT NON TER 1
FT NON TER 236
SQ SEQUENCE 236 AA; 27062 MW; 24D6BB040A80BB8 CRC64;

Query Match 87.2%; Score 34; DB 2; Length 236;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7
Db 129 GYQATW 135

RESULT 5
Q32816 PRELIMINARY; PRT; 253 AA.
AC Q32816;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Arginine/ornithine antiporter homolog ArcD (Fragment).
GN Name=arcD;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M31363;
RX MEDLINE=97369814; PubMed=9226255;
RA Duwat P., Cochu A., Ehrlich S.D., Gruss A.;
RT "Characterization of Lactococcus lactis UV-sensitive mutants obtained
RT by IS91 transposition.";
```

RL J. Bacteriol. 179:4473-4479 (1997).  
 DR EMBL; U81991; AAC45504.1; -.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.  
 DR GO; GO:0006865; P:amino acid transport; IEA.  
 DR InterPro; IPR002293; AA/rel\_permease1.  
 DR Transmembrane.  
 FW NON\_TER 253  
 SQ SEQUENCE 253 AA; 26569 MW; 1CB8FAEF6C38FBB1 CRC64;  
 Query Match 87.2%; Score 34; DB 2; Length 253;  
 Best Local Similarity 57.1%; Pred. No. 2.7e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GYWXW 7  
 DB 93 GYWLSAW 99  
 RESULT 6  
 ID Q8ET30 PRELIMINARY; PRT; 294 AA.  
 AC Q8ET30;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE ABC transporter permease.  
 GN OrderedLocusNames=OB0434;  
 OS Oceanobacillus iheyensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.  
 OX NCBI\_TaxID=182710;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=HTE831;  
 RX MEDLINE=22220767; PubMed=12235376;  
 RA Takami H., Takaki Y., Uchiyama I.;  
 RT "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya  
 RT Ridge and its unexpected adaptive capabilities to extreme  
 RT environments";  
 RL Nucleic Acids Res. 30:3927-3935 (2002).  
 CC - SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 CC - SIMILARITY: BELONGS TO THE ABC-3 SUBFAMILY OF INTEGRAL MEMBRANE  
 CC PROTEINS.  
 DR EMBL; AF004594; BAC12390.1; -.  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005524; P:ATP binding; IEA.  
 DR GO; GO:0004009; P:ATP-binding cassette (ABC) transporter acti...; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR001626; ABC\_3.  
 DR Pfam; PF00950; ABC-3; 1.  
 KW Complete proteome; Transmembrane; Transport.  
 SQ SEQUENCE 294 AA; 31323 MW; F75E50F22EA4071A CRC64;  
 Query Match 87.2%; Score 34; DB 2; Length 294;  
 Best Local Similarity 57.1%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GYWXW 7  
 DB 244 GYWIATW 250  
 RESULT 7  
 ID Q6F6U4 PRELIMINARY; PRT; 333 AA.  
 AC Q6F6U4;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Putative transporter; putative sodium/bile acid transporter family  
 DE protein.  
 GN OrderedLocusNames=ACTIAD3583;  
 OS Acinetobacter sp. (strain ADP1).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Moraxellaceae; Acinetobacter.  
 OX NCBI\_TaxID=62977;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,  
 RA Labarre L., Cruveillier S., Robert C., Duprat S., Wincker P.,  
 RA Ornaton L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;  
 RT "Unique features revealed by the genome sequence of Acinetobacter sp.  
 RT ADP1, a versatile and naturally transformation competent bacterium.";  
 RL Nucleic Acids Res. 0:0-0 (2004).  
 DR EMBL; CR543861; CAG70223.1; -.  
 DR InterPro; IPR002857; BilAC/Na\_sympor.  
 DR Pfam; PF01758; SBF; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 333 AA; 36530 MW; 7C887F5127A40682 CRC64;  
 Query Match 87.2%; Score 34; DB 2; Length 333;  
 Best Local Similarity 57.1%; Pred. No. 3.5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GYWXW 7  
 DB 252 GYWASRW 258  
 RESULT 8  
 ID Q9S1R7 PRELIMINARY; PRT; 345 AA.  
 AC Q9S1R7;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Hypothetical protein SCO0224.  
 GN OrderedLocusNames=SCO0224; ORFNames=SCJ9A.03c;  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M45;  
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Horneby T., Howarth S.,  
 RA Huang C.-H., Kieser F., Larke L., Murphy L.D., Oliver K., O'Neil S.,  
 RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete Streptomyces  
 RT coelicolor A3(2).";  
 RL Nature 417:141-147 (2002).  
 DR EMBL; AL939104; CAB53264.1; -.  
 DR PIR; T37139; T37139.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 345 AA; 36929 MW; 23643009936285B8 CRC64;  
 Query Match 87.2%; Score 34; DB 2; Length 345;  
 Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 GYWXW 7  
 DB 147 GYWAARW 153  
 RESULT 9  
 ID Q9KGV3 PRELIMINARY; PRT; 459 AA.  
 AC Q9KGV3;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE ArcD1.  
GN Name=arcD1;  
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).  
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.  
OX NCBI\_TaxID=1360;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ML3;  
RA Chou L., Weimer B., Xie Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ML3;  
RA Chou L.-S., Weimer B., Xie Y.;  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF282249; AAF86987.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.  
DR GO; GO:0006865; P:amino acid transport; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR002293; AA/permease1.  
DR InterPro; IPR004841; Permease region.  
DR Pfam; PF00324; AA\_permease; 1.  
KW Transmembrane; Transport.  
SQ SEQUENCE 459 AA; 49146 MW; 9718F27B7E937242 CRC64;  
Query Match 87.2%; Score 34; DB 2; Length 459;  
Best Local Similarity 57.1%; Pred. No. 4.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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Db 92 GYWLAW 98  
RESULT 10  
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ID Q84DL5 PRELIMINARY; PRT; 464 AA.  
AC Q84DL5;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Arginine/ornithine antiporter ArcD2.  
GN Name=arcD2;  
OS Oenococcus oeni (Leuconostoc oenos).  
OC Bacteria; Firmicutes; Lactobacillales; Oenococcus.  
OX NCBI\_TaxID=1247;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 23279;  
RX MEDLINE=22519090; PubMed=12631210;  
RA Divol B., Tonon T., Morichon S., Gindreau E., Lonvaud-Funel A.;  
RT "Molecular characterization of Oenococcus oeni genes encoding proteins involved in arginine transport."  
RL J. Appl. Microbiol. 94:738-746 (2003).  
DR EMBL; AF541253; AA083382.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.  
DR GO; GO:0006865; P:amino acid transport; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR002293; AA/permease1.  
DR InterPro; IPR004841; Permease region.  
DR Pfam; PF00324; AA\_permease; 1.  
KW Transmembrane; Transport.  
SQ SEQUENCE 464 AA; 50557 MW; 1C6EE79AFF9F8B84 CRC64;  
Query Match 87.2%; Score 34; DB 2; Length 464;  
Best Local Similarity 57.1%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GYWXW 7  
Db 94 GYWLSSW 100  
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ID Q6HNI4 PRELIMINARY; PRT; 465 AA.  
AC Q6HNI4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Probable arginine/ornithine antiporter protein.  
GN Name=arcD; ORFName=B79727\_0540;  
OS Bacillus thuringiensis serovar konkukian str. 97-27.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus thuringiensis serovar konkukian.  
OX NCBI\_TaxID=281309;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=97-27;  
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Tice H.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE017355; AAT62417.1; -.  
DR InterPro; IPR002293; AA/permease1.  
DR InterPro; IPR004841; Permease region.  
DR Pfam; PF00324; AA\_permease; 1.  
KW Transmembrane; Transport.  
SQ SEQUENCE 465 AA; 50153 MW; 534F038C0A379E04 CRC64;  
Query Match 87.2%; Score 34; DB 2; Length 465;  
Best Local Similarity 57.1%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GYWXW 7  
Db 96 GYWAANW 102  
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Q6I3F7  
ID Q6I3F7 PRELIMINARY; PRT; 465 AA.  
AC Q6I3F7;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Amino acid permease family protein.  
GN OrderedLocusNames=BAS0596;  
OS Bacillus anthracis.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=1392;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Spierne;  
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
RA Richardson P., Rubin E., Tice H.;  
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE017225; AAT52924.1; -.  
DR InterPro; IPR002293; AA/permease1.  
DR InterPro; IPR004841; Permease region.  
DR Pfam; PF00324; AA\_permease; 1.  
KW Transmembrane; Transport.  
SQ SEQUENCE 465 AA; 50192 MW; 45E4E63506085DF4 CRC64;  
Query Match 87.2%; Score 34; DB 2; Length 465;  
Best Local Similarity 57.1%; Pred. No. 4.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GYWXW 7

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Db          96 GYWAANW 102

RESULT 13
Q73DL5
ID Q73DL5      PRELIMINARY;      PRT;      465 AA.
AC Q73DL5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Amino acid permease family protein.
GN OrderedLocusNames=BC0697;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=222523;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14960714;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.B., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
RT "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pX01.";
RL Nucleic Acids Res. 32:977-988 (2004).
DR EMBL; AF017266; AAS39630.1; -.
DR TIGR; BCE0697; -.
DR InterPro; IPR002293; AA/permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Complete proteome; Transmembrane; Transport.
SQ SEQUENCE 465 AA; 50193 MW; C18384810EBC639D CRC64;

Query Match      87.2%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXWXXW 7
      |||||
Db      96 GYWAANW 102

RESULT 14
Q81HZ7
ID Q81HZ7      PRELIMINARY;      PRT;      465 AA.
AC Q81HZ7;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Arginine/ornithine antiporter.
GN ORFNames=BC0629;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=226900;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA Ivanova N., Sorokin A., Anderson I., Galleron N., Candelson B.,
RA Kaparal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
RT Bacillus anthracis.";
RL Nature 423:87-91 (2003).
DR EMBL; AF017000; AAP07646.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Transmembrane; Transport.

Query Match      87.2%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXWXXW 7
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Db      96 GYWAANW 102

SQ SEQUENCE 465 AA; 50040 MW; 9750B5D1019142F2 CRC64;

Query Match      87.2%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXWXXW 7
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Db      96 GYWAANW 102

RESULT 15
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ID Q81V71      PRELIMINARY;      PRT;      465 AA.
AC Q81V71; Q6KX71;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Amino acid permease family protein.
GN OrderedLocusNames=BA0629; ORFNames=GBAA0629;
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Oekstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouiri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Niernan W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF017026; AAP24646.1; -.
DR EMBL; AF017334; AAT29732.1; -.
DR TIGR; BA0629; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
DR GO; GO:0006865; P:amino acid transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR002293; AA/permease1.
DR InterPro; IPR004841; Permease_region.
DR Pfam; PF00324; AA_permease; 1.
KW Transmembrane; Transport.
SQ SEQUENCE 465 AA; 50250 MW; AA04D53505386FA9 CRC64;

Query Match      87.2%; Score 34; DB 2; Length 465;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 GYWXWXXW 7
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Db      96 GYWAANW 102

Search completed: December 30, 2004, 13:16:13
Job time : 74.8113 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:02:29 ; Search time 148 Seconds  
(without alignments)  
19,391 Million cell updates/sec

Title: US-10-046-922-32  
Perfect score: 8  
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 200273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 153769

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	1	2	ADD95004 Platelet
2	0	0.0	1	2	ADD94992 Platelet
3	0	0.0	1	2	ADD94993 Platelet
4	0	0.0	1	2	ADD95002 Platelet
5	0	0.0	1	2	ADD94997 Platelet
6	0	0.0	1	2	ADD94999 Platelet
7	0	0.0	1	2	ADD95003 Platelet
8	0	0.0	1	2	ADD94995 Platelet
9	0	0.0	1	2	ADD94998 Platelet
10	0	0.0	1	2	ADD95001 Platelet
11	0	0.0	1	2	ADD94990 Platelet
12	0	0.0	1	2	ADD94991 Platelet
13	0	0.0	1	2	ADD94994 Platelet
14	0	0.0	1	2	ADD94996 Platelet
15	0	0.0	1	2	ADD95000 Platelet
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17	0	0.0	1	4	AAm97834 Human pep
18	0	0.0	1	4	AAm97974 Human pep
19	0	0.0	1	4	AAm97643 Human pep
20	0	0.0	1	4	AAm98447 Human pep
21	0	0.0	1	4	AAm98354 Human pep
22	0	0.0	1	4	AAm53290 Human non
23	0	0.0	1	4	AAm53329 Human non
24	0	-0.0	1	4	AAm53291 Human non
25	0	0.0	1	4	AAm53328 Human non

26	0	0.0	1	4	AAM53219 Human non
27	0	0.0	1	4	AAM53218 Human non
28	0	0.0	1	4	AAB91029 Thyrotrop
29	0	0.0	1	4	AAB91739 Opioid pe
30	0	0.0	1	4	AAB92150 Polypepti
31	0	0.0	1	4	AAB91892 Apoptosis
32	0	0.0	1	4	AAB91546 Endotheli
33	0	0.0	1	4	AAB92392 Miscellan
34	0	0.0	1	4	AAB91665 Opioid pe
35	0	0.0	1	4	AAG99966 ERA bindi
36	0	0.0	1	4	AAM00011 ERA bindi
37	0	0.0	1	4	AAG99987 ERA bindi
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ALIGNMENTS

RESULT 1  
ADD95004  
ID ADD95004 standard; peptide; 1 AA.  
XX AC ADD95004;  
XX DT 29-JAN-2004 (first entry)  
XX DE Platelet aggregation inhibitor peptide #146.  
XX KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
FT Modified-site 1  
FT /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
XX PN WO9501371-A1.  
XX PD 12-JAN-1995.  
XX PF 22-JUN-1994; 94WO-JP000999.  
XX PR 30-JUN-1993; 93JP-00186755.  
XX PA (YAMA ) NIPPON STEEL CORP.  
XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX DR WPI; 1995-060950/08.  
XX FT New RGD peptide(s) useful as anti-platelet aggregation agents - contain  
XX PT guanidino or amidino gp. at N-terminal to increase stability.  
XX PS Disclosure; Page 11; 34pp; Japanese.  
XX CC The invention describes peptides of amino acid sequence (I) and their  
XX CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
XX CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
XX CC amidino group, (I) are provided with excellent stability so that their  
XX CC activity can be exhibited for an effective time after administration.  
XX CC Thereafter they are readily metabolised and expelled. This is the amino  
XX CC acid sequence of a platelet aggregation inhibitor peptide.  
XX SQ Sequence 1 AA;

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Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 R 1

RESULT 2
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ID ADD94992 standard; peptide; 1 AA.
XX
AC ADD94992;
XX
DT 29-JAN-2004 (first entry)
XX
DE Platelet aggregation inhibitor peptide #134.
XX
KW platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT defined)"
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PN WO9501371-Al.
XX
PD 12-JAN-1995.
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PF 22-JUN-1994; 94WO-JP000999.
XX
PR 30-JUN-1993; 93JP-00186755.
XX
PA (YAWA ) NIPPON STEEL CORP.
XX
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX
DR WPI; 1995-060950/08.
XX
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain
PT guanidino or amidino gp. at N-terminal to increase stability.
XX
PS Disclosure; Page 10; 34pp; Japanese.
XX
CC The invention describes peptides of amino acid sequence (I) and their
CC salts. (I) are useful as platelet aggregation inhibitors and are easily
CC absorbed by the body. Due to the presence of the N-terminal guanidino or
CC amidino group, (I) are provided with excellent stability so that their
CC activity can be exhibited for an effective time after administration.
CC Thereafter they are readily metabolised and expelled. This is the amino
CC acid sequence of a platelet aggregation inhibitor peptide.
XX
SQ Sequence 1 AA;
Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 R 1

RESULT 4
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ID ADD95002 standard; peptide; 1 AA.
XX
AC ADD95002;
XX
DT 29-JAN-2004 (first entry)
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DE Platelet aggregation inhibitor peptide #144.
XX
KW platelet aggregation inhibitor; guanidino group; amidino group.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT defined)"
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AC ADD94993;

Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
Db      1 R 1

RESULT 3
ADD94993
ID ADD94993 standard; peptide; 1 AA.
XX
AC ADD94993;
XX
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PN W09501371-Al.  
XX  
XX 12-JAN-1995.  
XX  
XX 22-JUN-1994; 94WO-JP000999.  
XX PF  
XX 30-JUN-1993; 93JP-00186755.  
XX PR  
XX (YAWA ) NIPPON STEEL CORP.  
XX PA  
XX Sato Y, Hayaashi Y, Katada J, Takiguchi Y;  
XX PI  
XX WPI; 1995-060950/08.  
DR  
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
XX guanidino or amidino gp. at N-terminal to increase stability.  
PT  
XX Disclosure; Page 10-11; 34pp; Japanese.  
PS  
XX The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
XX Sequence 1 AA;  
SQ

Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
DB 1 R 1

RESULT 5  
ADD94997  
ID ADD94997 standard; peptide; 1 AA.  
XX  
XX AC ADD94997;  
XX  
XX DT 29-JAN-2004 (first entry)  
XX  
XX DE Platelet aggregation inhibitor peptide #139.  
XX  
XX KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
XX OS Unidentified.  
XX

FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER= H2NC(=NH)(CH2)CO. Beta-Ala (not defined)"  
FT  
XX PN W09501371-Al.  
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XX PD 12-JAN-1995.  
XX  
XX PP 22-JUN-1994; 94WO-JP000999.  
XX  
XX PR 30-JUN-1993; 93JP-00186755.  
XX  
XX PA (YAWA ) NIPPON STEEL CORP.  
XX  
XX PI Sato Y, Hayaashi Y, Katada J, Takiguchi Y;  
XX  
XX DR WPI; 1995-060950/08.  
XX  
XX PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
XX guanidino or amidino gp. at N-terminal to increase stability.  
PS  
XX Disclosure; Page 10; 34pp; Japanese.  
XX  
XX The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
XX Sequence 1 AA;  
SQ

Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
DB 1 R 1

RESULT 5  
ADD94997  
ID ADD94997 standard; peptide; 1 AA.  
XX  
XX AC ADD94997;  
XX  
XX DT 29-JAN-2004 (first entry)  
XX  
XX DE Platelet aggregation inhibitor peptide #139.  
XX  
XX KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
XX OS Unidentified.  
XX

FH Key Location/Qualifiers  
FT Modified-site 1 /label= OTHER  
FT /note= "OTHER= H2NC(=NH)(CH2)CO. Beta-Ala (not defined)"  
FT  
XX PN W09501371-Al.  
XX  
XX PD 12-JAN-1995.  
XX  
XX PP 22-JUN-1994; 94WO-JP000999.  
XX  
XX PR 30-JUN-1993; 93JP-00186755.  
XX  
XX PA (YAWA ) NIPPON STEEL CORP.  
XX  
XX PI Sato Y, Hayaashi Y, Katada J, Takiguchi Y;  
XX  
XX DR WPI; 1995-060950/08.  
XX  
XX PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
XX guanidino or amidino gp. at N-terminal to increase stability.

Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

RESULT 7  
ADD95003  
ID ADD95003 standard; peptide; 1 AA.  
XX AC ADD95003;  
XX 29-JAN-2004 (first entry)  
DT  
DE Platelet aggregation inhibitor peptide #145.  
XX platelet aggregation inhibitor; guanidino group; amidino group.  
XX OS Unidentified.  
XX Key Location/Qualifiers  
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FT /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
XX WO9501371-AL.  
XX 12-JAN-1995.  
XX 22-JUN-1994; 94WO-JP000999.  
XX 30-JUN-1993; 93JP-00186755.  
XX (YAWA ) NIPPON STEEL CORP.  
XX Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
PI WPI; 1995-060950/08.  
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.  
XX Disclosure; Page 11; 34pp; Japanese.

QY 1 X 1  
Db 1 R 1

RESULT 8  
ADD94995  
ID ADD94995 standard; peptide; 1 AA.  
XX AC ADD94995;  
XX 29-JAN-2004 (first entry)  
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

RESULT 9  
ADD94998  
ID ADD94998 standard; peptide; 1 AA.  
XX AC ADD94998;  
XX 29-JAN-2004 (first entry)  
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DE Platelet aggregation inhibitor peptide #140.  
XX platelet aggregation inhibitor; guanidino group; amidino group.  
XX OS Unidentified.  
XX Key Location/Qualifiers  
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FT /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
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Query Match 0.0%; Score 0; DB 2; Length 1;  
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

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XX AC ADD94998;  
XX 29-JAN-2004 (first entry)  
DT  
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XX platelet aggregation inhibitor; guanidino group; amidino group.  
XX OS Unidentified.  
XX Key Location/Qualifiers  
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XX WO9501371-AL.  
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XX Platelet aggregation inhibitor peptide #137.  
DE platelet aggregation inhibitor; guanidino group; amidino group.  
XX Unidentified.  
XX Key Location/Qualifiers  
FT Modified-site 1  
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XX WO9501371-AL.  
XX 12-JAN-1995.  
XX 22-JUN-1994; 94WO-JP000999.  
XX 30-JUN-1993; 93JP-00186755.  
XX (YAWA ) NIPPON STEEL CORP.  
XX Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
PI WPI; 1995-060950/08.  
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.  
XX Disclosure; Page 10; 34pp; Japanese.

XX The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.

XX Sequence 1 AA;  
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Best Local Similarity 0.0%; Pred. No. 0;  
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QY 1 X 1  
Db 1 R 1

RESULT 9  
ADD94998  
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XX AC ADD94998;  
XX 29-JAN-2004 (first entry)  
DT  
DE Platelet aggregation inhibitor peptide #140.  
XX platelet aggregation inhibitor; guanidino group; amidino group.  
XX OS Unidentified.  
XX Key Location/Qualifiers  
FT Modified-site 1  
FT /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
XX WO9501371-AL.  
XX

PD 12-JAN-1995.  
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PF 22-JUN-1994; 94WO-JP000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
PI WPI; 1995-060950/08.  
DR  
XX  
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
Query Match 0.0%; Score 0; DB 2; Length 1;  
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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 X 1  
DB 1 R 1  
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AC ADD95001;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #143.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
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FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not  
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PD 12-JAN-1995.  
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PF 22-JUN-1994; 94WO-JP000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
PI WPI; 1995-060950/08.  
DR  
XX  
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX

PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 X 1  
DB 1 R 1  
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XX  
AC ADD94990;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #132.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
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FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not  
FT defined)"  
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XX  
PD 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
PI WPI; 1995-060950/08.  
DR  
XX  
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
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Qy 1 X 1  
Db 1 R 1

RESULT 12  
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XX AC ADD94991;  
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XX KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
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XX PR 30-JUN-1993; 93JP-00186755.  
XX PA (YAWA ) NIPPON STEEL CORP.  
XX Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX WPI; 1995-060950/08.  
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.  
XX Disclosure; Page 10; 34pp; Japanese.  
XX The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.

Qy 1 X 1  
Db 1 R 1

RESULT 13  
ADD94994  
ID ADD94994 standard; peptide; 1 AA.  
XX AC ADD94994;  
XX 29-JAN-2004 (first entry)  
XX DE Platelet aggregation inhibitor peptide #136.

XX platelet aggregation inhibitor; guanidino group; amidino group.  
XX Unidentified.  
XX Key Location/Qualifiers  
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FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
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XX PF 22-JUN-1994; 94WO-JP000999.  
XX PR 30-JUN-1993; 93JP-00186755.  
XX PA (YAWA ) NIPPON STEEL CORP.  
XX Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX WPI; 1995-060950/08.  
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.  
XX Disclosure; Page 10; 34pp; Japanese.  
XX The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.

Qy 1 X 1  
Db 1 R 1

RESULT 14  
ADD94996  
ID ADD94996 standard; peptide; 1 AA.  
XX AC ADD94996;  
XX 29-JAN-2004 (first entry)  
XX DE Platelet aggregation inhibitor peptide #138.  
XX KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
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Query Match 0.0%; Score 0; DB 2; Length 1;  
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PF 22-JUN-1994; 94WO-JP000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX WPI; 1995-060950/08.  
XX  
XX  
XX New RGD peptide(s) useful as anti-platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
XX The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
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Db 1 R 1  
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XX AC ADD95000;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
XX Platelet aggregation inhibitor peptide #142.  
DE  
XX platelet aggregation inhibitor; guanidino group; amidino group.  
KW  
XX Unidentified.  
OS  
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FT defined)"  
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XX (YAWA ) NIPPON STEEL CORP.  
XX  
XX Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
PI WPI; 1995-060950/08.  
XX  
XX New RGD peptide(s) useful as anti-platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
XX Disclosure; Page 10; 34pp; Japanese.  
PS  
XX

CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
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Db 1 R 1  
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Job time : 150 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:10:45 ; Search time 36 Seconds  
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14.737 Million cell updates/sec

Title: US-10-046-922-32  
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Scoring table: BLOSUM62  
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Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 73656

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Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	1	1	US-07-820-154A-12
2	0	0.0	1	1	US-07-791-213D-24
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4	0	0.0	1	1	US-08-174-365A-57
5	0	0.0	1	1	US-07-789-913-23
6	0	0.0	1	1	US-07-789-913-25
7	0	0.0	1	1	US-08-049-794-23
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23	0	0.0	1	2	US-09-138-439-23
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25	0	0.0	1	3	US-08-480-640A-12
26	0	0.0	1	3	US-08-613-400A-23
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28 0 0.0 1 3 US-08-801-092-10 Sequence 10, Appl  
29 0 0.0 1 3 US-08-801-092-17 Sequence 17, Appl  
30 0 0.0 1 3 US-08-801-092-24 Sequence 24, Appl  
31 0 0.0 1 3 US-08-801-092-31 Sequence 31, Appl  
32 0 0.0 1 3 US-08-801-092-38 Sequence 38, Appl  
33 0 0.0 1 3 US-08-801-092-45 Sequence 45, Appl  
34 0 0.0 1 3 US-09-298-017-23 Sequence 23, Appl  
35 0 0.0 1 3 US-09-298-017-25 Sequence 25, Appl  
36 0 0.0 1 3 US-08-295-802-12 Sequence 12, Appl  
37 0 0.0 1 3 US-09-392-979A-23 Sequence 23, Appl  
38 0 0.0 1 3 US-09-392-979A-25 Sequence 25, Appl  
39 0 0.0 1 3 US-09-103-663-16 Sequence 16, Appl  
40 0 0.0 1 3 US-08-488-237A-12 Sequence 12, Appl  
41 0 0.0 1 3 US-09-117-927-5 Sequence 5, Appl  
42 0 0.0 1 3 US-08-375-992A-12 Sequence 12, Appl  
43 0 0.0 1 3 US-09-315-113-10 Sequence 10, Appl  
44 0 0.0 1 3 US-09-315-113-17 Sequence 17, Appl  
45 0 0.0 1 3 US-09-315-113-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1  
US-07-820-154A-12  
; Sequence 12, Application US/07820154A  
; Patent No. 5382425  
; GENERAL INFORMATION:  
; APPLICANT: Cochran Ph.D., Mark D  
; APPLICANT: Junker M.S., David E  
; TITLE OF INVENTION: Recombinant Swinepox Virus  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/820.154A  
; FILING DATE: 19920113  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 977-9550  
; TELEFAX: (212) 664-0525  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-820-154A-12

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 V 1

RESULT 2  
US-07-791-213D-24

; Sequence 24, Application US/07791213D  
; Patent No. 5409895  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/791,213D  
; FILING DATE: 13-NOV-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-07-791-213D-24

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 C 1

RESULT 3  
US-07-791-213D-40  
; Sequence 40, Application US/07791213D  
; Patent No. 5409895  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Burns, Doane, Swecker & Mathis  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States

; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/791,213D  
; FILING DATE: 13-NOV-1991  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-07-791-213D-40

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 C 1

RESULT 4  
US-08-174-365A-57  
; Sequence 57, Application US/08174365A  
; Patent No. 5478809  
; GENERAL INFORMATION:  
; APPLICANT: Seichi TANIDA et al.  
; TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 144 mb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/174,365A  
; FILING DATE: December 28, 1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M. Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-8850  
; TELEFAX:  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 57:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acid  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified site  
LOCATION:

IDENTIFICATION METHOD:  
OTHER INFORMATION: /note = "Xaa is modified amino acid as  
OTHER INFORMATION: described in specification"  
US-08-174-365A-57

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 X 1

RESULT 5  
US-07-789-913-23

Sequence 23, Application US/07789913  
Patent No. 5559095  
GENERAL INFORMATION:  
APPLICANT: Miljanich, George P.  
APPLICANT: Bowersox, Stephen S.  
APPLICANT: Fox, James A.  
APPLICANT: Valentino, Karen L.  
APPLICANT: Bitner, Robert S.  
APPLICANT: Yamashiro, Donald H.  
TITLE OF INVENTION: Delayed Treatment Method of Reducing  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Peter Dehlinger  
STREET: 350 Cambridge Avenue, Suite 300  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/789,913  
FILING DATE: 19911112  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/561,766  
FILING DATE: 02-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/440,094  
FILING DATE: 22-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A.  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 5865-0005.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0960  
TELEFAX: (415) 324-0880  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: both  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO

ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: peptide fragment used in the claims  
US-07-789-913-23

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 C 1

RESULT 6

US-07-789-913-25  
Sequence 25, Application US/07789913  
Patent No. 5559095

GENERAL INFORMATION:  
APPLICANT: Miljanich, George P.  
APPLICANT: Bowersox, Stephen S.  
APPLICANT: Fox, James A.  
APPLICANT: Valentino, Karen L.  
APPLICANT: Bitner, Robert S.  
APPLICANT: Yamashiro, Donald H.  
TITLE OF INVENTION: Delayed Treatment Method of Reducing  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Law Offices of Peter Dehlinger  
STREET: 350 Cambridge Avenue, Suite 300  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/789,913  
FILING DATE: 19911112  
CLASSIFICATION: 514

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/561,766  
FILING DATE: 02-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/440,094  
FILING DATE: 22-NOV-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A.  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 5865-0005.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: both  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: peptide fragment used in the claims  
US-07-789-913-25

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 R 1

RESULT 7  
US-08-049-794-23  
; Sequence 23, Application US/08049794  
; Patent No. 5587454  
; GENERAL INFORMATION:  
; APPLICANT: JUSTICE, ALAN  
; APPLICANT: SINGH, TEJINDER  
; APPLICANT: GOHIL, KISHOR C  
; APPLICANT: VALENTINO, KAREN L  
; APPLICANT: MILJANICH, GEORGE P  
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND  
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Peter Dehlinger  
; STREET: 350 Cambridge Avenue, Suite 300  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/049,794  
; FILING DATE: 19930415  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/814,759  
; FILING DATE: 30-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stratford, Carol A.  
; REGISTRATION/DOCKET NUMBER: 34,444  
; REFERENCE/DOCKET NUMBER: 5865-0009.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE  
; INDIVIDUAL ISOLATE: 32  
US-08-049-794-23

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 X 1

Db 1 C 1

RESULT 8  
US-08-049-794-25  
; Sequence 25, Application US/08049794  
; Patent No. 5587454  
; GENERAL INFORMATION:  
; APPLICANT: JUSTICE, ALAN  
; APPLICANT: SINGH, TEJINDER  
; APPLICANT: GOHIL, KISHOR C  
; APPLICANT: VALENTINO, KAREN L

; APPLICANT: MILJANICH, GEORGE P  
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND  
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Law Offices of Peter Dehlinger  
; STREET: 350 Cambridge Avenue, Suite 300  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94306  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/049,794  
; FILING DATE: 19930415  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/814,759  
; FILING DATE: 30-DEC-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stratford, Carol A.  
; REGISTRATION/DOCKET NUMBER: 34,444  
; REFERENCE/DOCKET NUMBER: 5865-0009.30  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 324-0880  
; TELEFAX: (415) 324-0960  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE  
; INDIVIDUAL ISOLATE: 32  
US-08-049-794-25

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 1 X 1

Db 1 R 1

RESULT 9  
US-08-433-037-12  
; Sequence 12, Application US/08433037  
; Patent No. 5707828  
; GENERAL INFORMATION:  
; APPLICANT: Sreekrishna, Kotikanyadan  
; APPLICANT: Barr, Kathryn A.  
; APPLICANT: Brierley, Russell A.  
; APPLICANT: Thill, Gregory P.  
; APPLICANT: Tschopp, Juerg F.  
; TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN  
; TITLE OF INVENTION: PICHIA PASTORIS  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 11530-0299  
; COMPUTER READABLE FORM: disk  
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/433,037  
;; FILING DATE: 03-MAY-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Digiglio, Frank S.  
;; REGISTRATION NUMBER: 31,346  
;; REFERENCE/DOCKET NUMBER: 9108Z  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (516) 742-4343  
;; TELEFAX: (516) 742-4366  
;; TELEX: 230 901 SANS UR  
;; INFORMATION FOR SEQ ID NO: 12:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-433-037-12

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
DB 1 L 1

RESULT 10  
US-08-448-606-4  
; Sequence 4, Application US/08448606  
; Patent No. 572114  
; GENERAL INFORMATION:  
; APPLICANT: Abrahams n, Lars  
; APPLICANT: Holmgren, Erik  
; APPLICANT: Kalder n, Christina  
; APPLICANT: Lake, Mats  
; APPLICANT: Mikaelsson, sa  
; APPLICANT: Sejlitz, Torsten  
; TITLE OF INVENTION: Expression System For Producing  
; TITLE OF INVENTION: Apolipoprotein AI-M  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pollock, Vande Sande & Priddy  
; STREET: 1990 M Street, N.W., Suite 800  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.  
; ZIP: 20036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/448,606  
; FILING DATE: 25-AUG-1995  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/SE93/01061  
; FILING DATE: 09-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: SE 9203753-0  
; FILING DATE: 11-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amernick, Burton A.  
; REGISTRATION NUMBER: 24,852  
; REFERENCE/DOCKET NUMBER: 0151/00121  
; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (202)331-7111  
;; TELEFAX: (202) 293-6229  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1 amino acid  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-448-606-4

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
DB 1 Q 1

RESULT 11  
US-07-869-933-16  
; Sequence 16, Application US/07869933  
; Patent No. 5770396  
; GENERAL INFORMATION:  
; APPLICANT: KINET, Jean-Pierre  
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF  
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR  
; TITLE OF INVENTION: IMMUNOGLOBULIN  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 1800 Diagonal Road, Suite 500  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22313-0299  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/869,933  
; FILING DATE: 19920416  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703)836-9300  
; TELEFAX: (703)683-4109  
; TELEX: 899149  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-869-933-16

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
DB 1 M 1

RESULT 12  
US-08-293-150A-24  
; Sequence 24, Application US/08293150A

; Patent No. 5792629  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,150A  
; FILING DATE: 19-AUG-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/791,213  
; FILING DATE: 13-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M.  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-049  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-293-150A-24

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 C 1

RESULT 13  
US-08-293-150A-40  
; Sequence 40, Application US/08293150A  
; Patent No. 5792629  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria

; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,150A  
; FILING DATE: 19-AUG-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/791,213  
; FILING DATE: 13-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M.  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-049  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-293-150A-40

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 C 1

RESULT 14  
US-08-496-847-23  
; Sequence 23, Application US/08496847  
; Patent No. 5795864  
; GENERAL INFORMATION:  
; APPLICANT: Amstutz, Gary A.  
; APPLICANT: Bowersox, Stephen S.  
; APPLICANT: Gohil, Kishorchandra  
; APPLICANT: Adriaenssens, Peter I.  
; APPLICANT: Kristipati, Ramasharma  
; TITLE OF INVENTION: METHODS AND  
; TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94306-1546  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/496,847  
; FILING DATE: 27-JUN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stratford, Carol A

```
;
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
; US-08-496-847-23

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 C 1

RESULT 15
US-08-496-847-25
; Sequence 25, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
; APPLICANT: Amutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND
; FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,847
; FILING DATE: 27-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.31
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
; US-08-496-847-25

Query Match 0.0%; Score 0; DB 1; Length 1;
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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 R 1

Search completed: December 29, 2004, 21:20:23
Job time : 37 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:16:31 ; Search time 137 Seconds  
(without alignments)  
21.006 Million cell updates/sec

Title: US-10-046-922-32

Perfect score: 8

Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 83711

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	0	0.0	1	9 US-09-778-885-5	Sequence 5, Appli
2	0	0.0	1	9 US-09-909-348-4	Sequence 4, Appli
3	0	0.0	1	9 US-09-982-172-3	Sequence 3, Appli
4	0	0.0	1	9 US-09-982-172-4	Sequence 4, Appli
5	0	0.0	1	9 US-09-982-172-9	Sequence 9, Appli
6	0	0.0	1	9 US-09-982-172-11	Sequence 11, Appli
7	0	0.0	1	9 US-09-982-172-19	Sequence 19, Appli
8	0	0.0	1	9 US-09-982-172-31	Sequence 31, Appli
9	0	0.0	1	9 US-09-982-172-35	Sequence 35, Appli
10	0	0.0	1	9 US-09-982-172-37	Sequence 37, Appli
11	0	0.0	1	9 US-09-982-172-46	Sequence 46, Appli
12	0	0.0	1	9 US-09-982-172-69	Sequence 69, Appli
13	0	0.0	1	9 US-09-982-172-80	Sequence 80, Appli

Sequence 81, Appli  
Sequence 83, Appli  
Sequence 86, Appli  
Sequence 93, Appli  
Sequence 95, Appli  
Sequence 106, Appli  
Sequence 112, Appli  
Sequence 120, Appli  
Sequence 126, Appli  
Sequence 148, Appli  
Sequence 149, Appli  
Sequence 155, Appli  
Sequence 160, Appli  
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Sequence 184, Appli  
Sequence 186, Appli  
Sequence 325, Appli  
Sequence 500, Appli  
Sequence 744, Appli  
Sequence 1045, Ap

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16 0 0.0 1 9 US-09-982-172-86  
17 0 0.0 1 9 US-09-982-172-93  
18 0 0.0 1 9 US-09-982-172-95  
19 0 0.0 1 9 US-09-982-172-106  
20 0 0.0 1 9 US-09-982-172-112  
21 0 0.0 1 9 US-09-982-172-120  
22 0 0.0 1 9 US-09-982-172-126  
23 0 0.0 1 9 US-09-982-172-148  
24 0 0.0 1 9 US-09-982-172-149  
25 0 0.0 1 9 US-09-982-172-155  
26 0 0.0 1 9 US-09-982-172-160  
27 0 0.0 1 9 US-09-982-172-172  
28 0 0.0 1 9 US-09-982-172-173  
29 0 0.0 1 9 US-09-982-172-175  
30 0 0.0 1 9 US-09-982-172-189  
31 0 0.0 1 9 US-09-982-172-190  
32 0 0.0 1 9 US-09-982-172-191  
33 0 0.0 1 9 US-09-982-172-195  
34 0 0.0 1 9 US-09-982-172-200  
35 0 0.0 1 9 US-09-982-172-211  
36 0 0.0 1 10 US-09-809-391-395  
37 0 0.0 1 10 US-09-809-391-611  
38 0 0.0 1 10 US-09-882-171-395  
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40 0 0.0 1 11 US-09-833-245-184  
41 0 0.0 1 11 US-09-833-245-186  
42 0 0.0 1 11 US-09-833-245-325  
43 0 0.0 1 11 US-09-833-245-500  
44 0 0.0 1 11 US-09-833-245-744  
45 0 0.0 1 11 US-09-833-245-1045

#### ALIGNMENTS

#### RESULT 1

US-09-778-885-5  
; Sequence 5, Application US/09778885  
; Publication No. US20020039748A1  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Gao, Zeren  
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS  
; FILE OF INVENTION: AND METHODS FOR MAKING IT  
; FILE REFERENCE: 98-22  
; CURRENT APPLICATION NUMBER: US/09/778,885  
; CURRENT FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 09/320,095  
; PRIOR FILING DATE: 1999-05-26  
; PRIOR APPLICATION NUMBER: US 60/087,032  
; PRIOR FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: polypeptide motif  
; NAME/KEY: VARIANT  
; LOCATION: (2)...(2)  
; OTHER INFORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met,  
; OTHER INFORMATION: Pro, Trp or Val  
; NAME/KEY: VARIANT  
; LOCATION: (3)...(3)  
; OTHER INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or Pro  
; NAME/KEY: VARIANT  
; LOCATION: (4)...(4)  
; OTHER INFORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp,  
; OTHER INFORMATION: Tyr or Val

NAME/KEY: VARIANT  
LOCATION: (5)...(5)  
OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe,  
OTHER INFORMATION: Ser, Thr or Trp  
NAME/KEY: VARIANT  
LOCATION: (6)...(6)  
OTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Tyr  
OTHER INFORMATION: or Met  
NAME/KEY: VARIANT  
LOCATION: (7)...(7)  
OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gly, His, Leu,  
OTHER INFORMATION: Met, Phe or Trp  
NAME/KEY: VARIANT  
LOCATION: (8)...(8)  
OTHER INFORMATION: Xaa is Gly or Glu  
NAME/KEY: VARIANT  
LOCATION: (9)...(9)  
OTHER INFORMATION: Xaa is Pro, Arg, Leu, Val, Ser, Asp, Ile, Asn or Thr  
NAME/KEY: VARIANT  
LOCATION: (11)...(11)  
OTHER INFORMATION: Xaa is any residue except Ala, Cys, Glu, His, Ile,  
OTHER INFORMATION: Pro, Trp and Val  
NAME/KEY: VARIANT  
LOCATION: (12)...(12)  
OTHER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr  
OTHER INFORMATION: and Ser  
NAME/KEY: VARIANT  
LOCATION: (13)...(13)  
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, Pro, Thr  
OTHER INFORMATION: or Trp  
NAME/KEY: VARIANT  
LOCATION: (14)...(14)  
OTHER INFORMATION: Xaa is any residue except Arg, Asn, Cys, Gly, His,  
OTHER INFORMATION: Ser, Trp or Tyr  
NAME/KEY: VARIANT  
LOCATION: (15)...(15)  
OTHER INFORMATION: Xaa is any residue except Ala, Asp, Cys, Gly, His,  
OTHER INFORMATION: Met, Trp or Tyr  
NAME/KEY: VARIANT  
LOCATION: (16)...(16)  
OTHER INFORMATION: Xaa is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly or Ile  
NAME/KEY: VARIANT  
LOCATION: (17)...(17)  
OTHER INFORMATION: Xaa is Phe, Tyr, Ile, Trp or Leu  
NAME/KEY: VARIANT  
LOCATION: (18)...(18)  
OTHER INFORMATION: Xaa is Tyr, His, Phe, Trp, Asn or Ala  
NAME/KEY: VARIANT  
LOCATION: (19)...(19)  
OTHER INFORMATION: Xaa is Tyr or Phe  
NAME/KEY: VARIANT  
LOCATION: (20)...(20)  
OTHER INFORMATION: Xaa is Lys, Asn, Ser or Asp  
NAME/KEY: VARIANT  
LOCATION: (21)...(21)  
OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, His or Tyr  
NAME/KEY: VARIANT  
LOCATION: (22)...(22)  
OTHER INFORMATION: Xaa is any residue except Cys, Met, Pro or Trp  
NAME/KEY: VARIANT  
LOCATION: (23)...(23)  
OTHER INFORMATION: Xaa is Ala, Lys, Ser, Leu, Thr, Ile, Gln, Glu, Tyr or Val  
NAME/KEY: VARIANT  
LOCATION: (24)...(24)  
OTHER INFORMATION: Xaa is Lys, Gln, Asn, His, Gly, Arg or Met  
NAME/KEY: VARIANT  
LOCATION: (25)...(25)  
OTHER INFORMATION: Xaa is any residue except Asn, Asp, Cys, His, Ile, Pro, Trp, Tyr  
US-09-778-885-5  
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Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 V 1

## RESULT 2

US-09-909-348-4  
; Sequence 4, Application US/09909348  
; Patent No. US20020042373A1  
; GENERAL INFORMATION:  
; APPLICANT: Carney, Darrell H.  
; APPLICANT: Crowther, Roger S.  
; APPLICANT: Stierberg, Janet  
; APPLICANT: Bergmann, John  
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists  
; TITLE OF INVENTION: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re  
; FILE REFERENCE: 3033.1003-001  
; CURRENT APPLICATION NUMBER: US/09/909,348  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US 60/219,800  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide fragment of Thrombin  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(14)  
; OTHER INFORMATION: Xaa at position six is Glu or Gln  
; OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or  
US-09-909-348-4

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 V 1

## RESULT 3

US-09-982-172-3  
; Sequence 3, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERAT  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-3

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Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

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; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-4
;
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-4
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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 K 1
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; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-9
;
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
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; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-9
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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
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Db      1 K 1
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; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-11
;
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-11
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; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-11
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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
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Db      1 K 1
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; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-19
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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 X 1
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Db      1 K 1
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; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-31
;
; APPLICANT: Emil Israel Katz
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING
; TITLE OF INVENTION: UTILIZING EACH
; FILE REFERENCE: 01/22283
; CURRENT APPLICATION NUMBER: US/09/982,172
; CURRENT FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 253
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
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; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-31
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; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-31

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 X 1  
Db 1 K 1

## RESULT 9

US-09-982-172-35  
; Sequence 35, Application US/09982172  
; Patent No. US20020137119A1

## GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 35

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

## US-09-982-172-35

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 X 1  
Db 1 R 1

## RESULT 10

US-09-982-172-37  
; Sequence 37, Application US/09982172  
; Patent No. US20020137119A1

## GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 37

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

## US-09-982-172-37

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 X 1  
Db 1 K 1

## RESULT 11

US-09-982-172-46

; Sequence 46, Application US/09982172

; Patent No. US20020137119A1

## GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 46

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

## US-09-982-172-46

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 K 1

## RESULT 12

US-09-982-172-69

; Sequence 69, Application US/09982172

; Patent No. US20020137119A1

## GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172

; CURRENT FILING DATE: 2001-10-19

; NUMBER OF SEQ ID NOS: 253

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 69

; LENGTH: 1

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Computer generated synthetic peptide

## US-09-982-172-69

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 K 1

## RESULT 13

US-09-982-172-80

; Sequence 80, Application US/09982172

; Patent No. US20020137119A1

## GENERAL INFORMATION:

; APPLICANT: Emil Israel Katz

; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES

; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING

; TITLE OF INVENTION: UTILIZING EACH

; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 80  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-80

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. NO. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
DB 1 K 1

## RESULT 14

US-09-982-172-81  
; Sequence 81, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 81  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-81

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. NO. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
DB 1 R 1

## RESULT 15

US-09-982-172-83  
; Sequence 83, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 83  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-83

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. NO. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 X 1  
DB 1 R 1

Search completed: December 29, 2004, 21:30:09  
Job time : 138 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2004, 21:10:20 ; Search time 37 Seconds  
(without alignments)  
20.804 Million cell updates/sec

Title: US-10-046-922-32

Perfect score: 8

Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 606

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	3	3 RHSGT	thyroliberin - she
2	0	0.0	3	3 A92971	thyroliberin - eas
3	0	0.0	3	3 RHDTDO	thyroliberin - Bom
4	0	0.0	3	3 A22565	R-phycocerythrin al
5	0	0.0	3	3 PQ0010	angiotensin-conver
6	0	0.0	3	3 S13894	histidinol dehydro
7	0	0.0	3	3 A43391	TRH-like tripeptid
8	0	0.0	3	3 E37196	bradykinin-potenti
9	0	0.0	3	3 F37196	bradykinin-potenti
10	0	0.0	3	3 I50412	gene p20K protein
11	0	0.0	3	3 PT0636	T-cell receptor be
12	0	0.0	3	3 PT0578	T-cell receptor be
13	0	0.0	3	3 PT0571	T-cell receptor be
14	0	0.0	3	3 PT0622	T-cell receptor be
15	0	0.0	3	3 I78890	tyrosine protein k
16	0	0.0	3	3 S68328	blood cell protein
17	0	0.0	3	3 T13892	cytochrome-c oxida
18	0	0.0	3	3 GRHU	growth-modulating
19	0	0.0	3	3 RHPGT	thyroliberin - pig
20	0	0.0	3	3 A60898	bursin - chicken
21	0	0.0	3	3 A23751	spinal cord peptid
22	0	0.0	3	3 B23751	spinal cord peptid
23	0	0.0	3	3 A33802	thyrotropin-releas
24	0	0.0	4	1 ECXAA	antho-Ramide neur
25	0	0.0	4	2 S18401	thyroglobulin - do
26	0	0.0	4	2 A02147	phagocytosis-stimu
27	0	0.0	4	2 A37832	phenol 2-monooxyse
28	0	0.0	4	2 A48360	gamma subunit of p
29	0	0.0	4	2 A61300	22K superhelical D

30	0	0.0	4	2 A41890	protein D - Escher
31	0	0.0	4	2 S43014	hypothetical prote
32	0	0.0	4	2 D41654	hypothetical prote
33	0	0.0	4	2 B43848	cell surface adhes
34	0	0.0	4	2 I40505	hypothetical prote
35	0	0.0	4	2 I40870	phospholipase C IE
36	0	0.0	4	2 T46627	hypothetical prote
37	0	0.0	4	2 S53508	starvation-induced
38	0	0.0	4	2 T37897	glucan 1,4-alpha-g
39	0	0.0	4	2 T30569	hypothetical prote
40	0	0.0	4	2 I38888	COI intron 16 prot
41	0	0.0	4	2 A25844	aucto-RF amide neu
42	0	0.0	4	2 A34626	RPCH-related neuro
43	0	0.0	4	2 I51049	metallothionein-A
44	0	0.0	4	2 S39390	myosin-light-chain
45	0	0.0	4	2 I61883	protamine P1 - ora

ALIGNMENTS

RESULT 1

RHSHT

thyroliberin - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004

C:Accession: A93750; A01415

R:Desiderio Jr., D.M.; Burgus, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.

Org. Mass Spectrom. 5, 221-228, 1971

A>Title: The elucidation of the primary structure of the hypothalamic thyroïd stimulating

A:Reference number: A93750

A:Accession: A93750

A:Molecule type: protein

A:Residues: 1-3 <DES>

A:Cross-references: UNIPROT:P01151

R:Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.

Nature 226, 321-325, 1970

A>Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.

A:Reference number: A93161; MUID:70163386; PMID:4985794

A:Contents: annotation

A>Note: physicochemical characteristics and biological activities of the natural and synt

C:Superfamily: thyroliberin

C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred.No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

Db 1 Q 1

RESULT 2

A92971

thyroliberin - eastern newt (tentative sequence)

C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)

C>Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004

C:Accession: A92971; A01415

R:Grimm-Jorgensen, Y.; McKelvy, J.F.

J. Neurochem. 23, 471-478, 1974

A>Title: Bioynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain

A:Reference number: A92971; MUID:75035605; PMID:4214528

A:Accession: A92971

A:Molecule type: protein

A:Residues: 1-3 <GRI>

A:Cross-references: UNIPROT:P01151

A>Note: a peptide with the chromatographic and electrophoretic characteristics of thyroli

stidine, or glutamic acid

C:Superfamily: thyroliberin

C:Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic a

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 Q 1

RESULT 3  
RHTDIO  
thyroliberin - Bombina orientalis  
C;Species: Bombina orientalis  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004  
C;Accession: A90919; A01415  
R;Yasuhara, T.; Nakajima, T.  
Chem. Pharm. Bull. 23, 3301-3303, 1975  
A;Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.  
A;Reference number: A90919; MUID:76138399; PMID:815011  
A;Accession: A90919  
A;Molecule type: protein  
A;Residues: 1-3 <YAS>  
A;Cross-references: UNIPROT:P01151  
C;Superfamily: thyroliberin  
C;Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 Q 1

RESULT 4  
A22565  
R-phycoerythrin alpha-1 chain - red alga (Gastrocloonium coulteri) (fragment)  
C;Species: Gastrocloonium coulteri  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: A22565  
R;Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A;Reference number: A22565; MUID:85182601; PMID:3886644  
A;Accession: A22565  
A;Molecule type: protein  
A;Residues: 1-3 <KLO>

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 2 Y 2

RESULT 5  
PQ0010  
angiotensin-converting enzyme inhibitor (FLP-3) - common fig  
N;Alternate names: ficus latex peptide 3  
C;Species: Ficus carica (common fig)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: PQ0010  
R;Haruyama, S.; Miyoshi, S.; Tanaka, H.  
Agric. Biol. Chem. 53, 2763-2767, 1989  
A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 Q 1

RESULT 6  
S13894  
histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)  
C;Species: Brassica oleracea (wild cabbage)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: S13894  
R;Nagai, A.; Scheidegger, A.  
Arch. Biochem. Biophys. 284, 127-132, 1991  
A;Title: Purification and characterization of histidinol dehydrogenase from cabbage.  
A;Reference number: S13894; MUID:91112783; PMID:1989490  
A;Accession: S13894  
A;Molecule type: protein  
A;Residues: 1-3 <NAG>  
A;Experimental source: var. capitata  
C;Keywords: dimer; NAD; oxidoreductase

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 X 1

RESULT 7  
A43391  
TRH-like tripeptide - alfalfa  
C;Species: Medicago sativa (alfalfa)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: A43391  
R;Lackey, D.B.  
J. Biol. Chem. 267, 17508-17511, 1992  
A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglu-  
A;Reference number: A43391; MUID:92388092; PMID:1517203  
A;Accession: A43391  
A;Molecule type: protein  
A;Residues: 1-3 <LAC>  
C;Keywords: amidated carboxyl end; pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 Q 1

RESULT 8  
E37196  
bradykinin-potentiating peptide 5 - island jararaca  
C;Species: Bothrops insularis (island jararaca)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 30-Jun-2001  
C;Accession: E37196

R,Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptides

C:Species: Bothrops insularis (island jararaca)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

A:Accession: E37196

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-3 <CIN>

C:Keywords: pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 1 Q 1

#### RESULT 9

F37196

bradykinin-potentiating peptide 6 - island jararaca

C:Species: Bothrops insularis (island jararaca)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

A:Accession: F37196

R,Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptides

C:Species: Bothrops insularis (island jararaca)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

A:Accession: F37196

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-3 <CIN>

C:Keywords: pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 1 Q 1

#### RESULT 10

I50412

gene p20K protein - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

A:Accession: I50412

R,Mao, P.L.; Beauchemin, M.; Bedard, P.A.

J. Biol. Chem. 268, 8131-8139, 1993

A:Title: Outcomes-dependent activation of the p20K promoter in growth-arrested chicken

C:Species: Gallus gallus (chicken)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

A:Accession: I50412

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-3 <MAO>

A:Cross-references: GB:L02537; NID:G212616; PID:G212617

C:Genetics:

A:Gene: p20K

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 2 S 2

#### RESULT 11

PT0636

T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

A:Accession: PT0636

R,Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

C:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0636

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-3 <PEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 1 A 1

#### RESULT 12

PT0578

T-cell receptor beta chain V-D-J region (141-1BD) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

A:Accession: PT0578

R,Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

C:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0578

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-3 <PEE>

A:Experimental source: day 19 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 1 A 1

#### RESULT 13

PT0571

T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

A:Accession: PT0571

R,Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

C:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0571

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-3 <PEE>

A:Experimental source: day 19 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 A 1

## RESULT 14

PT0622  
T-cell receptor beta chain V-D-J region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: PT0622; PT0680; PT0582; PT0673  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0622  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <PEE>  
A;Experimental source: newborn thymus, strain BALB/c, clone 111-1P  
A;Accession: PT0680  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-3 <PEE1>  
A;Experimental source: day 18 fetal thymus, strain BALB/c clones 154-1J and 154-1F  
A;Accession: PT0582  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <PEE2>  
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2A  
C;Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 A 1

## RESULT 15

I78890  
tyrosine protein kinase - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: I78890  
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.  
Oncogene 9, 3437-3448, 1994  
A;Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protein kinase  
A;Reference number: I58407; MUID:95060800; PMID:7970703  
A;Accession: I78890  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-3 <RES>  
A;Cross-references: GB:L33339; NID:g609536; PIDN:AAA64432.1; PID:g609538  
C;Genetics:  
A;Gene: p52ntk

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 3 T 3

Search completed: December 29, 2004, 21:19:40  
Job time : 38 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:01:44 ; Search time 185 seconds  
(without alignments)  
24.881 Million cell updates/sec

Title: US-10-046-922-32

Perfect score: 8

Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 835

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_02:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	2	1 GWA SEPOF	P83570 sepi offic
2	0	0.0	3	1 GRWM HUMAN	P01157 homo sapien
3	0	0.0	3	1 LUXE VIBFI	P24272 vibrio fisc
4	0	0.0	3	1 THYL_PIG	P01151 sus scrofa
5	0	0.0	4	1 ACHL_ACHFU	P35904 achatina fu
6	0	0.0	4	1 DCML_PSECH	P19916 pseudomonas
7	0	0.0	4	1 DCMS_PSECH	P19918 pseudomonas
8	0	0.0	4	1 EOSI HUMAN	P02731 homo sapien
9	0	0.0	4	1 FAR3_HIRME	P42562 hirudo medi
10	0	0.0	4	1 FAR4_HIRME	P42563 hirudo medi
11	0	0.0	4	1 FFKA_ANTEL	P58705 anthopleura
12	0	0.0	4	1 FLRP_HIRME	P42561 hirudo medi
13	0	0.0	4	1 FLRN_ANTEL	P58707 anthopleura
14	0	0.0	4	1 FMRF_NACNI	P01162 macrocallis
15	0	0.0	4	1 FYRI_ANTEL	P58706 anthopleura
16	0	0.0	4	1 ILME_SEPOF	P83568 sepi offic
17	0	0.0	4	1 OCF1_OCTMI	P58648 octopus min
18	0	0.0	4	1 OCF3_OCTMI	P58649 octopus min
19	0	0.0	4	1 TUFT_HUMAN	P01858 homo sapien
20	0	0.0	4	1 YLM1_YEAST	P36515 saccharomyc
21	0	0.0	4	2 Q16047	Q16047 homo sapien
22	0	0.0	4	2 Q96AT0	Q96AT0 homo sapien
23	0	0.0	4	2 Q08433	Q08433 rattus sp.
24	0	0.0	5	1 ALI4_CARMA	P81817 carcinus ma
25	0	0.0	5	1 B10A_CITFR	P13071 citrobacter
26	0	0.0	5	1 B10B_CITFR	P12997 citrobacter
27	0	0.0	5	1 BPPT_BOTIN	P30425 bothrops in
28	0	0.0	5	1 EI03_LITRU	P82099 litoria rub
29	0	0.0	5	1 EI04_LITRU	P82100 litoria rub
30	0	0.0	5	1 FARP_AKTRH	P41853 artiposthi
31	0	0.0	5	1 FARP_CHICK	P83308 gallus gall

32	0	0.0	5	1 MPA4_JUNVI	P81826 juniperus v
33	0	0.0	5	1 PAP2_PARMA	P81864 pardachirus
34	0	0.0	5	1 PRCT_PERAM	P01373 periplaneta
35	0	0.0	5	1 PSK DAUCA	P58261 daucus caro
36	0	0.0	5	1 RE1I_LITRU	P82070 litoria rub
37	0	0.0	5	1 RE2I_LITRU	P82071 litoria rub
38	0	0.0	5	1 RE3I_LITRU	P82072 litoria rub
39	0	0.0	5	1 RE32_LITRU	P82073 litoria rub
40	0	0.0	5	1 SUGA_ACHDO	P19991 acheta dome
41	0	0.0	5	1 TPIS_CANFA	P54714 canis famil
42	0	0.0	5	1 TRM3_ECOLI	P13973 escherichia
43	0	0.0	5	1 UC22_MAIZE	P80628 zea mays (m
44	0	0.0	5	1 UF01_MOUSE	P38639 mus musculu
45	0	0.0	5	1 UXA4_CHLTR	P38005 chlamydia t

#### ALIGNMENTS

RESULT 1  
GWA SEPOF STANDARD; PRT; 2 AA.  
AC P83570;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Neuropeptide Gwa.  
OS Sepia officinalis (Common cuttlefish).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.  
OX NCBI\_TaxID=6610;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.  
RC TISSUE=Optic lobe;  
RX MEDLINE=98100358; PubMed=9437704;  
RA Henry J., Favrel P., Boucaud-Camou E.;  
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related  
RT peptide inhibiting the motility of the mature oviduct in the  
RT cuttlefish, Sepia officinalis.";  
RL Peptides 18:1469-1474(1997).  
CC -!- FUNCTION: Regulatory neuropeptide with myotropic activity  
CC targeting the distal oviduct. Inhibits the motility of the oviduct  
CC by decreasing tonus, frequency and amplitude of contractions.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 2 2 Tryptophan amide.  
SQ SEQUENCE 2 AA; 261 MW; 737810000000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 2;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 G 1

#### RESULT 2

GRWM HUMAN STANDARD; PRT; 3 AA.  
ID GRWM HUMAN  
AC P01157;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Growth-modulating peptide.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77162369; PubMed=858356;

RA Schlesinger D.H., Pickart L., Thaler M.M.;  
 RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";  
 RL Experientia 33:324-325(1977).  
 CC -I- MISCELLANEOUS: This serum tripeptide has been found to stimulate  
 CC growth of some cell types and to inhibit other types in vitro.  
 DR GO; GO:0001558; P:regulation of cell growth; NAS.  
 KW Direct protein sequencing.  
 SQ SEQUENCE 3 AA; 340 MW; 6331E8100000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
 Db 1 G 1

RESULT 3  
 LUXE VIBFI  
 ID LUXE VIBFI STANDARD; PRT; 3 AA.  
 AC P24272;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-  
 DE protein synthetase) (fragment).  
 GN Names:luxE;  
 OS Vibrio fischeri.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=668;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91072226; PubMed=2254256;  
 RT Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;  
 RT "A new Vibrio fischeri lux gene precedes a bidirectional termination  
 RT site for the lux operon.";  
 RL J. Bacteriol. 172:6797-6802(1990).  
 CC -I- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It  
 CC is a component of the fatty acid reductase complex responsible for  
 CC converting tetradecanoic acid to the aldehyde which serves as  
 CC substrate in the luciferase-catalyzed reaction.  
 CC -I- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +  
 CC an acyl-protein thiolester.  
 CC -I- PATHWAY: Bioluminescent fatty acid reduction system; second step.  
 CC -I- SIMILARITY: Belongs to the luxE family.

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 CC -----  
 DR EMBL; M62812; -; NOT\_ANNOTATED\_CDS.  
 KW Ligase; Luminescence.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 3 AA; 374 MW; 6AA3303000000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
 Db 1 I 1

RESULT 4  
 THYL\_PIG  
 ID THYL\_PIG STANDARD; PRT; 3 AA.

P01151;  
 AC 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin).  
 OS Sus scrofa (pig),  
 OS Ovis aries (Sheep),  
 OS Bombina orientalis (Oriental fire-bellied toad), and  
 OS Bombina orientalis viridescens (Eastern newt) (Triturus viridescens).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823, 9940, 8346, 8316;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=Pig; TISSUE=Hypothalamus;  
 RX MEDLINE=70136150; PubMed=4984938;  
 RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;  
 RT "Structure of porcine thyrotropin releasing hormone.";  
 RT Biochemistry 9:1103-1106(1970).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=Pig;  
 RX MEDLINE=70039904; PubMed=4982117;  
 RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;  
 RT "The identity of chemical and hormonal properties of the thyrotropin  
 RT releasing hormone and pyroglutamyl-histidyl-proline amide.";  
 RT Biochem. Biophys. Res. Commun. 37:705-710(1969).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=Sheep; TISSUE=Hypothalamus;  
 RA Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,  
 RA Ward D.N.;  
 RT "The elucidation of the primary structure of the hypothalamic thyroid  
 RT stimulating hormone releasing factor of ovine origin by means of mass  
 RT spectrometry.";  
 RL Org. Mass Spectrom. 5:221-228(1971).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=Sheep;  
 RX MEDLINE=70163386; PubMed=4985794;  
 RA Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,  
 RA Guillemin R.;  
 RT "Characterization of ovine hypothalamic hypophysiotropic TSH-releasing  
 RT factor.";  
 RL Nature 226:321-325(1970).  
 RN [5]  
 RP SEQUENCE.  
 RC SPECIES=B.orientalis; TISSUE=Skin;  
 RX MEDLINE=76138399; PubMed=815011;  
 RA Yasuhara T., Nakajima T.;  
 RT "Occurrence of PyT-His-Pro-NH2 in the frog skin.";  
 RL Chem. Pharm. Bull. 23:3301-3303(1975).  
 RN [6]  
 RP SEQUENCE.  
 RC SPECIES=N.viridescens;  
 RX MEDLINE=75035605; PubMed=4214528;  
 RA Grimm-Joergensen Y., McKelvy J.F.;  
 RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus  
 RT viridescens) brain in vitro. Isolation and characterization of  
 RT thyrotropin releasing factor.";  
 RL J. Neurochem. 23:471-478(1974).  
 CC -I- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH  
 CC in the anterior pituitary gland and as a neurotransmitter/  
 CC neuromodulator in the central and peripheral nervous systems.

DR PIR; A90919; RHTDRO.  
 DR PIR; A92971; A92971.  
 DR PIR; A93750; RSHST.  
 KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
 FT MOD\_RES 3 3 Proline amide.  
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B0000000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;

Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 Q 1

RESULT 5  
ACH1 ACHFU  
ID ACH1 ACHFU STANDARD; PRT; 4 AA.  
AC P35904; 1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Achatin-I.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.  
RC STRAIN=Perussac; TISSUE=Ganglion;  
RX MEDLINE=89273551; PubMed=2557281;  
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,  
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,  
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.,  
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina  
fulica Perussac containing a D-amino acid residue.",  
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).  
RN [2]  
RP CHARACTERIZATION.  
RC STRAIN=Perussac; TISSUE=Heart atrium;  
RX MEDLINE=91264856; PubMed=1675568;  
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,  
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.,  
RT "Purification of achatin-I from the atria of the African giant snail,  
Achatina fulica, and its possible function.",  
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).  
RN [3]  
RP X-RAY CRYSTALLOGRAPHY.  
RX MEDLINE=93014529; PubMed=1399265;  
RA Iwashita T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,  
RA Iwashita T., Nomoto K.,  
RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-  
Phe-Ala-Asp-OH), an endogenous neuroexcitatory tetrapeptide containing a D-amino acid  
residue.",  
RL Int. J. Pept. Protein Res. 39:258-264(1992).  
CC -|- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency  
and produces a spike broadening of the identified heart excitatory  
neuron (PON); also enhances the amplitude and frequency of the  
heart beat. Has also an effect on several other muscles.  
DR PIR: A32480; A32480.  
KW D-amino acid; Direct protein sequencing; Hormone.  
FT MOD\_RES 2 2 D-phenylalanine.  
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 3 A 3

RESULT 6  
DCML PSECH  
ID DCML PSECH STANDARD; PRT; 4 AA.  
AC P19976;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO  
dehydrogenase subunit L) (CO-DH L) (Fragment).  
GN Name=cutL;  
OC Pseudomonas carboxydohydrogena.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OX NCBI\_TaxID=290;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90055678; PubMed=2818128;  
RA Kraut M., Hugendieck I., Herwig S., Meyer O.,  
RT "Homology and distribution of CO dehydrogenase structural genes in  
carboxydohydrogenic bacteria.",  
RL Arch. Microbiol. 152:335-341(1989).  
CC -|- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
dioxide.  
CC -|- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).  
CC -|- COFACTOR: Binds 1 copper(I) ion, 1 molybdenum(VI) ion and 1  
molybdopterin cytosine dinucleotide (MCD) per subunit.  
CC -|- SUBUNIT: Heterotrimer consisting of a large, a medium and a small  
subunit.  
DR PIR: PL0140; PL0140.  
KW Direct protein sequencing; Molybdenum; Oxidoreductase.  
FT NON\_TER 4 4  
SQ SEQUENCE 4 AA; 441 MW; 7761E876F00000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 M 1

RESULT 7  
DCMS PSECH  
ID DCMS PSECH STANDARD; PRT; 4 AA.  
AC P19918;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO  
dehydrogenase subunit S) (CO-DH S) (Fragment).  
GN Name=cuts;  
OC Pseudomonas carboxydohydrogena.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OX NCBI\_TaxID=290;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=90055678; PubMed=2818128;  
RA Kraut M., Hugendieck I., Herwig S., Meyer O.,  
RT "Homology and distribution of CO dehydrogenase structural genes in  
carboxydohydrogenic bacteria.",  
RL Arch. Microbiol. 152:335-341(1989).  
CC -|- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon  
dioxide.  
CC -|- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).  
CC -|- COFACTOR: Binds 2 2Fe-2S clusters (By similarity).  
CC -|- SUBUNIT: Heterotrimer consisting of a large, a medium and a small  
subunit.  
DR PIR: PL0146; PL0146.  
KW 2Fe-2S; Direct protein sequencing; Iron; Iron-sulfur; Metal-binding;  
FT NON\_TER 4 4  
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F00000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

```

Db      2 A 2
RESULT 8
EESI HUMAN
ID _EESI_HUMAN STANDARD; PRT; 4 AA.
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eosinophilic tetrapeptides.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76078412; PubMed=1060093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilic tetrapeptides of
RT human lung tissue: identification as eosinophil chemotactic factor of
RT anaphylaxis."
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -|- MISCELLANEOUS: These peptides are released from mast cells in lung
CC (and other tissues) during hypersensitivity reactions
CC (anaphylaxis). Their activities, preferentially affecting
CC eosinophils, include chemotaxis, chemotactic deactivation, release
CC of enzymes, and stimulation of the hexose monophosphate shunt.
DR GO: GO:0006935; P:chemotaxis; IDA.
DR GO: GO:0006955; P:immune response; IDA.
KW Direct protein sequencing.
FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).
FT FTID=VAR_005201.
SQ SEQUENCE 4 AA; 390 MW; 6805B862A0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 3 S 3
RESULT 9
FAR3 HIRME
ID _FAR3_HIRME STANDARD; PRT; 4 AA.
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide YMRP-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RFS 4 4 Phenylalanine amide.
SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 3 S 3
RESULT 10
FAR4 HIRME
ID _FAR4_HIRME STANDARD; PRT; 4 AA.
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRFamide-like neuropeptide YMRP-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RFS 4 4 Phenylalanine amide.
SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 Y 1
RESULT 11
FFKA ANTEL
ID _FFKA_ANTEL STANDARD; PRT; 4 AA.
AC P58705;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antho-Kkaamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92028852; PubMed=1681803;
RA Notheracker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-Kkaamide), a
RT novel neuropeptide from sea anemones."
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Notheracker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Kkaamide and Antho-Riamide."
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -|- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Neuron specific.
DR PIR; JQ1273; JQ1273.
KW Amidation; Direct protein sequencing; Neuropeptide.

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FT MOD\_RES 1 1 3-phenyllactic acid.  
 FT MOD\_RES 4 4 Alanine amide.  
 SQ SEQUENCE 4 AA; 512 MW; 6D339C9A00000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

Db 4 A 4

# RESULT 12

FLRF\_HIRME STANDARD; PRT; 4 AA.  
 ID FLRF\_HIRME  
 AC P42561.  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE FLRFamide.  
 OS Hirudo medicinalis (Medicinal leech), and  
 OS Helisoma trivolvis (Snail).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.  
 OX NCBI\_TaxID=6421, 27815;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=H. medicinalis;  
 RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of Rfamamide neuropeptides in the medicinal leech.";  
 RL Peptides 12:897-908(1991).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=H. trivolvis; TISSUE=Kidney;  
 RX MEDLINE=94286417; PubMed=7912428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma  
 trivolvis.";  
 RL Peptides 15:31-36(1994).  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 family.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 4 4 Phenylalanine amide.  
 SQ SEQUENCE 4 AA; 582 MW; 69D40729A000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

Db 1 F 1

# RESULT 13

FLRN\_ANCEL STANDARD; PRT; 4 AA.  
 ID FLRN\_ANCEL  
 AC P58707;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Antho-RNamide.  
 OS Anthopleura elegantissima (Sea anemone).  
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
 OC Nynanthaeae; Actiniidae; Anthopleura.  
 OX NCBI\_TaxID=6110;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=H. trivolvis; TISSUE=Kidney;  
 RX MEDLINE=90319122; PubMed=1973541;  
 RA Grimmeikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,

RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;  
 RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea  
 anemone neuropeptide containing an unusual amino-terminal blocking  
 group.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- TISSUE SPECIFICITY: Neuron specific.  
 CC -I- MASS SPECTROMETRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.  
 DR PIR; A35779; A35779.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 1 1 3-phenyllactic acid.  
 FT MOD\_RES 4 4 Asparagine amide.  
 SQ SEQUENCE 4 AA; 549 MW; 64540729A000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
 Best Local Similarity 0.0%; Pred. No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 X 1

Db 1 F 1

# RESULT 14

FMRF\_MACNI STANDARD; PRT; 4 AA.  
 ID FMRF\_MACNI  
 AC P01162;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE FMRFamide (Peak C) (Cardioexcitatory neuropeptide).  
 OS Macrocallista nimbosa (Sun-ray clam),  
 OS Nereis virens (Sandworm),  
 OS Hirudo medicinalis (Medicinal leech), and  
 OS Helisoma trivolvis (Snail).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;  
 OC Veneroidea; Veneridae; Macrocallista.  
 OX NCBI\_TaxID=6594, 6353, 6421, 27815;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC SPECIES=M. nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;  
 RX MEDLINE=77215956; PubMed=877582;  
 RA Price D.A., Greenberg M.J.;  
 RT "Structure of a molluscan cardioexcitatory neuropeptide.";  
 RL Science 197:670-671(1977).  
 RN [2]  
 RP SEQUENCE, AND CHARACTERIZATION  
 RC SPECIES=M. nimbosa; TISSUE=Ganglion;  
 RX MEDLINE=78012038; PubMed=909875;  
 RA Price D.A., Greenberg M.J.;  
 RT "Purification and characterization of a cardioexcitatory neuropeptide  
 from the central ganglia of a bivalve mollusc.";  
 RL Prep. Biochem. 7:261-281(1977).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=N. virens;  
 RX MEDLINE=90259866; PubMed=2342992;  
 RA Krainiak K.G., Price D.A.;  
 RT "Authentic FMRFamide is present in the polychaete Nereis virens.";  
 RL Peptides 11:75-77(1990).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=H. medicinalis;  
 RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of Rfamamide neuropeptides in the medicinal leech.";  
 RL Peptides 12:897-908(1991).  
 RN [5]  
 RP SEQUENCE.  
 RC SPECIES=H. trivolvis; TISSUE=Kidney;  
 RX MEDLINE=94286417; PubMed=7912428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma

Job time : 187 secs

RT trivolvins.;  
RL Peptides 15:31-36(1994).  
CC -|- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological  
CC activities include augmentation, induction, and regularization of  
CC cardiac contraction.  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- SIMILARITY: Belongs to the PARP (PMRFamide related peptide)  
CC family.  
DR PIR; A01426; EGNK.  
DR PIR; A60418; A60418.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD RES 4 4 Phenylalanine amide.  
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;  
  
Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 X 1  
DB 1 F 1  
  
RESULT 15  
FYRI ANTEL STANDARD; PRT; 4 AA.  
AC P58706; 2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Antho-Riamide I [Contains: Antho-Riamide II].  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthaeae; Actiniidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92270459; PubMed=1821096;  
RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,  
RA Gimmelikhuijzen C.J.P.;  
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,  
RT biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its des-  
RT phenyllactyl fragment Tyr-Arg-Ile-NH2.";  
RL Peptides 12:1165-1173(1991).  
RN [2]  
RP FUNCTION.  
RX MEDLINE=93391436; PubMed=8397415;  
RA McFarlane I.D., Hudman D., Nothacker H.-P., Gimmelikhuijzen C.J.P.;  
RT "The expansion behaviour of sea anemones may be coordinated by two  
RT inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";  
RL Proc. R. Soc. Lond. B, Biol. Sci. 253:183-188(1993).  
CC -|- FUNCTION: Inhibits spontaneous contractions in several muscle  
CC groups. May be involved in the expansion phase of feeding  
CC behaviour in sea anemones.  
CC -|- SUBCELLULAR LOCATION: Secreted.  
CC -|- TISSUE SPECIFICITY: Neuron specific.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT CHAIN 1 4 Antho-Riamide I.  
FT CHAIN 2 4 Antho-Riamide II.  
FT MOD RES 1 1 3-phenyllactic acid.  
FT MOD RES 4 4 Isoleucine amide.  
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Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 X 1  
DB 1 F 1

Search completed: December 29, 2004, 21:16:24

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:55:07 ; Search time 55.6981 Seconds  
(without alignments)  
51.525 Million cell updates/sec

Title: US-10-046-922-32  
Perfect score: 8  
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	1	2	Add95004 Platelet
2	0	0.0	1	2	Add94992 Platelet
3	0	0.0	1	2	Add94993 Platelet
4	0	0.0	1	2	Add95002 Platelet
5	0	0.0	1	2	Add94997 Platelet
6	0	0.0	1	2	Add94999 Platelet
7	0	0.0	1	2	Add95003 Platelet
8	0	0.0	1	2	Add94995 Platelet
9	0	0.0	1	2	Add94998 Platelet
10	0	0.0	1	2	Add95001 Platelet
11	0	0.0	1	2	Add94990 Platelet
12	0	0.0	1	2	Add94991 Platelet
13	0	0.0	1	2	Add94994 Platelet
14	0	0.0	1	2	Add94996 Platelet
15	0	0.0	1	2	Add95000 Platelet
16	0	0.0	1	2	AAY46652 Immunogen
17	0	0.0	1	4	AAM97834 Human pep
18	0	0.0	1	4	AAM97974 Human pep
19	0	0.0	1	4	AAM97643 Human pep
20	0	0.0	1	4	AAM98447 Human pep
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23	0	0.0	1	4	AAM53329 Human non
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25	0	0.0	1	4	AAM53328 Human non

26	0	0.0	1	4	AAM53219 Human non
27	0	0.0	1	4	AAM53218 Human non
28	0	0.0	1	4	AAB91029 Thyrotrop
29	0	0.0	1	4	AAB91739 Opioid pe
30	0	0.0	1	4	AAB92150 Polypepti
31	0	0.0	1	4	AAB91892 Apoptosia
32	0	0.0	1	4	AAB91546 Endotheli
33	0	0.0	1	4	AAB92392 Miscellan
34	0	0.0	1	4	AAB91665 Opioid pe
35	0	0.0	1	4	AAG99966 ERA bindi
36	0	0.0	1	4	AAM00011 ERA bindi
37	0	0.0	1	4	AAG99987 ERA bindi
38	0	0.0	1	4	AAG99983 ERA bindi
39	0	0.0	1	4	AAM00013 ERA bindi
40	0	0.0	1	4	AAM00016 ERA bindi
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42	0	0.0	1	4	AAM00010 ERA bindi
43	0	0.0	1	4	ABB66809 Drosophil
44	0	0.0	1	4	ABB66810 Drosophil
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ALIGNMENTS

RESULT 1  
ADD95004  
ID ADD95004 standard; peptide; 1 AA.  
XX AC ADD95004;  
XX DT 29-JAN-2004 (first entry)  
XX DE Platelet aggregation inhibitor peptide #146.  
XX KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX OS Unidentified.  
XX FH Key Location/Qualifiers  
FT Modified-site 1  
FT /label= OTHER  
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
XX PN WO9501371-A1.  
XX PD 12-JAN-1995.  
XX PF 22-JUN-1994; 94WO-JP000999.  
XX PR 30-JUN-1993; 93JP-00186755.  
XX PA (YAWA ) NIPPON STEEL CORP.  
XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX DR WPI; 1995-060950/08.  
XX PT New RGD peptide(s) useful as anti-platelet aggregation agents - contain  
XX guanidino or amidino gp. at N-terminal to increase stability.  
XX PS Disclosure; Page 11; 34pp; Japanese.  
XX CC The invention describes peptides of amino acid sequence (I) and their  
XX salts. (I) are useful as platelet aggregation inhibitors and are easily  
XX absorbed by the body. Due to the presence of the N-terminal guanidino or  
XX amidino group, (I) are provided with excellent stability so that their  
XX activity can be exhibited for an effective time after administration.  
XX Thereafter they are readily metabolised and expelled. This is the amino  
XX acid sequence of a platelet aggregation inhibitor peptide.  
XX SQ Sequence 1 AA;

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Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 R 1

RESULT 2
ADD94992
ID ADD94992 standard; peptide; 1 AA.
XX AC ADD94992;
XX AC
XX 29-JAN-2004 (first entry)
XX DE Platelet aggregation inhibitor peptide #134.
XX KW platelet aggregation inhibitor; guanidino group; amidino group.
XX OS Unidentified.
XX FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT defined)"
XX WO9501371-A1.
XX PN 12-JAN-1995.
XX PD
XX PF 22-JUN-1994; 94WO-JP000999.
XX PR 30-JUN-1993; 93JP-00186755.
XX PA (YAWA ) NIPPON STEEL CORP.
XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX WPI; 1995-060950/08.
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain
XX guanidino or amidino gp. at N-terminal to increase stability.
XX PS Disclosure; Page 10; 34pp; Japanese.
XX CC The invention describes peptides of amino acid sequence (I) and their
XX salts. (I) are useful as platelet aggregation inhibitors and are easily
XX absorbed by the body. Due to the presence of the N-terminal guanidino or
XX amidino group, (I) are provided with excellent stability so that their
XX activity can be exhibited for an effective time after administration.
XX Thereafter they are readily metabolised and expelled. This is the amino
XX acid sequence of a platelet aggregation inhibitor peptide.
XX SQ Sequence 1 AA;

Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 R 1

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ID ADD94993 standard; peptide; 1 AA.
XX AC ADD94993;
XX AC
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XX 29-JAN-2004 (first entry)
XX DE Platelet aggregation inhibitor peptide #135.
XX KW platelet aggregation inhibitor; guanidino group; amidino group.
XX OS Unidentified.
XX FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT defined)"
XX WO9501371-A1.
XX PN 12-JAN-1995.
XX PD
XX PF 22-JUN-1994; 94WO-JP000999.
XX PR 30-JUN-1993; 93JP-00186755.
XX PA (YAWA ) NIPPON STEEL CORP.
XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;
XX WPI; 1995-060950/08.
XX New RGD peptide(s) useful as anti:platelet aggregation agents - contain
XX guanidino or amidino gp. at N-terminal to increase stability.
XX PS Disclosure; Page 10; 34pp; Japanese.
XX CC The invention describes peptides of amino acid sequence (I) and their
XX salts. (I) are useful as platelet aggregation inhibitors and are easily
XX absorbed by the body. Due to the presence of the N-terminal guanidino or
XX amidino group, (I) are provided with excellent stability so that their
XX activity can be exhibited for an effective time after administration.
XX Thereafter they are readily metabolised and expelled. This is the amino
XX acid sequence of a platelet aggregation inhibitor peptide.
XX SQ Sequence 1 AA;

Query Match      0.0%; Score 0; DB 2; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 R 1

RESULT 4
ADD95002
ID ADD95002 standard; peptide; 1 AA.
XX AC ADD95002;
XX AC
XX 29-JAN-2004 (first entry)
XX DE Platelet aggregation inhibitor peptide #144.
XX KW platelet aggregation inhibitor; guanidino group; amidino group.
XX OS Unidentified.
XX FH Key Location/Qualifiers
FT Modified-site 1
FT /label= OTHER
FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not
FT defined)"
XX
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PN W09501371-A1.  
XX  
PD 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10-11; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
SQ Sequence 1 AA;  
Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 X 1  
DB 1 R 1  
RESULT 5  
ADD94997  
ID ADD94997 standard; peptide; 1 AA.  
XX  
AC ADD94997;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Platelet aggregation inhibitor peptide #139.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT /label= OTHER  
FT /note= "OTHER= H2NC(=NH)(CH2)CO. Beta-Ala (not defined)"  
XX  
PN W09501371-A1.  
XX  
PD 12-JAN-1995.  
XX  
PF 22-JUN-1994; 94WO-JP000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
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SQ Sequence 1 AA;  
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XX  
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DE Platelet aggregation inhibitor peptide #141.  
XX  
KW platelet aggregation inhibitor; guanidino group; amidino group.  
XX  
OS Unidentified.  
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PD 12-JAN-1995.  
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PF 22-JUN-1994; 94WO-JP000999.  
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PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain

PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
XX  
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Query Match 0.0%; Score 0; DB 2; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
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DB 1 R 1  
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AC ADD94999;  
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XX  
PR 30-JUN-1993; 93JP-00186755.  
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PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
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PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
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CC acid sequence of a platelet aggregation inhibitor peptide.  
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PF 22-JUN-1994; 94WO-JP000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
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PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayaashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
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PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
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AC ADD94990;  
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PD 22-JUN-1994; 94WO-JP000999.  
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XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayaashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
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XX  
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PD 22-JUN-1994; 94WO-JP000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayaashi Y, Katada J, Takiguchi Y;  
XX  
DR WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX

QY 1 X 1  
Db 1 R 1

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XX AC ADD94991;  
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XX PD 12-JAN-1995.  
XX PF 22-JUN-1994; 94WO-JP000999.  
XX PR 30-JUN-1993; 93JP-00186755.  
XX PA (YAWA ) NIPPON STEEL CORP.  
XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX WPI; 1995-060950/08.  
XX PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.  
XX PS Disclosure; Page 10; 34pp; Japanese.  
XX CC The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.  
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XX PA (YAWA ) NIPPON STEEL CORP.  
XX PI Sato Y, Hayashi Y, Katada J, Takiguchi Y;  
XX WPI; 1995-060950/08.  
XX PT New RGD peptide(s) useful as anti:platelet aggregation agents - contain guanidino or amidino gp. at N-terminal to increase stability.  
XX PS Disclosure; Page 10; 34pp; Japanese.  
XX CC The invention describes peptides of amino acid sequence (I) and their salts. (I) are useful as platelet aggregation inhibitors and are easily absorbed by the body. Due to the presence of the N-terminal guanidino or amidino group, (I) are provided with excellent stability so that their activity can be exhibited for an effective time after administration. Thereafter they are readily metabolised and expelled. This is the amino acid sequence of a platelet aggregation inhibitor peptide.  
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FT /note= "OTHER= H2NC(=NH)NH(CH2)CO. Beta-Ala (not defined)"  
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XX PD 12-JAN-1995.  
XX DE Platelet aggregation inhibitor peptide #136.

PF 22-JUN-1994; 94WO-JP000999.  
XX  
PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayaashi Y, Katada J, Takiguchi Y;  
XX WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti-platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
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PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayaashi Y, Katada J, Takiguchi Y;  
XX WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti-platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX  
CC The invention describes peptides of amino acid sequence (I) and their  
CC salts. (I) are useful as platelet aggregation inhibitors and are easily  
CC absorbed by the body. Due to the presence of the N-terminal guanidino or  
CC amidino group, (I) are provided with excellent stability so that their  
CC activity can be exhibited for an effective time after administration.  
CC Thereafter they are readily metabolised and expelled. This is the amino  
CC acid sequence of a platelet aggregation inhibitor peptide.  
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DE Platelet aggregation inhibitor peptide #142.  
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PR 30-JUN-1993; 93JP-00186755.  
XX  
PA (YAWA ) NIPPON STEEL CORP.  
XX  
PI Sato Y, Hayaashi Y, Katada J, Takiguchi Y;  
XX WPI; 1995-060950/08.  
XX  
PT New RGD peptide(s) useful as anti-platelet aggregation agents - contain  
PT guanidino or amidino gp. at N-terminal to increase stability.  
XX  
PS Disclosure; Page 10; 34pp; Japanese.  
XX

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:59:07 ; Search time 18.4151 Seconds  
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Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
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Listing first 45 summaries

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SUMMARIES

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36	0	0.0	1	3	US-08-295-802-12	Sequence 12, Appl
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ALIGNMENTS

RESULT 1  
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; Sequence 12, Application US/07820154A  
; Patent No. 5382425  
; GENERAL INFORMATION:  
; APPLICANT: Cochran Ph.D., Mark D  
; APPLICANT: Junker M.S., David E  
; TITLE OF INVENTION: Recombinant Swinepox Virus  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: John P. White  
; STREET: 30 Rockefeller Plaza  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10112  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07820,154A  
; FILING DATE: 19920113  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)977-9550  
; TELEFAX: (212)664-0525  
; TELEX: 422523  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-820-154A-12

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Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 V 1

RESULT 2  
US-07-791-213D-24

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; Sequence 24, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,213D
; FILING DATE: 13-NOV-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-306745
; FILING DATE: 13-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 029650-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-791-213D-24

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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 C 1

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; Sequence 40, Application US/07791213D
; Patent No. 5409895
; GENERAL INFORMATION:
; APPLICANT: MORISHITA, Hideaki
; APPLICANT: KANAMORI, Toshinori
; APPLICANT: NOBUHARA, Masahiro
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE
; SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF
; TREATING USING THE SAME
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 C 1

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; Sequence 57, Application US/08174365A
; Patent No. 5478809
; GENERAL INFORMATION:
; APPLICANT: Seiichi TANIDA et al.
; TITLE OF INVENTION: 4-THIAHEPTANOIC ACID DERIVATIVES
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/174,365A
; FILING DATE: December 28, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 57:
```

SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acid  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified site  
LOCATION:

IDENTIFICATION METHOD:  
OTHER INFORMATION: /note = "Xaa is modified amino acid as  
OTHER INFORMATION: described in specification"  
US-08-174-365A-57

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 X 1  
DB 1 X 1

## RESULT 5

US-07-789-913-23

; Sequence 23, Application US/07789913

; Patent No. 5559095

; GENERAL INFORMATION:

; APPLICANT: Miljanich, George P.

; APPLICANT: Bowersox, Stephen S.

; APPLICANT: Fox, James A.

; APPLICANT: Valentino, Karen L.

; APPLICANT: Bitner, Robert S.

; APPLICANT: Yamashiro, Donald H.

; TITLE OF INVENTION: Delayed Treatment Method of Reducing

; TITLE OF INVENTION: Ischemia-Related Neuronal Damage

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Peter Dehlinger

; STREET: 350 Cambridge Avenue, Suite 300

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/789,913

; FILING DATE: 19911112

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/561,766

; FILING DATE: 02-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/440,094

; FILING DATE: 22-NOV-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Stratford, Carol A.

; REGISTRATION NUMBER: 34,444

; REFERENCE/DOCKET NUMBER: 5865-0005.30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: both

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:  
; INDIVIDUAL ISOLATE: peptide fragment used in the claims  
US-07-789-913-23

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
DB 1 C 1

## RESULT 6

US-07-789-913-25

; Sequence 25, Application US/07789913

; Patent No. 5559095

; GENERAL INFORMATION:

; APPLICANT: Miljanich, George P.

; APPLICANT: Bowersox, Stephen S.

; APPLICANT: Fox, James A.

; APPLICANT: Valentino, Karen L.

; APPLICANT: Bitner, Robert S.

; APPLICANT: Yamashiro, Donald H.

; TITLE OF INVENTION: Delayed Treatment Method of Reducing

; TITLE OF INVENTION: Ischemia-Related Neuronal Damage

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Peter Dehlinger

; STREET: 350 Cambridge Avenue, Suite 300

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/789,913

; FILING DATE: 19911112

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/561,766

; FILING DATE: 02-AUG-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/440,094

; FILING DATE: 22-NOV-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Stratford, Carol A.

; REGISTRATION NUMBER: 34,444

; REFERENCE/DOCKET NUMBER: 5865-0005.30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0880

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 25:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: both

; MOLECULE TYPE: peptide

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: peptide fragment used in the claims  
US-07-789-913-25

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 R 1

RESULT 7

US-08-049-794-23

; Sequence 23, Application US/08049794

; Patent No. 5587454

; GENERAL INFORMATION:

; APPLICANT: JUSTICE, ALAN

; APPLICANT: SINGH, TEJINDER

; APPLICANT: GOHIL, KISHOR C

; APPLICANT: VALENTINO, KAREN L

; APPLICANT: MILJANICH, GEORGE P

; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Peter Dehlinger

; STREET: 350 Cambridge Avenue, Suite 300

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/049,794

; FILING DATE: 19930415

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/814,759

; FILING DATE: 30-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Stratford, Carol A.

; REGISTRATION NUMBER: 34,444

; REFERENCE/DOCKET NUMBER: 5865-0009.30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0960

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE

; INDIVIDUAL ISOLATE: 32

US-08-049-794-23

Query Match 0.0%; Score 0; DB 1; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 C 1

RESULT 8

US-08-049-794-25

; Sequence 25, Application US/08049794

; Patent No. 5587454

; GENERAL INFORMATION:

; APPLICANT: JUSTICE, ALAN

; APPLICANT: SINGH, TEJINDER

; APPLICANT: GOHIL, KISHOR C

; APPLICANT: VALENTINO, KAREN L

; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND

; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Law Offices of Peter Dehlinger

; STREET: 350 Cambridge Avenue, Suite 300

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94306

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/049,794

; FILING DATE: 19930415

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/814,759

; FILING DATE: 30-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Stratford, Carol A.

; REGISTRATION NUMBER: 34,444

; REFERENCE/DOCKET NUMBER: 5865-0009.30

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 324-0960

; TELEFAX: (415) 324-0960

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ORIGINAL SOURCE:

; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE

; INDIVIDUAL ISOLATE: 32

US-08-049-794-23

Query Match 0.0%; Score 0; DB 1; Length 1;

Best Local Similarity 0.0%; Pred. No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 R 1

RESULT 9

US-08-433-037-12

; Sequence 12, Application US/08433037

; Patent No. 5707828

; GENERAL INFORMATION:

; APPLICANT: Sreekrishna, Kotikanyadan

; APPLICANT: Barr, Kathryn A.

; APPLICANT: Brierley, Russell A.

; APPLICANT: Thill, Gregory P.

; APPLICANT: Tschoep, Juerg F.

; TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN

; TITLE OF INVENTION: PICHIA PASTORIS

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Presser

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 11530-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/433,037
/ FILING DATE: 03-MAY-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Digiglio, Frank S.
/ REGISTRATION NUMBER: 31,346
/ REFERENCE/DOCKET NUMBER: 9108Z
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (516) 742-4343
/ TELEFAX: (516) 742-4366
/ TELEX: 230 901 SANS UR
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-433-037-12

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 L 1

RESULT 10
US-08-448-606-4
; Sequence 4, Application US/08448606
; Patent No. 5721114
; GENERAL INFORMATION:
; APPLICANT: Abrahams n, Lars
; APPLICANT: Holmgren, Erik
; APPLICANT: Kalder n, Christina
; APPLICANT: Lake, Mats
; APPLICANT: Mikaelsson, sa
; APPLICANT: Sejlitz, Torsten
; TITLE OF INVENTION: Expression System For Producing
; TITLE OF INVENTION: Apolipoprotein AI-M
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pollock, Vande Sande & Priddy
; STREET: 1990 M Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,606
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/SE93/01061
; FILING DATE: 09-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9203753-0
; FILING DATE: 11-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Amernick, Burton A.
; REGISTRATION NUMBER: 24,852
; REFERENCE/DOCKET NUMBER: 0151/00121
; TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (202)331-7111
/ TELEFAX: (202) 293-6229
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1 amino acid
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-448-606-4

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 Q 1

RESULT 11
US-07-869-933-16
; Sequence 16, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; TITLE OF INVENTION: IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-869-933-16

Query Match 0.0%; Score 0; DB 1; Length 1;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 M 1

RESULT 12
US-08-293-150A-24
; Sequence 24, Application US/08293150A
```

; Patent No. 5792629  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,150A  
; FILING DATE: 19-AUG-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/791,213  
; FILING DATE: 13-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M.  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-049  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-293-150A-24

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 C 1

RESULT 13  
US-08-293-150A-40  
; Sequence 40, Application US/08293150A  
; Patent No. 5792629  
; GENERAL INFORMATION:  
; APPLICANT: MORISHITA, Hideaki  
; APPLICANT: KANAMORI, Toshinori  
; APPLICANT: NOBUHARA, Masahiro  
; TITLE OF INVENTION: POLYPEPTIDE, DNA FRAGMENT ENCODING THE  
; TITLE OF INVENTION: SAME AND PROCESS FOR PRODUCING THE SAME, AND ENZYME  
; TITLE OF INVENTION: INHIBITION PROCESS, DRUG COMPOSITION AND METHODS OF  
; TITLE OF INVENTION: TREATING USING THE SAME  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: P.O. Box 1404  
; CITY: Alexandria

; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/293,150A  
; FILING DATE: 19-AUG-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/791,213  
; FILING DATE: 13-NOV-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 2-306745  
; FILING DATE: 13-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meuth, Donna M.  
; REGISTRATION NUMBER: 36,607  
; REFERENCE/DOCKET NUMBER: 029650-049  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-293-150A-40

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 C 1

RESULT 14  
US-08-496-847-23  
; Sequence 23, Application US/08496847  
; Patent No. 5795864  
; GENERAL INFORMATION:  
; APPLICANT: Amstutz, Gary A.  
; APPLICANT: Bowersox, Stephen S.  
; APPLICANT: Gohil, Kishorchandra  
; APPLICANT: Adriaenssens, Peter I.  
; APPLICANT: Kristipati, Ramasharma  
; TITLE OF INVENTION: METHODS AND  
; TITLE OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Dehlinger & Associates  
; STREET: 350 Cambridge Avenue, Suite 250  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: US  
; ZIP: 94306-1546  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/496,847  
; FILING DATE: 27-JUN-1995  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stratford, Carol A

REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 5865-0009.31  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT  
US-08-496-847-23

Query Match 0.0%; Score 0; DB 1; Length 1;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 C 1

RESULT 15  
US-08-496-847-25  
Sequence 25, Application US/08496847  
Patent No. 5795864  
GENERAL INFORMATION:  
APPLICANT: Amstutz, Gary A.  
APPLICANT: Bowersox, Stephen S.  
APPLICANT: Gohil, Kishorchandra  
APPLICANT: Adriaenssens, Peter I.  
APPLICANT: Krutipati, Ramasharma  
TITLE OF INVENTION: METHODS AND  
FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: US  
ZIP: 94306-1546  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/496,847  
FILING DATE: 27-JUN-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Stratford, Carol A  
REGISTRATION NUMBER: 34,444  
REFERENCE/DOCKET NUMBER: 5865-0009.31  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880  
TELEFAX: 650-324-0960  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT  
US-08-496-847-25

Query Match 0.0%; Score 0; DB 1; Length 1;

Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 R 1

Search completed: December 30, 2004, 13:19:16  
Job time : 19.4151 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 13:08:04 ; Search time 59.6226 Seconds  
(without alignments)  
48.267 Million cell updates/sec

Title: US-10-046-922-32  
Perfect score: 8  
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	0	0.0	1	9 US-09-778-885-5	Sequence 5, Appli
2	0	0.0	1	9 US-09-909-348-4	Sequence 4, Appli
3	0	0.0	1	9 US-09-982-172-3	Sequence 3, Appli
4	0	0.0	1	9 US-09-982-172-4	Sequence 4, Appli
5	0	0.0	1	9 US-09-982-172-9	Sequence 9, Appli
6	0	0.0	1	9 US-09-982-172-11	Sequence 11, Appli
7	0	0.0	1	9 US-09-982-172-19	Sequence 19, Appli
8	0	0.0	1	9 US-09-982-172-31	Sequence 31, Appli
9	0	0.0	1	9 US-09-982-172-35	Sequence 35, Appli
10	0	0.0	1	9 US-09-982-172-37	Sequence 37, Appli
11	0	0.0	1	9 US-09-982-172-46	Sequence 46, Appli
12	0	0.0	1	9 US-09-982-172-69	Sequence 69, Appli
13	0	0.0	1	9 US-09-982-172-80	Sequence 80, Appli

14	0	0.0	1	9 US-09-982-172-81	Sequence 81, Appli
15	0	0.0	1	9 US-09-982-172-83	Sequence 83, Appli
16	0	0.0	1	9 US-09-982-172-86	Sequence 86, Appli
17	0	0.0	1	9 US-09-982-172-93	Sequence 93, Appli
18	0	0.0	1	9 US-09-982-172-95	Sequence 95, Appli
19	0	0.0	1	9 US-09-982-172-106	Sequence 106, Appli
20	0	0.0	1	9 US-09-982-172-112	Sequence 112, Appli
21	0	0.0	1	9 US-09-982-172-120	Sequence 120, Appli
22	0	0.0	1	9 US-09-982-172-126	Sequence 126, Appli
23	0	0.0	1	9 US-09-982-172-148	Sequence 148, Appli
24	0	0.0	1	9 US-09-982-172-149	Sequence 149, Appli
25	0	0.0	1	9 US-09-982-172-155	Sequence 155, Appli
26	0	0.0	1	9 US-09-982-172-160	Sequence 160, Appli
27	0	0.0	1	9 US-09-982-172-172	Sequence 172, Appli
28	0	0.0	1	9 US-09-982-172-173	Sequence 173, Appli
29	0	0.0	1	9 US-09-982-172-175	Sequence 175, Appli
30	0	0.0	1	9 US-09-982-172-189	Sequence 189, Appli
31	0	0.0	1	9 US-09-982-172-190	Sequence 190, Appli
32	0	0.0	1	9 US-09-982-172-191	Sequence 191, Appli
33	0	0.0	1	9 US-09-982-172-195	Sequence 195, Appli
34	0	0.0	1	9 US-09-982-172-200	Sequence 200, Appli
35	0	0.0	1	9 US-09-982-172-211	Sequence 211, Appli
36	0	0.0	1	10 US-09-809-391-395	Sequence 395, Appli
37	0	0.0	1	10 US-09-809-391-611	Sequence 611, Appli
38	0	0.0	1	10 US-09-882-171-395	Sequence 395, Appli
39	0	0.0	1	10 US-09-882-171-611	Sequence 611, Appli
40	0	0.0	1	11 US-09-833-245-184	Sequence 184, Appli
41	0	0.0	1	11 US-09-833-245-186	Sequence 186, Appli
42	0	0.0	1	11 US-09-833-245-325	Sequence 325, Appli
43	0	0.0	1	11 US-09-833-245-500	Sequence 500, Appli
44	0	0.0	1	11 US-09-833-245-744	Sequence 744, Appli
45	0	0.0	1	11 US-09-833-245-1045	Sequence 1045, Ap

ALIGNMENTS

RESULT 1  
US-09-778-885-5  
; Sequence 5, Application US/09778885  
; Publication No. US20020039748A1  
; GENERAL INFORMATION:  
; APPLICANT: Conklin, Darrell C.  
; APPLICANT: Foster, Donald C.  
; APPLICANT: Gao, Zeren  
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS  
; TITLE OF INVENTION: AND METHODS FOR MAKING IT  
; FILE REFERENCE: 98-22  
; CURRENT APPLICATION NUMBER: US/09/778,885  
; PRIOR FILING DATE: 2001-02-06  
; PRIOR APPLICATION NUMBER: 09/320,095  
; PRIOR FILING DATE: 1999-05-26  
; PRIOR APPLICATION NUMBER: US 60/087,032  
; PRIOR FILING DATE: 1998-05-28  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 51  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: polypeptide motif  
; NAME/KEY: VARIANT  
; LOCATION: (2)...(2)  
; OTHER INFORMATION: Xaa is any residue except Asp, Cys, Gly, His, Met,  
; OTHER INFORMATION: Pro, Trp or Val  
; NAME/KEY: VARIANT  
; LOCATION: (3)...(3)  
; OTHER INFORMATION: Xaa is Leu, Glu, Met, Gln, Phe, Ser, Thr, Ala or Pro  
; NAME/KEY: VARIANT  
; LOCATION: (4)...(4)  
; OTHER INFORMATION: Xaa is any residue except Arg, Cys, Met, Phe, Trp,  
; OTHER INFORMATION: Tyr or Val

; NAME/KEY: VARIANT  
; LOCATION: (5)...(5)  
; OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gln, Gly, Phe,  
; OTHER INFORMATION: Ser, Thr or Trp  
; NAME/KEY: VARIANT  
; LOCATION: (6)...(6)  
; OTHER INFORMATION: Xaa is Arg, Glu, Asn, Ala, Val, Asp, Lys, Ser, Tyr  
; OTHER INFORMATION: or Met  
; NAME/KEY: VARIANT  
; LOCATION: (7)...(7)  
; OTHER INFORMATION: Xaa is any residue except Asn, Cys, Gly, His, Leu,  
; OTHER INFORMATION: Met, Phe or Trp  
; NAME/KEY: VARIANT  
; LOCATION: (8)...(8)  
; OTHER INFORMATION: Xaa is Gly or Glu  
; NAME/KEY: VARIANT  
; LOCATION: (9)...(9)  
; OTHER INFORMATION: Xaa is Pro, Arg, Leu, Val, Ser, Asp, Ile, Asn or Thr  
; NAME/KEY: VARIANT  
; LOCATION: (11)...(11)  
; OTHER INFORMATION: Xaa is any residue except Ala, Cys, Glu, His, Ile,  
; OTHER INFORMATION: Pro, Trp and Val  
; NAME/KEY: VARIANT  
; LOCATION: (12)...(12)  
; OTHER INFORMATION: Xaa is Arg, Lys, Ala, Asp, Gln, Phe, Gly, Glu, Thr  
; OTHER INFORMATION: and Ser  
; NAME/KEY: VARIANT  
; LOCATION: (13)...(13)  
; OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, Pro, Thr  
; OTHER INFORMATION: or Trp  
; NAME/KEY: VARIANT  
; LOCATION: (14)...(14)  
; OTHER INFORMATION: Xaa is any residue except Arg, Asn, Cys, Gly, His,  
; OTHER INFORMATION: Ser, Trp or Tyr  
; NAME/KEY: VARIANT  
; LOCATION: (15)...(15)  
; OTHER INFORMATION: Xaa is any residue except Ala, Asp, Cys, Gly, His,  
; OTHER INFORMATION: Met, Trp or Tyr  
; NAME/KEY: VARIANT  
; LOCATION: (16)...(16)  
; OTHER INFORMATION: Xaa is Ser, Ala, Arg, Val, Gln, Lys, Leu, Gly or Ile  
; NAME/KEY: VARIANT  
; LOCATION: (17)...(17)  
; OTHER INFORMATION: Xaa is Phe, Tyr, Ile, Trp or Leu  
; NAME/KEY: VARIANT  
; LOCATION: (18)...(18)  
; OTHER INFORMATION: Xaa is Tyr, His, Phe, Trp, Asn or Ala  
; NAME/KEY: VARIANT  
; LOCATION: (19)...(19)  
; OTHER INFORMATION: Xaa is Tyr or Phe  
; NAME/KEY: VARIANT  
; LOCATION: (20)...(20)  
; OTHER INFORMATION: Xaa is Lys, Asn, Ser or Asp  
; NAME/KEY: VARIANT  
; LOCATION: (21)...(21)  
; OTHER INFORMATION: Xaa is any residue except Asp, Cys, Glu, His or Tyr  
; NAME/KEY: VARIANT  
; LOCATION: (22)...(22)  
; OTHER INFORMATION: Xaa is any residue except Cys, Met, Pro or Trp  
; NAME/KEY: VARIANT  
; LOCATION: (23)...(23)  
; OTHER INFORMATION: Xaa is Ala, Lys, Ser, Leu, Thr, Ile, Gln, Glu, Tyr or Val  
; NAME/KEY: VARIANT  
; LOCATION: (24)...(24)  
; OTHER INFORMATION: Xaa is Lys, Gln, Asn, His, Gly, Arg or Met  
; NAME/KEY: VARIANT  
; LOCATION: (25)...(25)  
; OTHER INFORMATION: Xaa is any residue except Asn, Asp, Cys, His, Ile, Pro, Trp, Tyr  
US-09-778-885-5

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 V 1

## RESULT 2

US-09-909-348-4  
; Sequence 4, Application US/09909348  
; Patent No. US20020042373A1  
; GENERAL INFORMATION:  
; APPLICANT: Carney, Darrell H.  
; APPLICANT: Crowther, Roger S.  
; APPLICANT: Stierberg, Janet  
; APPLICANT: Bergmann, John  
; TITLE OF INVENTION: Stimulation Of Cartilage Growth With Agonists  
; FILE REFERENCE: Of The No. US20020042373A1-Proteolytically Activated Thrombin Re  
; FILE REFERENCE: 3033.1003-001  
; CURRENT FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US/09/909,348  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US 60/219,800  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide fragment of Thrombin  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(14)  
; OTHER INFORMATION: Xaa at position six is Glu or Gln  
; OTHER INFORMATION: Xaa at position thirteen is Phe, Met, Leu, His or  
US-09-909-348-4

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 V 1

## RESULT 3

US-09-982-172-3  
; Sequence 3, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATI  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-3

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 K 1

RESULT 4  
US-09-982-172-4  
; Sequence 4, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-4

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 K 1

RESULT 5  
US-09-982-172-9  
; Sequence 9, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-9

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 K 1

RESULT 6  
US-09-982-172-11  
; Sequence 11, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-11

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 K 1

; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-11

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 K 1

RESULT 7  
US-09-982-172-19  
; Sequence 19, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 19  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-19

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 K 1

RESULT 8  
US-09-982-172-31  
; Sequence 31, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 31  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-31

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 K 1

; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-31

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 X 1  
Db 1 K 1

## RESULT 9

US-09-982-172-35  
; Sequence 35, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 35  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-35

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 X 1  
Db 1 R 1

## RESULT 10

US-09-982-172-37  
; Sequence 37, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-37

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 X 1  
Db 1 K 1

## RESULT 11

US-09-982-172-46  
; Sequence 46, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 46  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-46

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 X 1  
Db 1 K 1

## RESULT 12

US-09-982-172-69  
; Sequence 69, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 69  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-69

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 X 1  
Db 1 K 1

## RESULT 13

US-09-982-172-80  
; Sequence 80, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283

; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 80  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-80

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 K 1

## RESULT 14

US-09-982-172-81  
; Sequence 81, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 81  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-81

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 R 1

## RESULT 15

US-09-982-172-83  
; Sequence 83, Application US/09982172  
; Patent No. US20020137119A1  
; GENERAL INFORMATION:  
; APPLICANT: Emil Israel Katz  
; TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBODIES  
; TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENERATING  
; TITLE OF INVENTION: UTILIZING EACH  
; FILE REFERENCE: 01/22283  
; CURRENT APPLICATION NUMBER: US/09/982,172  
; CURRENT FILING DATE: 2001-10-19  
; NUMBER OF SEQ ID NOS: 253  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 83  
; LENGTH: 1  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Computer generated synthetic peptide  
US-09-982-172-83

Query Match 0.0%; Score 0; DB 9; Length 1;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 X 1  
Db 1 R 1

Search completed: December 30, 2004, 13:49:58  
Job time : 60.8226 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:59:17 ; Search time 9.20755 Seconds  
(without alignments)  
83.598 Million cell updates/sec

Title: US-10-046-922-32

Perfect score: 8

Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: p1r1:\*

2: p1r2:\*

3: p1r3:\*

4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	0	0.0	3	3 RHGHT	thyroliberin - she
2	0	0.0	3	3 A92971	thyroliberin - eas
3	0	0.0	3	3 RHDTTO	thyroliberin - Bom
4	0	0.0	3	3 A22565	R-phycoerythrin al
5	0	0.0	3	3 PQ0010	angiotensin-conver
6	0	0.0	3	3 S13894	histidinol dehydro
7	0	0.0	3	3 A43391	TRH-like tripeptid
8	0	0.0	3	3 E37196	bradykinin-potenti
9	0	0.0	3	3 F37196	bradykinin-potenti
10	0	0.0	3	3 I50412	gene p20K protein
11	0	0.0	3	3 PT0636	T-cell receptor be
12	0	0.0	3	3 PT0578	T-cell receptor be
13	0	0.0	3	3 PT0571	T-cell receptor be
14	0	0.0	3	3 PT0522	tyrosine protein k
15	0	0.0	3	3 I78890	blood cell protein
16	0	0.0	3	3 S68328	cytochrome-c oxida
17	0	0.0	3	3 T13892	growth-modulating
18	0	0.0	3	3 GHUPT	thyroliberin - pig
19	0	0.0	3	3 RHVGT	burin - chicken
20	0	0.0	3	3 A60898	spinal cord peptid
21	0	0.0	3	3 A23751	spinal cord peptid
22	0	0.0	3	3 B23751	thyrotropin-releas
23	0	0.0	3	3 A33802	antho-Ramide neur
24	0	0.0	4	1 ECXAA	thyroglobulin - do
25	0	0.0	4	2 S18401	phagocytosis-stimu
26	0	0.0	4	2 A02147	phenol 2-monooxyge
27	0	0.0	4	2 A37832	gamma subunit of p
28	0	0.0	4	2 A48360	22K superhelical D
29	0	0.0	4	2 A61300	

30	0	0.0	4	2 A41890	protein D - Escher
31	0	0.0	4	2 S43014	hypothetical prote
32	0	0.0	4	2 D41654	hypothetical prote
33	0	0.0	4	2 B43848	cell surface adhes
34	0	0.0	4	2 I40505	hypothetical prote
35	0	0.0	4	2 I40870	phospholipase C (E
36	0	0.0	4	2 T46627	hypothetical prote
37	0	0.0	4	2 S3508	starvation-induced
38	0	0.0	4	2 A27897	glucan 1,4-alpha-g
39	0	0.0	4	2 T30569	hypothetical prote
40	0	0.0	4	2 I38888	COI intron 16 prot
41	0	0.0	4	2 A35844	auto-BF amide neu
42	0	0.0	4	2 A34626	RPCH-related neuro
43	0	0.0	4	2 I51049	metallothionein-A
44	0	0.0	4	2 S39390	myosin-light-chain
45	0	0.0	4	2 I61883	protamine P1 - Ora

ALIGNMENTS

RESULT 1

RHSHT

thyroliberin - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004

C:Accession: A93750; A01415

R:Desiderio Jr., D.M.; Burgus, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.

Org. Mass Spectrom. 5; 221-228, 1971

A:Title: The elucidation of the primary structure of the hypothalamic thyroïd stimulating

A:Reference number: A93750

A:Accession: A93750

A:Molecule type: protein

A:Residues: 1-3 <DES>

A:Cross-references: UNIPROT:P01151

R:Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.

Nature 226, 321-325, 1970

A:Title: Characterization of ovine hypothalamic hypophyiotropic TSH-releasing factor.

A:Reference number: A93161; MUID:70163386; PMID:4985794

A:Contents: annotation

A:Note: physicochemical characteristics and biological activities of the natural and synt

C:Superfamily: thyroliberin

C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F:1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental

F:3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred.No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 Q 1

RESULT 2

A92971

thyroliberin - eastern newt (tentative sequence)

C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004

C:Accession: A92971; A01415

R:Grimm-Jorgensen, Y.; McKelvy, J.F.

J. Neurochem. 23, 471-478, 1974

A:Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain

A:Reference number: A92971; MUID:75035605; PMID:4214528

A:Accession: A92971

A:Molecule type: protein

A:Residues: 1-3 <GRI>

A:Cross-references: UNIPROT:P01151

A:Note: a peptide with the chromatographic and electrophoretic characteristics of thyroli

stidine, or glutamic acid

C:Superfamily: thyroliberin

C:Keywords: amidated carboxyl end; cutaneous gland; hormone; hypothalamus; pyroglutamic

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 Q 1

## RESULT 3

RHTDTQ

thyroliberin - Bombina orientalis

C;Species: Bombina orientalis

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 09-Jul-2004

C;Accession: A90919; A01415

R;Yasuhara, T.; Nakajima, T.

Chem. Pharm. Bull. 23, 3301-3303, 1975

A;Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.

A;Reference number: A90919; MUID:76138399; PMID:815011

A;Accession: A90919

A;Molecule type: protein

A;Residues: 1-3 &lt;VAS&gt;

A;Cross-references: UNIPROT:P01151

C;Superfamily: thyroliberin

C;Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 Q 1

## RESULT 4

A22565

R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)

C;Species: Gastroclonium coulteri

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C;Accession: A22565

R;Klotz, A.V.; Glazer, A.N.

J. Biol. Chem. 260, 4856-4863, 1985

A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.

A;Reference number: A22565; MUID:85182601; PMID:3886644

A;Accession: A22565

A;Molecule type: protein

A;Residues: 1-3 &lt;KLO&gt;

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 2 Y 2

## RESULT 5

PQ0010

angiotensin-converting enzyme inhibitor (FLP-3) - common fig

N;Alternate names: ficus latex peptide 3

C;Species: Ficus carica (common fig)

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C;Accession: PQ0010

R;Maruyama, S.; Miyoshi, S.; Tanaka, H.

Agric. Biol. Chem. 53, 2763-2767, 1989

A;Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.

A;Reference number: PQ0008

A;Accession: PQ0010

A;Molecule type: protein

A;Residues: 1-3 &lt;MAR&gt;

A;Experimental source: latex

C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 L 1

## RESULT 6

S13894

histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)

C;Species: Brassica oleracea (wild cabbage)

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C;Accession: S13894

R;Nagai, A.; Scheidegger, A.

Arch. Biochem. Biophys. 284, 127-132, 1991

A;Title: Purification and characterization of histidinol dehydrogenase from cabbage.

A;Reference number: S13894; MUID:91112783; PMID:1989490

A;Accession: S13894

A;Molecule type: protein

A;Residues: 1-3 &lt;NAG&gt;

A;Experimental source: var. capitata

C;Keywords: dimer; NAD; oxidoreductase

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 X 1

## RESULT 7

A43391

TRH-like tripeptide - alfalfa

C;Species: Medicago sativa (alfalfa)

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C;Accession: A43391

R;Lackey, D.B.

J. Biol. Chem. 267, 17508-17511, 1992

A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglu-

A;Reference number: A43391; MUID:92388092; PMID:1517203

A;Accession: A43391

A;Molecule type: protein

A;Residues: 1-3 &lt;LAC&gt;

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1

Db 1 Q 1

## RESULT 8

E37196

bradykinin-potentiating peptide 5 - island jararaca

C;Species: Bothrops insularis (island jararaca)

C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 30-Jun-2001

C;Accession: E37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptides  
C:Species: Bothrops insularis (island jararaca)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: F37196

A:Reference number: A37196; PMID:2386615

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-3 <CIN>

A:Keywords: pyrrolidone carboxylic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred.No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 1 Q 1

#### RESULT 9

F37196

bradykinin-potentiating peptide 6 - island jararaca

C:Species: Bothrops insularis (island jararaca)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: F37196

R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.

J. Protein Chem. 9, 221-227, 1990

A:Title: Primary structure and biological activity of bradykinin potentiating peptides  
C:Species: Bothrops insularis (island jararaca)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: F37196

A:Reference number: A37196; PMID:2386615

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-3 <CIN>

A:Keywords: pyrrolidone carboxylic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred.No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 1 Q 1

#### RESULT 10

I50412

gene p20K protein - chicken (fragment)

C:Species: Gallus gallus (chicken)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: I50412

R;Mao, P.L.; Beauchemin, M.; Bedard, P.A.

J. Biol. Chem. 268, 8131-8139, 1993

A:Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken  
C:Species: Gallus gallus (chicken)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: I50412

A:Reference number: A46643; PMID:8463325

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-3 <MAO>

A:Cross-references: GB:L02537; NID:G212616; PID:G212617

C:Genetics:

A:Gene: p20K

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred.No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 2 S 2

#### RESULT 11

PT0636

T-cell receptor beta chain V-D-J region (100-2AT) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: PT0636

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; PMID:91277601; PMID:1711558

A:Accession: PT0636

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-3 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred.No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 1 A 1

#### RESULT 12

PT0578

T-cell receptor beta chain V-D-J region (141-1BD) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: PT0578

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; PMID:91277601; PMID:1711558

A:Accession: PT0578

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-3 <PEE>

A:Experimental source: day 19 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred.No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 1 A 1

#### RESULT 13

PT0571

T-cell receptor beta chain V-D-J region (141-1CM) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001

C:Accession: PT0571

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; PMID:91277601; PMID:1711558

A:Accession: PT0571

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-3 <FEE>

A:Experimental source: day 19 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;

Best Local Similarity 0.0%; Pred.No. 0;

Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

DB 2 S 2

Qy 1 X 1  
Db 1 A 1

## RESULT 14

PT0622  
T-cell receptor beta chain V-D-J region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: PT0622; PT0680; PT0582; PT0673  
R;Feeney, A.J.  
J. Exp. Med. 174, 115-124, 1991  
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
A;Reference number: PT0509; MUID:91277601; PMID:1711558  
A;Accession: PT0622  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <FEE>  
A;Experimental source: newborn thymus, strain BALB/c, clone 111-1P  
A;Accession: PT0680  
A;Status: translation not shown  
A;Molecule type: DNA  
A;Residues: 1-3 <FEE1>  
A;Experimental source: day 18 fetal thymus, strain BALB/c clones 154-1J and 154-1P  
A;Accession: PT0582  
A;Status: translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-3 <FEE2>  
A;Experimental source: day 19 fetal thymus, strain BALB/c, clone 159-2A  
C;Keywords: T-cell receptor

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 1 A 1

## RESULT 15

I78890  
tyrosine protein kinase - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Jun-2001  
C;Accession: I78890  
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.  
Oncogene 9, 3437-3448, 1994  
A;Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protein kinase gene.  
A;Reference number: I58407; MUID:95060800; PMID:7970703  
A;Accession: I78890  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-3 <RES>  
A;Cross-references: GB:I33339; NID:g609536; PIDN:AAA64432.1; PID:g609538  
C;Genetics:  
A;Gene: p52ntk

Query Match 0.0%; Score 0; DB 3; Length 3;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1  
Db 3 T 3

Search completed: December 30, 2004, 13:17:07  
Job time : 9.37421 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 30, 2004, 12:57:52 ; Search time 73.8113 Seconds  
(without alignments)  
62.362 Million cell updates/sec

Title: US-10-046-922-32  
Perfect score: 8  
Sequence: 1 XXXXXXXX 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	0	0.0	2	1 GWA_SEPOF	P83570 sepi offic
2	0	0.0	3	1 GRWM_HUMAN	P01157 homo sapien
3	0	0.0	3	1 LUXE_VIBFI	P24272 vibrio fisc
4	0	0.0	3	1 THYL_PIG	P01151 sus scrofa
5	0	0.0	4	1 ACHL_ACHFU	P35904 achatina fu
6	0	0.0	4	1 DCML_PSECH	P19916 pseudomonas
7	0	0.0	4	1 DCMS_PSECH	P19918 pseudomonas
8	0	0.0	4	1 EOSI_HUMAN	P02731 homo sapien
9	0	0.0	4	1 PAR3_HIRME	P42562 hirudo medi
10	0	0.0	4	1 PAR4_HIRME	P42563 hirudo medi
11	0	0.0	4	1 FFKA_ATEL	P58705 anthopleura
12	0	0.0	4	1 FLRP_HIRME	P42561 hirudo medi
13	0	0.0	4	1 FLRN_ATEL	P58707 anthopleura
14	0	0.0	4	1 FMRF_MACNI	P01162 macrocallis
15	0	0.0	4	1 FYRI_ATEL	P58706 anthopleura
16	0	0.0	4	1 ILME_SEPOF	P83568 sepi offic
17	0	0.0	4	1 OCPI_OCTMI	P58648 octopus min
18	0	0.0	4	1 OCP3_OCTMI	P58649 octopus min
19	0	0.0	4	1 TUFT_HUMAN	P01858 homo sapien
20	0	0.0	4	1 YLMI_YEAST	P36515 saccharomyc
21	0	0.0	4	2 Q16047	Q16047 homo sapien
22	0	0.0	4	2 Q96AT0	Q96AT0 homo sapien
23	0	0.0	4	2 Q08433	Q08433 rattus sp.
24	0	0.0	5	1 ALI4_CARMA	P18187 carinus ma
25	0	0.0	5	1 BIOA_CITFR	P13071 citrobacter
26	0	0.0	5	1 BIOB_CITFR	P12997 citrobacter
27	0	0.0	5	1 BPP7_BOTIN	P30425 bothrops in
28	0	0.0	5	1 EI03_LITRU	P82099 litoria rub
29	0	0.0	5	1 EI04_LITRU	P82100 litoria rub
30	0	0.0	5	1 FARP_ARTTR	P41853 artiopesthi
31	0	0.0	5	1 FARP_CHICK	P83308 gallus gall

32	0	0.0	5	1 MPA4_JUNVI	P81826 juniperus v
33	0	0.0	5	1 PAP2_PARMA	P81864 pardachirus
34	0	0.0	5	1 PRCT_PERAM	P01373 periplaneta
35	0	0.0	5	1 PSK_DAUCA	P58261 daucus caro
36	0	0.0	5	1 RELI_LITRU	P82070 litoria rub
37	0	0.0	5	1 RE21_LITRU	P82071 litoria rub
38	0	0.0	5	1 RE31_LITRU	P82072 litoria rub
39	0	0.0	5	1 RE32_LITRU	P82073 litoria rub
40	0	0.0	5	1 SUGA_ACHDO	P19991 acheta dome
41	0	0.0	5	1 TPIS_CANFA	P54714 canis fami
42	0	0.0	5	1 TRM3_ESCOLI	P13973 escherichia
43	0	0.0	5	1 UC22_WAIZE	P80628 zea mays (m
44	0	0.0	5	1 UF01_MOUSE	P38639 mus musculu
45	0	0.0	5	1 UXA4_CHLTR	P38005 chlamydia t

ALIGNMENTS

RESULT 1  
GWA\_SEPOF STANDARD; PRT; 2 AA.  
AC P83570;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Neuropeptide Gwa.  
OS Sepia officinalis (Common cuttlefish).  
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
OC Decapodiformes; Sepioidea; Sepiidae; Sepia.  
OX NCBI\_TaxID=6610;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.  
RC TISSUE=Optic lobe;  
RX MEDLINE=98100358; PubMed=9437704;  
RA Henry J., Favrel P., Boucaud-Camou E.;  
RT "Isolation and identification of a novel Ala-Pro-Gly-Trp-amide-related  
RT peptide inhibiting the motility of the mature oviduct in the  
RT cuttlefish, Sepia officinalis.";  
RL Peptides 18:1469-1474 (1997).  
CC -!- FUNCTION: Regulatory neuropeptide with myotropic activity  
CC targeting the distal oviduct. Inhibits the motility of the oviduct  
CC by decreasing tonus, frequency and amplitude of contractions.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=259.9; METHOD=NALDI; RANGE=1-2; NOTE=Ref.1.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 2 2 Tryptophan amide.  
SQ SEQUENCE 2 AA; 261 MW; 737810000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 2;  
Best Local Similarity 0.0%; Pred.No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1  
Db 1 G 1

RESULT 2  
GRWM\_HUMAN STANDARD; PRT; 3 AA.  
ID GRWM\_HUMAN  
AC P01157;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Growth-modulating peptide.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=77162369; PubMed=858356;

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RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experientia 33:324-325(1977).
CC -|- MISCELLANEOUS: This serum tripeptide has been found to stimulate
CC growth of some cell types and to inhibit other types in vitro.
DR GO; GO:0001558; P:regulation of cell growth; NAS.
KW Direct protein sequencing.
SQ SEQUENCE 3 AA; 340 MW; 6331BE81000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 G 1

RESULT 3
LUXE_VIBFI STANDARD; PRT; 3 AA.
AC P24272;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE protein synthetase) (Fragment).
GN Name=luxE;
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072226; PubMed=2254256;
RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT site for the lux operon.";
RL J. Bacteriol. 172:6797-6802(1990).
CC -|- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It
CC is a component of the fatty acid reductase complex responsible for
CC converting tetradecanoic acid to the aldehyde which serves as
CC substrate in the luciferase-catalyzed reaction.
CC -|- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
CC an acyl-protein thioester.
CC -|- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC -|- SIMILARITY: Belongs to the luxE family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; M62812; -; NOT ANNOTATED_CDS.
KW Ligase; Luminescence.
FT NON TER 1
SQ SEQUENCE 3 AA; 374 MW; 6AA33030000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;
Best Local Similarity 0.0%; Pred.No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 X 1
Db 1 I 1

RESULT 4
THYL_PIG STANDARD; PRT; 3 AA.
ID THYL_PIG

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AC P01151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Protirelin).
DR Sus scrofa (Pig),
OS Ovis aries (Sheep),
OS Bombina orientalis (Oriental fire-bellied toad), and
OS Neophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823, 9940, 8346, 8316;
RN [1]
RP SEQUENCE
RC SPECIES=Pig; TISSUE=Hypothalamus;
RX MEDLINE=70136150; PubMed=4984938;
RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
RT "Structure of porcine thyrotropin releasing hormone.";
RL Biochemistry 9:1103-1106(1970).
RN [2]
RP SYNTHESIS.
RC SPECIES=Pig;
RX MEDLINE=70039904; PubMed=4982117;
RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
RT "The identity of chemical and hormonal properties of the thyrotropin
RT releasing hormone and pyroglutamyl-histidyl-proline amide.";
RL Biochem. Biophys. Res. Commun. 37:705-710(1969).
RN [3]
RP SEQUENCE.
RC SPECIES=Sheep; TISSUE=Hypothalamus;
RA Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
RA Ward D.N.;
RT "The elucidation of the primary structure of the hypothalamic thyroid
RT stimulating hormone releasing factor of ovine origin by means of mass
RT spectrometry.";
RL Org. Mass Spectrom. 5:221-228(1971).
RN [4]
RP SYNTHESIS.
RC SPECIES=Sheep;
RX MEDLINE=70163386; PubMed=4985794;
RA Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W.,
RA Guillemin R.;
RT "Characterization of ovine hypothalamic hypophysiotropic TSH-releasing
RT factor.";
RL Nature 226:321-325(1970).
RN [5]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Skin;
RX MEDLINE=76138399; PubMed=815011;
RA Yasuhara T., Nakajima T.;
RT "Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
RL Chem. Pharm. Bull. 23:3301-3303(1975).
RN [6]
RP SEQUENCE.
RC SPECIES=N.viridescens;
RX MEDLINE=75035605; PubMed=4214528;
RA Grimm-Joergensen Y., McKelvy J.F.;
RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
RT viridescens) brain in vitro. Isolation and characterization of
RT thyrotropin releasing factor.";
RL J. Neurochem. 23:471-478(1974).
CC -|- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
CC in the anterior pituitary gland and as a neurotransmitter/
CC neuromodulator in the central and peripheral nervous systems.
DR PIR; A90919; RHTDRO.
DR PIR; A92971; A92971.
DR PIR; A93750; RHSHT.
KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 3 3 Proline amide.
SQ SEQUENCE 3 AA; 380 MW; 7761F6B0000000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 3;

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Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 Q 1

RESULT 5
ACH1 ACHFU STANDARD; PRT; 4 AA.
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Achatin-I.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]_
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RC STRAIN=Perussac; TISSUE=Ganglion;
RX MEDLINE=89273551; PubMed=2597281;
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,
RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
fulica Perussac containing a D-amino acid residue.";
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
RP CHARACTERIZATION.
RC STRAIN=Perussac; TISSUE=Heart atrium;
RX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Munooka Y., Kobayashi M.;
RT "Purification of achatin-I from the atria of the African giant snail,
Achatina fulica, and its possible function.";
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=93014529; PubMed=1399265;
RA Iwashita T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA Iwashita T., Nomoto K.;
RT "Crystal structure and molecular conformation of achatin-I (H-Gly-D-
Phe-Ala-Asp-OH), an endogenous neuropeptide containing a D-amino acid
residue.";
RL Int. J. Pept. Protein Res. 39:258-264(1992).
CC -!- FUNCTION: Neuroexcitatory peptide; increases the impulse frequency
and produces a spike broadening of the identified heart excitatory
neuron (PON); also enhances the amplitude and frequency of the
heart beat. Has also an effect on several other muscles.
DR PIR; A32480; A32480.
KW D-amino acid; Direct protein sequencing; Hormone.
FT MOD RES 2 2 D-phenylalanine.
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 3 A 3

RESULT 6
DCML PSECH STANDARD; PRT; 4 AA.
ID DCML PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE Carbon monoxide dehydrogenase subunit L (CO-DH L) (Fragment).
GN Name=cutL;
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]_
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
carboxydohydrogenic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
CC -!- COFACTOR: Binds 1 copper(I) ion, 1 molybdenum(VI) ion and 1
molybdopterin cytosine dinucleotide (MCD) per subunit.
CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
subunit.
DR PIR; PL0140; PL0140.
KW Direct protein sequencing; Molybdenum; Oxidoreductase.
FT NON TER 4 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
DB 1 M 1

RESULT 7
DCMS PSECH STANDARD; PRT; 4 AA.
ID DCMS PSECH STANDARD; PRT; 4 AA.
AC P19918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (SC 1.2.99.2) (CO
dehydrogenase subunit S) (CO-DH S) (Fragment).
GN Name=cutS;
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]_
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
carboxydohydrogenic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
CC -!- COFACTOR: Binds 2 2Fe-2S clusters (By similarity).
CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
subunit.
DR PIR; PL0146; PL0146.
KW 2Fe-2S; Direct protein sequencing; Iron; Iron-sulfur; Metal-binding;
KW Oxidoreductase.
FT NON TER 4 4
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

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Db      2 A 2

RESULT 8
EOSI HUMAN
ID EOSI HUMAN STANDARD; PRT; 4 AA.
AC P02731;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Eosinophilic tetrapeptides.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76078412; PubMed=1060093;
RA Goetzl E.J., Austen K.F.;
RT "Purification and synthesis of eosinophilic tetrapeptides of
human lung tissue: identification as eosinophil chemotactic factor of
anaphylaxis."
RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
CC -1- MISCELLANEOUS: These peptides are released from mast cells in lung
(anaphylaxis). Their activities, preferentially affecting
eosinophils, include chemotaxis, chemotactic deactivation, release
of enzymes, and stimulation of the hexose monophosphate shunt.
DR GO:0006935; P:chemotaxis; IDA.
DR GO:0006955; P:immune response; IDA.
KW Direct protein sequencing.
FT VARIANT 1 1 V -> A (IN OTHER PEPTIDE).
FT FTID=VAR_005201.
SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 3 S 3

RESULT 9
FAR3 HIRME
ID FAR3 HIRME STANDARD; PRT; 4 AA.
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRFamide-like neuropeptide YMRP-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 4 4 Phenylalanine amide.
SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 3 S 3

RESULT 10
FAR4 HIRME
ID FAR4 HIRME STANDARD; PRT; 4 AA.
AC P42563;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRFamide-like neuropeptide YMRP-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE.
RX MEDLINE=92195954; PubMed=1686933;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908(1991).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 4 4 Phenylalanine amide.
SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;
Best Local Similarity 0.0%; Pred. No. 0;
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1
Db 1 Y 1

RESULT 11
FFKA ANTEL
ID FFKA ANTEL STANDARD; PRT; 4 AA.
AC P58705;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antho-KAamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nymnaethae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92028852; PubMed=1681803;
RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a
novel neuropeptide from sea anemones."
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
inhibitory neuropeptides, Antho-KAamide and Antho-Riamide."
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
groups. May be involved in the expansion phase of feeding
behaviour in sea anemones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Neuron specific.
DR PIR; JQ1273; JQ1273.
KW Amidation; Direct protein sequencing; Neuropeptide.

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FT MOD\_RES 1 1 3-phenyllactic acid.  
 FT MOD\_RES 4 4 Alanine amide.  
 SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
 Best Local Similarity 0.0%; Pred.No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 4 A 4

# RESULT 12

FLRF\_HIRME STANDARD; PRT; 4 AA.  
 AC P42561;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE FLRFamide.  
 OS Hirudo medicinalis (Medicinal leech), and  
 OS Helisoma trivolvis (Snail).  
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;  
 OC Arhynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.  
 OX NCBI\_TaxID=6421, 27815;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=H.medicalialis;  
 RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of RFamide neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=H.trivolvis; TISSUE=Kidney;  
 RX MEDLINE=94286417; PubMed=7912428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma  
 trivolvis".  
 RL Peptides 15:31-36(1994).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)  
 family.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 4 4 Phenylalanine amide.  
 SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;

QY 1 X 1

Db 1 F 1

# RESULT 13

FLRN\_ANCEL STANDARD; PRT; 4 AA.  
 AC P58707;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Antho-RNamide.  
 OS Anthopleura elegantissima (Sea anemone).  
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;  
 OC Nynanthae; Actiniidae; Anthopleura.  
 OX NCBI\_TaxID=6110;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RX MEDLINE=90319122; PubMed=1973541;  
 RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,

QY 1 X 1

Db 1 F 1

# RESULT 14

FMRF\_MACNI STANDARD; PRT; 4 AA.  
 AC P01162;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE FMRFamide (Peak C) (Cardioexcitatory neuropeptide).  
 OS Macrocallista nimbosa (Sun-ray clam),  
 OS Nereis virens (Sandworm),  
 OS Hirudo medicinalis (Medicinal leech), and  
 OS Helisoma trivolvis (Snail).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;  
 OC Veneroidea; Veneridae; Macrocallista.  
 OX NCBI\_TaxID=6594, 6353, 6421, 27815;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RC SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and visceral ganglion;  
 RX MEDLINE=77215956; PubMed=877582;  
 RA Price D.A., Greenberg M.J.;  
 RT "Structure of a molluscan cardioexcitatory neuropeptide."  
 RL Science 197:670-671(1977).  
 RN [2]  
 RP SEQUENCE, AND CHARACTERIZATION.  
 RC SPECIES=M.nimbosa; TISSUE=Ganglion;  
 RX MEDLINE=78012038; PubMed=909875;  
 RA Price D.A., Greenberg M.J.;  
 RT "Purification and characterization of a cardioexcitatory neuropeptide  
 from the central ganglia of a bivalve mollusc."  
 RL Prep. Biochem. 7:261-281(1977).  
 RN [3]  
 RP SEQUENCE.  
 RC SPECIES=N.virens;  
 RX MEDLINE=90259866; PubMed=2342992;  
 RA Krajniak K.G., Price D.A.;  
 RT "Authentic FMRFamide is present in the polychaete Nereis virens."  
 RL Peptides 11:75-77(1990).  
 RN [4]  
 RP SEQUENCE.  
 RC SPECIES=H.medicalialis;  
 RX MEDLINE=92195954; PubMed=1686933;  
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;  
 RT "Identification of RFamide neuropeptides in the medicinal leech."  
 RL Peptides 12:897-908(1991).  
 RN [5]  
 RP SEQUENCE.  
 RC SPECIES=H.trivolvis; TISSUE=Kidney;  
 RX MEDLINE=94286417; PubMed=7912428;  
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;  
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma

RA Reinscheid R.K., Nothacker H.-P., Staley A.L.;  
 RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea  
 anemone neuropeptide containing an unusual amino-terminal blocking  
 group.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Neuron specific.  
 CC -!- MASS SPECTROMETRY: MW=549.3; METHOD=FPAB; RANGE=1-4; NOTE=Ref.1.  
 DR PIR; A35779; A35779.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 1 1 3-phenyllactic acid.  
 FT MOD\_RES 4 4 Asparagine amide.  
 SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 0.0%; Score 0; DB 1; Length 4;  
 Best Local Similarity 0.0%; Pred.No. 0;  
 Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 X 1

Db 1 F 1

Job time : 75.8113 secs

RT trivolvias";  
RL Peptides 15:31-36(1994).  
CC -!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological  
CC activities include augmentation, induction, and regularization of  
CC cardiac contraction.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the FARP (FWRamide related peptide)  
CC family.  
DR PIR; A01426; ECNK.  
DR PIR; A60418; A60418.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT MOD\_RES 4 4 Phenylalanine amide.  
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;  
  
Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 X 1  
Db 1 F 1  
  
RESULT 15  
FYRI ANTEL STANDARD; PRT; 4 AA.  
AC P58706;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Antho-Riamide I [Contains: Antho-Riamide II].  
OS Anthopleura elegantissima (Sea anemone).  
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Actiniaria;  
OC Nynanthaeae; Actiniidae; Anthopleura.  
OX NCBI\_TaxID=6110;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92270459; PubMed=1821096;  
RA Nothacker H.-P.; Rinehart K.L. Jr., McFarlane I.D.,  
RA Grimmelikhuijzen C.J.P.;  
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,  
RT biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its des-  
RT phenyllactyl fragment Tyr-Arg-Ile-NH2.";  
RL Peptides 12:1165-1173(1991).  
RN [2]  
RN FUNCTION.  
RP MEDLINE=93391436; PubMed=8397415;  
RX McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;  
RA "The expansion behaviour of sea anemones may be coordinated by two  
RT inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";  
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).  
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle  
CC groups. May be involved in the expansion phase of feeding  
CC behaviour in sea anemones.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Neuron specific.  
KW Amidation; Direct protein sequencing; Neuropeptide.  
FT CHAIN 1 4 Antho-Riamide I.  
FT CHAIN 2 4 Antho-Riamide II.  
FT MOD\_RES 1 1 3-phenyllactic acid.  
FT MOD\_RES 4 4 Isoleucine amide.  
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;  
  
Query Match 0.0%; Score 0; DB 1; Length 4;  
Best Local Similarity 0.0%; Pred. No. 0;  
Matches 0; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 X 1  
Db 1 F 1

Search completed: December 30, 2004, 13:16:01

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 21:19:46 ; Search time 94 Seconds  
(without alignments)  
38.163 Million cell updates/sec

Title: US-10-046-922-33  
Perfect score: 26  
Sequence: 1 CXXXXXXXC 10

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 444336

Minimum DB seq length: 0  
Maximum DB seq length: 10

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04: \*  
1: Genesecp1980s: \*  
2: Genesecp1990s: \*  
3: Genesecp2000s: \*  
4: Genesecp2001s: \*  
5: Genesecp2002s: \*  
6: Genesecp2003as: \*  
7: Genesecp2003bs: \*  
8: Genesecp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	61.5	10	1 AAP71548	Aap71548 AIDS viru
2	16	61.5	10	2 AAR28918	Aar28918 Peptide f
3	15	57.7	10	5 ABBA6640	Abba6640 Desmocoll
4	15	57.7	10	5 ABBA6650	Abba6650 Desmocoll
5	15	57.7	10	5 ABBA6630	Abba6630 Desmocoll
6	15	57.7	10	5 ABBA6621	Abba6621 Desmocoll
7	15	57.7	10	5 ABBA7079	Abba7079 Desmocoll
8	15	57.7	10	5 ABBA7083	Abba7083 Desmocoll
9	15	57.7	10	5 ABBA6612	Abba6612 Desmocoll
10	15	57.7	10	5 ABBA7075	Abba7075 Desmocoll
11	14	53.8	10	2 AAW09521	Aaw09521 Thrombopo
12	14	53.8	10	2 AAW36672	Aaw36672 Thrombopo
13	14	53.8	10	3 AAY64329	Aay64329 Cadherin-
14	14	53.8	10	3 AAY64331	Aay64331 Cadherin-
15	14	53.8	10	4 AAU25891	Aau25891 Human thr
16	14	53.8	10	4 AAG95975	Aag95975 Human com
17	14	53.8	10	4 AAG95917	Aag95917 Human com
18	14	53.8	10	5 ABP53955	Abp53955 VEGFR-3 b
19	14	53.8	10	5 ABBA6625	Abba6625 Desmocoll
20	14	53.8	10	5 ABBA6635	Abba6635 Desmocoll
21	14	53.8	10	5 ABBA6607	Abba6607 Desmocoll
22	14	53.8	10	5 ABBA6616	Abba6616 Desmocoll
23	14	53.8	10	5 ABBA6645	Abba6645 Desmocoll
24	14	53.8	10	5 AAU93236	Aau93236 Granulocy
25	14	53.8	10	5 AAU98193	Aau98193 Prostate

RESULT 1  
AAP71548  
ID AAP71548 standard; peptide; 10 AA.  
XX AC AAP71548;  
XX DT 25-MAR-2003 (revised)  
DT 07-MAY-1991 (first entry)  
XX DE AIDS virus receptor site blocking peptide (1).  
XX KW AIDS; virus; receptor site; HIV; vaccine; antibodies; T4 viral receptor;  
KW envelope glycoprotein; gp120; peptide T.  
XX OS Synthetic.  
XX PN EP249390-A.  
XX PD 16-DEC-1987.  
XX PF 03-JUN-1987; 87EP-00304913.  
XX PR 03-JUN-1986; 86US-00869919.  
PR 26-JUN-1986; 86US-00878586.  
PR 12-DEC-1986; 86US-00940919.  
PR 11-MAY-1987; 87US-00048148.  
PR 03-JUN-1987; 87EP-00304939.  
XX (PERT/) PERT C B.  
PA (USDC ) US SEC OF COMMERCE.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICE.  
PA (USGO ) US GOVERNMENT.  
XX PI Pert CB, Ruff MR, Farrar WL;  
XX WPI; 1987-350068/50.  
XX PT New peptide(s) related to AIDS virus - which inhibit AIDS virus binding  
to receptor sites and prevent cell infectivity with AIDS virus.  
XX Claim 1-2; Page 8; 12pp; English.  
XX The peptide may have the Cys residues at one or both the N- and C-  
terminals omitted. The resulting octapeptide in the HIV envelope  
glycoprotein (gp120) was identified by computer-assisted analysis. The  
peptide was termed "peptide T" because of the high threonine content. The  
peptide has been found to bind T4 viral receptors. The peptide blocks  
effectively receptor sites of cells and prevents cell infectivity with

ALIGNMENTS

26	14	53.8	10	7 ADD24107	Add24107 Melanin-c
27	14	53.8	10	8 ADH27064	Adh27064 Melanin-c
28	14	53.8	10	8 ADH27062	Adh27062 Melanin-c
29	14	53.8	10	8 ADO44204	Ado44204 Amino aci
30	14	53.8	10	8 ADP22727	Adp22727 Melanin-c
31	14	53.8	10	8 ADQ26193	Adq26193 Melanin-c
32	14	53.8	10	8 ADP71265	Adp71265 Melanin c
33	13	50.0	10	1 AAP91867	Aap91867 Cyclic pe
34	13	50.0	10	2 AAW03419	Aaw03419 Fibronec
35	13	50.0	10	2 AAW25669	Aaw25669 MAb anti-
36	13	50.0	10	2 AAW09546	Aaw09546 Thrombopo
37	13	50.0	10	2 AAW09564	Aaw09564 Thrombopo
38	13	50.0	10	2 AAW09565	Aaw09565 Thrombopo
39	13	50.0	10	2 AAW35433	Aaw35433 Thrombopo
40	13	50.0	10	2 AAW36715	Aaw36715 Thrombopo
41	13	50.0	10	2 AAW35432	Aaw35432 Thrombopo
42	13	50.0	10	2 AAW36716	Aaw36716 Thrombopo
43	13	50.0	10	2 AAW36697	Aaw36697 Thrombopo
44	13	50.0	10	2 AAW65945	Aaw65945 Molecule
45	13	50.0	10	2 AAW57567	Aaw57567 Molecular



XX AC ABB46650;  
 XX 30-JAN-2002 (first entry)  
 XX DE Desmocollin-1 CAR cyclic peptide 52.  
 XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
 KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.  
 XX OS Synthetic.  
 XX WO200172956-A2.  
 XX PN 04-OCT-2001.  
 XX PD 27-MAR-2001; 2001WO-IB001400.  
 XX PF 27-MAR-2000; 2000US-00535852.  
 XX PR (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX PA Blaschuk OW, Symonds JM, Gour BJ;  
 XX DR WPI; 2002-025778/03.  
 XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin  
 PT mediated cell adhesion, useful for facilitating wound healing and/or  
 PT reducing scar tissue, treating cancer and inducing apoptosis.  
 XX PS Claim 23; Page 109; 127pp; English.  
 XX CC The invention relates to modulating agents for inhibiting or enhancing  
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence  
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
 CC sequence, a substance such as an antibody or antigen-binding fragment  
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a  
 CC polynucleotide encoding a polypeptide that comprises a desmosomal  
 CC cadherin CAR sequence or analogue. The modulating agents have  
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to  
 CC facilitate wound healing and/or reduce scar tissue, for enhancing  
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
 CC treating an autoimmune blistering disorder and to treat cancer (e.g.  
 CC carcinoma, leukaemia or melanoma) and induce apoptosis  
 XX Sequence 10 AA;  
 SQ Query Match 57.7%; Score 15; DB 5; Length 10;  
 Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 CXXXXXXXC 10  
 Db 1 CIYAYATTAC 10  
 RESULT 5  
 ABB46630  
 ID ABB46630 standard; peptide; 10 AA.  
 XX AC ABB46630;  
 XX 30-JAN-2002 (first entry)  
 XX DE Desmocollin-1 CAR cyclic peptide 32.  
 XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
 KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.  
 XX OS Synthetic.

XX PN WO200172956-A2.  
 XX PD 04-OCT-2001.  
 XX PF 27-MAR-2001; 2001WO-IB001400.  
 XX PR 27-MAR-2000; 2000US-00535852.  
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX PI Blaschuk OW, Symonds JM, Gour BJ;  
 XX DR WPI; 2002-025778/03.  
 XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin  
 PT mediated cell adhesion, useful for facilitating wound healing and/or  
 PT reducing scar tissue, treating cancer and inducing apoptosis.  
 XX PS Claim 23; Page 109; 127pp; English.  
 XX CC The invention relates to modulating agents for inhibiting or enhancing  
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence  
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
 CC sequence, a substance such as an antibody or antigen-binding fragment  
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a  
 CC polynucleotide encoding a polypeptide that comprises a desmosomal  
 CC cadherin CAR sequence or analogue. The modulating agents have  
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to  
 CC facilitate wound healing and/or reduce scar tissue, for enhancing  
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
 CC treating an autoimmune blistering disorder and to treat cancer (e.g.  
 CC carcinoma, leukaemia or melanoma) and induce apoptosis  
 XX Sequence 10 AA;  
 SQ Query Match 57.7%; Score 15; DB 5; Length 10;  
 Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 CXXXXXXXC 10  
 Db 1 CIYAYATTAC 10  
 RESULT 6  
 ABB46621  
 ID ABB46621 standard; peptide; 10 AA.  
 XX AC ABB46621;  
 XX 30-JAN-2002 (first entry)  
 XX DE Desmocollin-1 CAR cyclic peptide 23.  
 XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
 KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.  
 XX OS Synthetic.  
 XX WO200172956-A2.  
 XX PN 04-OCT-2001.  
 XX PD 27-MAR-2001; 2001WO-IB001400.  
 XX PF 27-MAR-2000; 2000US-00535852.  
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX PI Blaschuk OW, Symonds JM, Gour BJ;

XX WPI; 2002-025778/03.  
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin  
 PT mediated cell adhesion, useful for facilitating wound healing and/or  
 PT reducing scar tissue, treating cancer and inducing apoptosis.  
 XX  
 PS Claim 23; Page 109; 127pp; English.  
 XX The invention relates to modulating agents for inhibiting or enhancing  
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence  
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
 CC sequence, a substance such as an antibody or antigen-binding fragment  
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a  
 CC polynucleotide encoding a polypeptide that comprises a desmosomal  
 CC cadherin CAR sequence or analogue. The modulating agents have  
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to  
 CC facilitate wound healing and/or reduce scar tissue, for enhancing  
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
 CC treating an autoimmune blistering disorder and to treat cancer (e.g.  
 CC carcinoma, leukaemia or melanoma) and induce apoptosis  
 XX  
 SQ Sequence 10 AA;  
 Query Match 57.7%; Score 15; DB 5; Length 10;  
 Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 CXXXXXXXC 10  
 |  
 Db 1 CYAYATTADC 10  
 RESULT 7  
 ABB47079  
 ID ABB47079 standard; peptide; 10 AA.  
 AC ABB47079;  
 XX  
 XX 30-JAN-2002 (first entry)  
 XX Desmocollin-3/4 CAR cyclic peptide 14.  
 XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
 KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.  
 XX  
 XX Synthetic.  
 XX  
 XX WO200172956-A2.  
 XX 04-OCT-2001.  
 XX 27-MAR-2001; 2001WO-IB001400.  
 XX 27-MAR-2000; 2000US-00535852.  
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX Blaschuk OW, Symonds JM, Gour BJ;  
 XX WPI; 2002-025778/03.  
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin  
 PT mediated cell adhesion, useful for facilitating wound healing and/or  
 PT reducing scar tissue, treating cancer and inducing apoptosis.  
 XX  
 PS Claim 23; Page 112; 127pp; English.  
 XX The invention relates to modulating agents for inhibiting or enhancing  
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence

CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
 CC sequence, a substance such as an antibody or antigen-binding fragment  
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a  
 CC polynucleotide encoding a polypeptide that comprises a desmosomal  
 CC cadherin CAR sequence or analogue. The modulating agents have  
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to  
 CC facilitate wound healing and/or reduce scar tissue, for enhancing  
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
 CC treating an autoimmune blistering disorder and to treat cancer (e.g.  
 CC carcinoma, leukaemia or melanoma) and induce apoptosis  
 XX  
 SQ Sequence 10 AA;  
 Query Match 57.7%; Score 15; DB 5; Length 10;  
 Best Local Similarity 20.0%; Pred. No. 1.2e+02;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 CXXXXXXXC 10  
 |  
 Db 1 CIAYASTADC 10  
 RESULT 8  
 ABB47083  
 ID ABB47083 standard; peptide; 10 AA.  
 AC ABB47083;  
 XX  
 XX 30-JAN-2002 (first entry)  
 XX Desmocollin-3/4 CAR cyclic peptide 18.  
 XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;  
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;  
 KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.  
 XX  
 XX Synthetic.  
 XX  
 XX WO200172956-A2.  
 XX 04-OCT-2001.  
 XX 27-MAR-2001; 2001WO-IB001400.  
 XX 27-MAR-2000; 2000US-00535852.  
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX Blaschuk OW, Symonds JM, Gour BJ;  
 XX WPI; 2002-025778/03.  
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin  
 PT mediated cell adhesion, useful for facilitating wound healing and/or  
 PT reducing scar tissue, treating cancer and inducing apoptosis.  
 XX  
 PS Claim 23; Page 112; 127pp; English.  
 XX The invention relates to modulating agents for inhibiting or enhancing  
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent  
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence  
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR  
 CC sequence, a substance such as an antibody or antigen-binding fragment  
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a  
 CC polynucleotide encoding a polypeptide that comprises a desmosomal  
 CC cadherin CAR sequence or analogue. The modulating agents have  
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to  
 CC facilitate wound healing and/or reduce scar tissue, for enhancing  
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),  
 CC treating an autoimmune blistering disorder and to treat cancer (e.g.  
 CC carcinoma, leukaemia or melanoma) and induce apoptosis  
 XX  
 SQ Sequence 10 AA;

Query Match	57.7%;	Score 15;	DB 5;	Length 10;	
Best Local Similarity	20.0%;	Pred. No. 1.2e+02;			
Matches	2;	Conservative	0;	Mismatches	8;
				Indels	0;
				Gaps	0;
QY	1	CXXXXXXXC	10		
DB	1	CLIAVASTAC	10		
RESULT 9					
ID	ABB46612	standard; peptide;	10 AA.		
XX	AC	ABB46612;			
XX	AC	ABB46612;			
XX	DT	30-JAN-2002 (first entry)			
XX	XX				
DE	DE	Dsmocollin-1 CAR cyclic peptide 14.			
XX	XX				
KW	KW	Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;			
KW	KW	cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;			
KW	KW	organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.			
XX	OS	Synthetic.			
XX	OS				
PN	PN	WO200172956-A2.			
XX	XX				
DT	DT	04-OCT-2001.			
XX	XX				
DE	DE	Desmocollin-1 CAR cyclic peptide 14.			
XX	XX				
KW	KW	Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;			
KW	KW	cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;			
KW	KW	organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.			
XX	OS	Synthetic.			
XX	OS				
PN	PN	WO200172956-A2.			
XX	XX				
DT	DT	04-OCT-2001.			
XX	XX				
PF	PF	27-MAR-2000; 2000US-00535852.			
XX	XX				
PR	PR	(ADHE-) ADHEREX TECHNOLOGIES INC.			
XX	XX				
PA	PA	Blaschuk OW, Symonds JM, Gour BJ;			
XX	XX				
PS	PS	Claim 23; Page 109; 127pp; English.			
XX	XX				
CC	CC	The invention relates to modulating agents for inhibiting or enhancing			
CC	CC	desmosomal cadherin mediated cell adhesion, comprising a modulating agent			
CC	CC	comprising a desmosomal cadherin cell adhesion recognition CAR sequence			
CC	CC	(ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR			
CC	CC	sequence, a substance such as an antibody or antigen-binding fragment			
CC	CC	that specifically binds a desmosomal cadherin CAR sequence and/or a			
CC	CC	polynucleotide encoding a polypeptide that comprises a desmosomal			
CC	CC	cadherin CAR sequence or analogue. The modulating agents have			
CC	CC	immunosuppressive, cytostatic and antiapoptotic activity and are used to			
CC	CC	facilitate wound healing and/or reduce scar tissue, for enhancing			
CC	CC	adhesion of foreign tissue implants (e.g. skin graft or organ implant),			
CC	CC	treating an autoimmune blistering disorder and to treat cancer (e.g.			
CC	CC	carcinoma, leukaemia or melanoma) and induce apoptosis			
XX	XX				
SQ	SQ	Sequence 10 AA;			
Query Match	57.7%;	Score 15;	DB 5;	Length 10;	
Best Local Similarity	20.0%;	Pred. No. 1.2e+02;			
Matches	2;	Conservative	0;	Mismatches	8;
				Indels	0;
				Gaps	0;
QY	1	CXXXXXXXC	10		
DB	1	CAYATTADGC	10		
RESULT 10					
ID	ABB47075	standard; peptide;	10 AA.		
XX	AC	ABB47075;			
XX	AC	ABB47075;			
XX	DT	30-JAN-2002 (first entry)			
XX	XX				
DE	DE	Dsmocollin-3/4 CAR cyclic peptide 10.			
XX	XX				
KW	KW	Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;			
KW	KW	cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;			
KW	KW	organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.			
XX	OS	Synthetic.			
XX	OS				
PN	PN	WO200172956-A2.			
XX	XX				
DT	DT	04-OCT-2001.			
XX	XX				
DE	DE	Desmocollin-1 CAR cyclic peptide 14.			
XX	XX				
KW	KW	Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;			
KW	KW	cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;			
KW	KW	organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.			
XX	OS	Synthetic.			
XX	OS				
PN	PN	WO200172956-A2.			
XX	XX				
DT	DT	04-OCT-2001.			
XX	XX				
PF	PF	27-MAR-2000; 2000US-00535852.			

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XX WO9640189-A1.
XX
XX 19-DEC-1996.
XX
XX 05-JUN-1996; 96WO-US008998.
XX
XX 07-JUN-1995; 95US-00472371.
XX
XX 07-JUN-1995; 95US-00473604.
XX
XX 07-JUN-1995; 95US-00476168.
XX
XX 07-JUN-1995; 95US-00478128.
XX
XX 07-JUN-1995; 95US-00484090.
XX
XX 07-JUN-1995; 95US-00485301.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
XX Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX WPI; 1997-051883/05.
XX
XX Thrombopoietin receptor-binding/activating peptide(s) and peptide
XX mimetic(s) - useful in treatment of haematological disorders, esp.
XX thrombocytopenia resulting from chemotherapy, etc.
XX
XX Disclosure; Page 27; 106pp; English.
XX
XX The present sequence is a peptide which binds to thrombopoietin (TPO)
XX receptor (TR). The compound can be used for treating patients suffering
XX from haematological disorders and thrombocytopenia resulting from
XX chemotherapy, radiation therapy or bone marrow transfusions. The peptide
XX may also be used to maintain the proliferation and growth of TPO-
XX dependent cell lines and for use in biological research, for detecting
XX TPO receptors on living cells
XX
XX Sequence 10 AA;
XX
XX Query Match 53.8%; Score 14; DB 2; Length 10;
XX Best Local Similarity 20.0%; Pred. No. 4.8e+02;
XX Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 1 CXXXXXXXC 10
XX |
XX Db 1 CSRADFLAAC 10
XX
XX RESULT 13
XX AAY64329
XX ID AAY64329 standard; peptide; 10 AA.
XX
XX AC AAY64329;
XX
XX XX
XX DT 02-MAR-2000 (first entry)
XX
XX XX
XX DE Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3644.
XX
XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
XX KW inhibition; cadherin extracellular domain; cell adhesion recognition;
XX KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
XX KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
XX KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
XX KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
XX KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
XX KW neurological disease; cyclic.
XX
XX OS Synthetic.
XX
XX OS Homo sapiens.
XX
XX XX
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 1..10
XX
XX XX
XX PN WO9957149-A2.
XX
XX XX
XX PD 11-NOV-1999.
XX
XX XX
XX PF 05-MAY-1999; 99WO-CA000363.
XX
XX XX
XX PR 05-MAY-1998; 98US-00073040.
XX
XX PR 06-NOV-1998; 98US-00187859.
XX
XX PR 20-JAN-1999; 99US-00234395.
XX
XX PR 08-MAR-1999; 99US-00264516.
XX
XX XX
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX XX
XX PI Blaschuk OW, Gour BJ, Byers S;
XX
XX XX
XX DR WPI; 2000-038791/03.

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XX WO9640189-A1.
XX
XX 19-DEC-1996.
XX
XX 05-JUN-1996; 96WO-US008998.
XX
XX 07-JUN-1995; 95US-00472371.
XX
XX 07-JUN-1995; 95US-00473604.
XX
XX 07-JUN-1995; 95US-00476168.
XX
XX 07-JUN-1995; 95US-00478128.
XX
XX 07-JUN-1995; 95US-00484090.
XX
XX 07-JUN-1995; 95US-00485301.
XX
XX (GLAX ) GLAXO GROUP LTD.
XX
XX Dower WJ, Barrett RW, Cwiria SE, Duffin DJ, Gates CM, Johnson SS;
XX Mattheakis LC, Schatz PJ, Wagstrom CR, Wrighton NC;
XX WPI; 1997-051883/05.
XX
XX Thrombopoietin receptor-binding/activating peptide(s) and peptide
XX mimetic(s) - useful in treatment of haematological disorders, esp.
XX thrombocytopenia resulting from chemotherapy, etc.
XX
XX Disclosure; Page 27; 106pp; English.
XX
XX The present sequence is a peptide which binds to thrombopoietin (TPO)
XX receptor (TR). The compound can be used for treating patients suffering
XX from haematological disorders and thrombocytopenia resulting from
XX chemotherapy, radiation therapy or bone marrow transfusions. The peptide
XX may also be used to maintain the proliferation and growth of TPO-
XX dependent cell lines and for use in biological research, for detecting
XX TPO receptors on living cells
XX
XX Sequence 10 AA;
XX
XX Query Match 53.8%; Score 14; DB 2; Length 10;
XX Best Local Similarity 20.0%; Pred. No. 4.8e+02;
XX Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
XX
XX QY 1 CXXXXXXXC 10
XX |
XX Db 1 CSRADFLAAC 10
XX
XX RESULT 12
XX AAW36672
XX ID AAW36672 standard; peptide; 10 AA.
XX
XX AC AAW36672;
XX
XX XX
XX DT 27-FEB-1998 (first entry)
XX
XX XX
XX DE Thrombopoietin receptor binding peptide.
XX
XX XX
XX KW Thrombopoietin receptor; binding peptide; treatment; agonist;
XX KW haematological disorder; thrombocytopenia; chemotherapy;
XX KW radiation therapy; bone marrow transfusion; diagnosis;
XX KW signal transduction; receptor activation; cell culture.
XX
XX OS Synthetic.
XX
XX XX
XX PN WO9640750-A1.
XX
XX XX
XX PD 19-DEC-1996.
XX
XX XX
XX PF 07-JUN-1996; 96WO-US009623.
XX
XX XX
XX PR 07-JUN-1995; 95US-00478128.
XX
XX PR 07-JUN-1995; 95US-00485301.
XX
XX XX
XX PA (GLAX ) GLAXO GROUP LTD.

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XX New cadherin modulating agents, used for modulating nonclassical cadherin  
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid  
PT arthritis, multiple sclerosis, diabetes or a neurological disease.  
XX  
PS Claim 102; Page 218; 252pp; English.  
XX  
CC The present invention describes cadherin modulating agents (MA)  
CC comprising peptides which comprise a nonclassical cadherin cell adhesion  
CC recognition (CAR) sequence. The MAs can be used for modulating  
CC nonclassical cadherin-mediated functions. They can be used for e.g.  
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a  
CC mammal, enhancing delivery of a drug through the skin of a mammal,  
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in  
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting  
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-  
CC expressing cell, preventing or treating obesity in a mammal, stimulating  
CC blood vessel regression in a mammal, enhancing drug delivery to the  
CC central nervous system, treating a demyelinating neurological disease,  
CC increasing vasopermeability in a mammal, enhancing adhesion of  
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in  
CC a mammal, or preventing pregnancy in a mammal. They can also be used for  
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing  
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a  
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age  
CC -related macular degeneration, multiple sclerosis and diabetes. The  
CC products can also be used for detection and diagnosis and in bioreactors.  
CC AAY60592 to AAY64572 represent specifically claimed peptides, and  
CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in  
CC the exemplification of the present invention  
XX  
SQ Sequence 10 AA;  
Query Match 53.8%; Score 14; DB 3; Length 10;  
Best Local Similarity 20.0%; Pred. No. 4.8e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 1 CXXXXXXXXC 10  
DB 1 CFTIDSSGC 10  
RESULT 14  
AAY64331  
ID AAY64331 standard; peptide; 10 AA.  
XX  
AC AAY64331;  
XX  
DT 02-MAR-2000 (first entry)  
XX  
DE Cadherin-related neuronal receptor CAR cyclic peptide SEQ ID NO:3646.  
XX  
KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;  
KW inhibition; cadherin extracellular domain; cell adhesion recognition;  
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;  
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;  
KW cadherin related neuronal receptor; Li-cadherin; protocadherin;  
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;  
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;  
KW neurological disease; cyclic.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Disulfide-bond 1..10  
FT  
XX W09957149-A2.  
PN  
PD 11-NOV-1999.  
XX  
XX 05-MAY-1999; 99WO-CA000363.  
XX

PR 05-MAY-1998; 98US-00073040.  
PR 06-NOV-1998; 98US-00187859.  
PR 20-JAN-1999; 99US-00234395.  
PR 08-MAR-1999; 99US-00264516.  
PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
XX  
PI Blaschuk OW, Gour BJ, Byers S;  
XX  
DR WPI; 2000-038791/03.  
XX  
PT New cadherin modulating agents, used for modulating nonclassical cadherin  
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid  
PT arthritis, multiple sclerosis, diabetes or a neurological disease.  
XX  
PS Claim 102; Page 218; 252pp; English.  
XX  
CC The present invention describes cadherin modulating agents (MA)  
CC comprising peptides which comprise a nonclassical cadherin cell adhesion  
CC recognition (CAR) sequence. The MAs can be used for modulating  
CC nonclassical cadherin-mediated functions. They can be used for e.g.  
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a  
CC mammal, enhancing delivery of a drug through the skin of a mammal,  
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in  
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting  
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-  
CC expressing cell, preventing or treating obesity in a mammal, stimulating  
CC blood vessel regression in a mammal, enhancing drug delivery to the  
CC central nervous system, treating a demyelinating neurological disease,  
CC increasing vasopermeability in a mammal, enhancing adhesion of  
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in  
CC a mammal, or preventing pregnancy in a mammal. They can also be used for  
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing  
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a  
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age  
CC -related macular degeneration, multiple sclerosis and diabetes. The  
CC products can also be used for detection and diagnosis and in bioreactors.  
CC AAY60592 to AAY64572 represent specifically claimed peptides, and  
CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in  
CC the exemplification of the present invention  
XX  
SQ Sequence 10 AA;  
Query Match 53.8%; Score 14; DB 3; Length 10;  
Best Local Similarity 20.0%; Pred. No. 4.8e+02;  
Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
QY 1 CXXXXXXXXC 10  
DB 1 CKFTIDSSSC 10  
RESULT 15  
AAU25891  
ID AAU25891 standard; peptide; 10 AA.  
XX  
AC AAU25891;  
XX  
DT 17-DEC-2001 (first entry)  
XX  
DE Human thrombopoietin receptor (TPO-R) activator peptide #77.  
XX  
KW Peptide mimetic; human; thrombopoietin receptor; TPO-R; TPO; cytokine;  
KW haemostatic; thrombocytopenia; chemotherapy; radiation therapy; ELISA;  
KW bone marrow transplantation; haematological disorder; platelet disorder;  
KW enzyme-linked immunosorbent assay; in situ staining; biological fluid;  
KW tissue homogenate; fluorescence-activated cell sorting; Western blotting;  
KW in vitro expansion; megakaryocyte; Headpiece Dimer gene; lacI gene.  
XX  
OS Homo sapiens.  
XX  
XX US6251864-B1.  
PN  
XX

PD 26-JUN-2001.  
 XX  
 PF 01-MAR-2000; 2000US-00516704.  
 XX  
 PR 07-JUN-1995; 95US-00478128.  
 PR 07-JUN-1995; 95US-00485301.  
 PR 07-JUN-1996; 96WO-US009623.  
 PR 15-AUG-1996; 96US-00699027.  
 XX  
 PA (GLAX ) GLAXO GROUP LTD.  
 XX  
 PI Dower WJ, Barrett RW, Cwirla SE, Gates CM, Schatz PJ;  
 PI Balasubramanian P, Wagstrom CR, Hendren RW, Podduturi S;  
 PI Yin Q;  
 XX  
 DR WPI; 2001-564142/63.  
 XX  
 XX Activating thrombopoietin receptors in cells, used to treat  
 PT thrombocytopenia and hematological disorders, comprises contacting cells  
 PT with peptides and peptide mimetics attached to hydrophilic polymers.  
 XX  
 PS Disclosure; Col 21; 128pp; English.  
 XX  
 CC Sequences AAU25815-AAU26049 represent peptides and peptide mimetics that  
 CC bind to and activate the human thrombopoietin receptor (TPO-R). Methods  
 CC of activating thrombopoietin receptors in cells comprise contacting the  
 CC cells with effective amounts of peptides and peptide mimetics attached to  
 CC hydrophilic polymers. The methods are used to treat thrombocytopenia such  
 CC as that due to chemotherapy, radiation therapy or bone-marrow  
 CC transplantation and to prevent thrombocytopenia in patients at risk. The  
 CC sequences are used to treat and prevent hematological disorders  
 CC including thrombocytopenia and platelet disorders. They are used in vitro  
 CC as unique tools for understanding the biological role of thrombopoietin  
 CC (TPO) and to develop other compounds that bind to and activate the TPO  
 CC receptor. The peptides can be used to detect TPO receptors on living  
 CC cells and fixed cells, in biological fluids, in tissue homogenates, and  
 CC in purified or natural biological materials. They may also be used for in  
 CC situ staining, fluorescence-activated cell sorting, Western blotting and  
 CC enzyme-linked immunosorbent assay (ELISA). In addition, the peptides can  
 CC be used for in vitro expansion of megakaryocytes and their committed  
 CC progenitors alone or in conjunction with additional cytokines  
 XX  
 SQ Sequence 10 AA;  
 Query Match 53.8%; Score 14; DB 4; Length 10;  
 Best Local Similarity 20.0%; Pred. No. 4.8e+02;  
 Matches 2; Conservative 0; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 CXXXXXXXC 10  
 DB 1 CSRADFLAC 10

Search completed: December 29, 2004, 21:35:28  
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